

gb_pat:AX284076	16	16.00	102.18	2.5e+03	AX284076 Sequence 41 from Patent	gb_pat:I54062	17	16.00	101.77	2.6e+03	I54062 Sequence 1803 from pat
gb_pat:AX300970	16	16.00	102.18	2.5e+03	AX300970 Sequence 41 from Patent	gb_pat:I54124	17	16.00	101.77	2.6e+03	I54124 Sequence 1865 from pat
gb_pat:I41042	16	16.00	102.18	2.5e+03	I41042 Sequence 11 from patent U	gb_pat:I94434	17	16.00	101.77	2.6e+03	I94434 Sequence 597 from pat
gb_pat:I41043	16	16.00	102.18	2.5e+03	I41043 Sequence 12 from patent U	em_pat:E09908	17	16.00	101.77	2.6e+03	E09908 Probe I7T-2 for detect
gb_pat:I47692	16	16.00	102.18	2.5e+03	I47692 Sequence 4 from patent US	gb_pat:AX31539	18	16.00	101.39	2.8e+03	AX31539 Synthetic H.pylori det
gb_pat:AR016252	17	16.00	101.77	2.6e+03	AR016252 Sequence 6 from patent	gb_pat:AR02296	18	16.00	101.39	2.8e+03	AR02296 Sequence 35 from pat
gb_pat:AR039563	17	16.00	101.77	2.6e+03	AR039563 Sequence 411 from patent	gb_pat:AR011218	18	16.00	101.39	2.8e+03	AR011218 Sequence 86 from pat
gb_pat:AR039565	17	16.00	101.77	2.6e+03	AR039565 Sequence 413 from patent	gb_pat:AR053147	18	16.00	101.39	2.8e+03	AR053147 Sequence 53 from pat
gb_pat:AR039567	17	16.00	101.77	2.6e+03	AR039567 Sequence 415 from patent	gb_pat:AR144877	18	16.00	101.39	2.8e+03	AR144877 Sequence 122 from pa
gb_pat:AR039569	17	16.00	101.77	2.6e+03	AR039569 Sequence 417 from patent	gb_pat:AX048677	18	16.00	101.39	2.8e+03	AX048677 Sequence 122 from Pa
gb_pat:AR039571	17	16.00	101.77	2.6e+03	AR039571 Sequence 419 from patent	gb_pat:AX076467	18	16.00	101.39	2.8e+03	AX076467 Sequence 12 from Pat
gb_pat:AR039573	17	16.00	101.77	2.6e+03	AR039573 Sequence 421 from patent	gb_pat:AX078832	18	16.00	101.39	2.8e+03	AX078832 Sequence 6 from Pat
gb_pat:AR045997	17	16.00	101.77	2.6e+03	AR045997 Sequence 790 from patent	gb_pat:AX078833	18	16.00	101.39	2.8e+03	AX078833 Sequence 7 from Pat
gb_pat:AR046273	17	16.00	101.77	2.6e+03	AR046273 Sequence 1066 from patent	gb_pat:AX078834	18	16.00	101.39	2.8e+03	AX078834 Sequence 8 from Pat
gb_pat:AR046275	17	16.00	101.77	2.6e+03	AR046275 Sequence 1068 from patent	gb_pat:AX078843	18	16.00	101.39	2.8e+03	AX078843 Sequence 17 from Pat
gb_pat:AR046277	17	16.00	101.77	2.6e+03	AR046277 Sequence 1070 from patent	gb_pat:AX078849	18	16.00	101.39	2.8e+03	AX078849 Sequence 23 from Pat
gb_pat:AR046279	17	16.00	101.77	2.6e+03	AR046279 Sequence 1072 from patent	gb_pat:AX078860	18	16.00	101.39	2.8e+03	AX078860 Sequence 34 from Pat
gb_pat:AR046281	17	16.00	101.77	2.6e+03	AR046281 Sequence 1074 from patent	gb_pat:AX135861	18	16.00	101.39	2.8e+03	AX135861 Sequence 2 from Pat
gb_pat:AR046283	17	16.00	101.77	2.6e+03	AR046283 Sequence 1076 from patent	gb_pat:AX135862	18	16.00	101.39	2.8e+03	AX135862 Sequence 2 from Pat
gb_pat:AR046285	17	16.00	101.77	2.6e+03	AR046285 Sequence 1078 from patent	gb_pat:AX191970	18	16.00	101.39	2.8e+03	AX191970 Probes, methods and
gb_pat:AR046998	17	16.00	101.77	2.6e+03	AR046998 Sequence 1791 from patent	gb_pat:BD009430	18	16.00	101.39	2.8e+03	BD009430 Probes, methods and
gb_pat:AR047000	17	16.00	101.77	2.6e+03	AR047000 Sequence 1793 from patent	gb_pat:E08099	18	16.00	101.39	2.8e+03	E08099 Synthetic RNA fragment
gb_pat:AR047002	17	16.00	101.77	2.6e+03	AR047002 Sequence 1795 from patent	gb_pat:E32450	18	16.00	101.39	2.8e+03	E32450 Mammal-derived tissue
gb_pat:AR047004	17	16.00	101.77	2.6e+03	AR047004 Sequence 1797 from patent	gb_pat:E32451	18	16.00	101.39	2.8e+03	E32451 Mammal-derived tissue
gb_pat:AR047006	17	16.00	101.77	2.6e+03	AR047006 Sequence 1799 from patent	gb_pat:E32452	18	16.00	101.39	2.8e+03	E32452 Mammal-derived tissue
gb_pat:AR047008	17	16.00	101.77	2.6e+03	AR047008 Sequence 1801 from patent	gb_pat:E32453	18	16.00	101.39	2.8e+03	E32453 Mammal-derived tissue
gb_pat:AR047010	17	16.00	101.77	2.6e+03	AR047010 Sequence 1803 from patent	gb_pat:E32454	18	16.00	101.39	2.8e+03	E32454 Mammal-derived tissue
gb_pat:AR047072	17	16.00	101.77	2.6e+03	AR047072 Sequence 1865 from patent	gb_pat:E32455	18	16.00	101.39	2.8e+03	E32455 Mammal-derived tissue
gb_pat:AR04983	17	16.00	101.77	2.6e+03	AR04983 Sequence 21 from patent	gb_pat:E32456	18	16.00	101.39	2.8e+03	E32456 Mammal-derived tissue
gb_pat:AR101754	17	16.00	101.77	2.6e+03	AR101754 Sequence 16 from patent	gb_pat:E32457	18	16.00	101.39	2.8e+03	E32457 Mammal-derived tissue
gb_pat:AR1166243	17	16.00	101.77	2.6e+03	AR1166243 Sequence 16 from patent	gb_pat:E32458	18	16.00	101.39	2.8e+03	E32458 Mammal-derived tissue
gb_pat:AX216730	17	16.00	101.77	2.6e+03	AX216730 Sequence 2172 from patent	gb_pat:E32459	18	16.00	101.39	2.8e+03	E32459 Mammal-derived tissue
gb_pat:AX217526	17	16.00	101.77	2.6e+03	AX217526 Sequence 2968 from patent	gb_pat:E32460	18	16.00	101.39	2.8e+03	E32460 Mammal-derived tissue
gb_pat:AX217527	17	16.00	101.77	2.6e+03	AX217527 Sequence 2969 from patent	gb_pat:E32461	18	16.00	101.39	2.8e+03	E32461 Mammal-derived tissue
gb_pat:AX217528	17	16.00	101.77	2.6e+03	AX217528 Sequence 2970 from patent	gb_pat:I04015	18	16.00	101.39	2.8e+03	I04015 Sequence 11 from Patent
gb_pat:AX217529	17	16.00	101.77	2.6e+03	AX217529 Sequence 2971 from patent	gb_pat:I17856	18	16.00	101.39	2.8e+03	I17856 Sequence 86 from patent
gb_pat:AX217530	17	16.00	101.77	2.6e+03	AX217530 Sequence 2972 from patent	gb_pat:I673187	18	16.00	101.39	2.8e+03	I673187 Sequence 1 from patent
gb_pat:AX217531	17	16.00	101.77	2.6e+03	AX217531 Sequence 2973 from patent	gb_pat:A62427	19	16.00	101.03	2.9e+03	A62427 Sequence 35 from Patent
gb_pat:AX217532	17	16.00	101.77	2.6e+03	AX217532 Sequence 2974 from patent	gb_pat:AR029157	19	16.00	101.03	2.9e+03	AR029157 Sequence 33 from pat
gb_pat:AX217533	17	16.00	101.77	2.6e+03	AX217533 Sequence 2975 from patent	gb_pat:AR036541	19	16.00	101.03	2.9e+03	AR036541 Sequence 33 from pat
gb_pat:AX218159	17	16.00	101.77	2.6e+03	AX218159 Sequence 3601 from patent	gb_pat:AR096074	19	16.00	101.03	2.9e+03	AR096074 Sequence 33 from pat
gb_pat:AX218200	17	16.00	101.77	2.6e+03	AX218200 Sequence 3642 from patent	gb_pat:AR102546	19	16.00	101.03	2.9e+03	AR102546 Sequence 35 from pat
gb_pat:AX218290	17	16.00	101.77	2.6e+03	AX218290 Sequence 3732 from patent	gb_pat:AR111930	19	16.00	101.03	2.9e+03	AR111930 Sequence 4 from pat
gb_pat:AX227570	17	16.00	101.77	2.6e+03	AX227570 Sequence 942 from Patent	gb_pat:AR124827	19	16.00	101.03	2.9e+03	AR124827 Sequence 4 from pat
gb_pat:AX263364	17	16.00	101.77	2.6e+03	AX263364 Sequence 755 from Patent	gb_pat:AR135275	19	16.00	101.03	2.9e+03	AR135275 Sequence 4 from pat
gb_pat:AX263365	17	16.00	101.77	2.6e+03	AX263365 Sequence 756 from Patent	gb_pat:AR141345	19	16.00	101.03	2.9e+03	AR141345 Sequence 12 from P
gb_pat:AX263596	17	16.00	101.77	2.6e+03	AX263596 Sequence 987 from Patent	gb_pat:AX131071	19	16.00	101.03	2.9e+03	AX131071 Sequence 2289 from P
gb_pat:AX263597	17	16.00	101.77	2.6e+03	AX263597 Sequence 988 from Patent	gb_pat:AX131072	19	16.00	101.03	2.9e+03	AX131072 Sequence 2290 from P
gb_pat:AX264244	17	16.00	101.77	2.6e+03	AX264244 Sequence 1635 from Patent	gb_pat:AX131073	19	16.00	101.03	2.9e+03	AX131073 Sequence 2291 from P
gb_pat:AX264245	17	16.00	101.77	2.6e+03	AX264245 Sequence 1636 from Patent	gb_pat:AX131074	19	16.00	101.03	2.9e+03	AX131074 Sequence 2292 from P
gb_pat:BD007682	17	16.00	101.77	2.6e+03	BD007682 795, a novel gene relat	gb_pat:AX131075	19	16.00	101.03	2.9e+03	AX131075 Sequence 2293 from P
gb_pat:BD007683	17	16.00	101.77	2.6e+03	BD007683 795, a novel gene relat	gb_pat:AX131076	19	16.00	101.03	2.9e+03	AX131076 Sequence 2294 from P
gb_pat:BD007684	17	16.00	101.77	2.6e+03	BD007684 795, a novel gene relat	gb_pat:AX131077	19	16.00	101.03	2.9e+03	AX131077 Sequence 2295 from P
gb_pat:E08103	17	16.00	101.77	2.6e+03	E08103 Synthetic oligonucleotide	gb_pat:AX131078	19	16.00	101.03	2.9e+03	AX131078 Sequence 2296 from P
gb_pat:E34258	17	16.00	101.77	2.6e+03	E34258 Pollinosis-associated ger	gb_pat:AX131973	19	16.00	101.03	2.9e+03	AX131973 Sequence 3191 from P
gb_pat:E34259	17	16.00	101.77	2.6e+03	E34259 Pollinosis-associated ger	gb_pat:AX131974	19	16.00	101.03	2.9e+03	AX131974 Sequence 3192 from P
gb_pat:E34260	17	16.00	101.77	2.6e+03	E34260 Pollinosis-associated ger	gb_pat:AX131975	19	16.00	101.03	2.9e+03	AX131975 Sequence 3193 from P
gb_pat:E59657	17	16.00	101.77	2.6e+03	E59657 Method for preparing nucl	gb_pat:AX131976	19	16.00	101.03	2.9e+03	AX131976 Sequence 3194 from P
gb_pat:I37584	17	16.00	101.77	2.6e+03	I37584 Sequence 597 from patent	gb_pat:AX131977	19	16.00	101.03	2.9e+03	AX131977 Sequence 3195 from P
gb_pat:I53049	17	16.00	101.77	2.6e+03	I53049 Sequence 790 from patent	gb_pat:AX131978	19	16.00	101.03	2.9e+03	AX131978 Sequence 3196 from P
gb_pat:I53325	17	16.00	101.77	2.6e+03	I53325 Sequence 1066 from patent	gb_pat:AX132829	19	16.00	101.03	2.9e+03	AX132829 Sequence 4047 from P
gb_pat:I53327	17	16.00	101.77	2.6e+03	I53327 Sequence 1068 from patent	gb_pat:AX132830	19	16.00	101.03	2.9e+03	AX132830 Sequence 4048 from P
gb_pat:I53329	17	16.00	101.77	2.6e+03	I53329 Sequence 1070 from patent	gb_pat:AX132831	19	16.00	101.03	2.9e+03	AX132831 Sequence 4049 from P
gb_pat:I53331	17	16.00	101.77	2.6e+03	I53331 Sequence 1072 from patent	gb_pat:AX132832	19	16.00	101.03	2.9e+03	AX132832 Sequence 4050 from P
gb_pat:I53333	17	16.00	101.77	2.6e+03	I53333 Sequence 1074 from patent	gb_pat:AX132833	19	16.00	101.03	2.9e+03	AX132833 Sequence 4051 from P
gb_pat:I53335	17	16.00	101.77	2.6e+03	I53335 Sequence 1076 from patent	gb_pat:AX132834	19	16.00	101.03	2.9e+03	AX132834 Sequence 4052 from P
gb_pat:I53337	17	16.00	101.77	2.6e+03	I53337 Sequence 1078 from patent	gb_pat:AX132835	19	16.00	101.03	2.9e+03	AX132835 Sequence 4053 from P
gb_pat:I54050	17	16.00	101.77	2.6e+03	I54050 Sequence 1791 from patent	gb_pat:AX132836	19	16.00	101.03	2.9e+03	AX132836 Sequence 4054 from P
gb_pat:I54052	17	16.00	101.77	2.6e+03	I54052 Sequence 1793 from patent	gb_pat:AX132837	19	16.00	101.03	2.9e+03	AX132837 Sequence 4055 from P
gb_pat:I54054	17	16.00	101.77	2.6e+03	I54054 Sequence 1795 from patent	gb_pat:AX149159	19	16.00	101.03	2.9e+03	AX149159 Sequence 361 from P
gb_pat:I54056	17	16.00	101.77	2.6e+03	I54056 Sequence 1797 from patent	gb_pat:AX339205	19	16.00	101.03	2.9e+03	AX339205 Sequence 4 from Pat
gb_pat:I54058	17	16.00	101.77	2.6e+03	I54058 Sequence 1799 from patent	gb_pat:AX352885	19	16.00	101.03	2.9e+03	AX352885 Sequence 91 from Pat
gb_pat:I54060	17	16.00	101.77	2.6e+03	I54060 Sequence 1801 from patent	gb_pat:AX352891	19	16.00	101.03	2.9e+03	AX352891 Sequence 97 from Pat
						gb_pat:AX352892	19	16.00	101.03	2.9e+03	AX352892 Sequence 98 from Pat

gb_pat:AX352893	19	1	AX352893	Sequence 99 from Patent	16.00	101.03	2.9e+03	gb_pat:AX136904	20	1	AX136904	Sequence 6 from Pat	16.00	100.68	3.0e+03
gb_pat:AX352895	19	1	AX352895	Sequence 101 from Patent	16.00	101.03	2.9e+03	gb_pat:AX148814	20	1	AX148814	Sequence 16 from Pat	16.00	100.68	3.0e+03
gb_pat:AX352902	19	1	AX352902	Sequence 108 from Patent	16.00	101.03	2.9e+03	gb_pat:AX148971	20	1	AX148971	Sequence 173 from Pat	16.00	100.68	3.0e+03
gb_pat:AX352904	19	1	AX352904	Sequence 110 from Patent	16.00	101.03	2.9e+03	gb_pat:AX167857	20	1	AX167857	Sequence 41 from Pat	16.00	100.68	3.0e+03
gb_pat:AX352911	19	1	AX352911	Sequence 117 from Patent	16.00	101.03	2.9e+03	gb_pat:AX167928	20	1	AX167928	Sequence 112 from Pat	16.00	100.68	3.0e+03
gb_pat:AX352922	19	1	AX352922	Sequence 128 from Patent	16.00	101.03	2.9e+03	gb_pat:AX167929	20	1	AX167929	Sequence 113 from Pat	16.00	100.68	3.0e+03
gb_pat:AX352923	19	1	AX352923	Sequence 129 from Patent	16.00	101.03	2.9e+03	gb_pat:AX167930	20	1	AX167930	Sequence 114 from Pat	16.00	100.68	3.0e+03
gb_pat:AX352925	19	1	AX352925	Sequence 131 from Patent	16.00	101.03	2.9e+03	gb_pat:AX167935	20	1	AX167935	Sequence 11 from Pat	16.00	100.68	3.0e+03
gb_pat:AX352927	19	1	AX352927	Sequence 133 from Patent	16.00	101.03	2.9e+03	gb_pat:AX294371	20	1	AX294371	Sequence 6133 from P	16.00	100.68	3.0e+03
gb_pat:AX352933	19	1	AX352933	Sequence 139 from Patent	16.00	101.03	2.9e+03	gb_pat:AX355136	20	1	AX355136	Sequence 184 from Pat	16.00	100.68	3.0e+03
gb_pat:AX352937	19	1	AX352937	Sequence 143 from Patent	16.00	101.03	2.9e+03	gb_pat:AX355404	20	1	AX355404	Sequence 432 from Pat	16.00	100.68	3.0e+03
gb_pat:AX352943	19	1	AX352943	Sequence 149 from Patent	16.00	101.03	2.9e+03	gb_pat:AX355709	20	1	AX355709	Sequence 737 from Pat	16.00	100.68	3.0e+03
gb_pat:AX353097	19	1	AX353097	Sequence 303 from Patent	16.00	101.03	2.9e+03	gb_pat:BD001838	20	1	BD001838	Method for identifiy	16.00	100.68	3.0e+03
gb_pat:BD008242	19	1	BD008242	Gene coding for protein	16.00	101.03	2.9e+03	gb_pat:BD008240	20	1	BD008240	Gene coding for prot	16.00	100.68	3.0e+03
gb_pat:E29790	19	1	E29790	Method for discriminating	16.00	101.03	2.9e+03	gb_pat:E05831	20	1	E05831	DNA sequence for synth	16.00	100.68	3.0e+03
gb_pat:134186	19	1	134186	Sequence 2 from patent US	16.00	101.03	2.9e+03	gb_pat:E06910	20	1	E06910	Synthetic DNA for hybr	16.00	100.68	3.0e+03
gb_pat:AX10788	19	1	AX10788	Oligonucleotide 1 from pa	16.00	100.68	3.0e+03	gb_pat:E29051	20	1	E29051	Mutant S182(Ps-1) gene	16.00	100.68	3.0e+03
gb_pat:AX10129	19	1	AX10129	Sequence 5 from Patent WC	16.00	100.68	3.0e+03	gb_pat:E29055	20	1	E29055	Mutant S182(Ps-1) gene	16.00	100.68	3.0e+03
gb_pat:AX1887	20	1	AX1887	Sequence 1 from Patent WC	16.00	100.68	3.0e+03	gb_pat:E29057	20	1	E29057	Mutant S182(Ps-1) gene	16.00	100.68	3.0e+03
gb_pat:AR000176	20	1	AR000176	Sequence 7 from Patent	16.00	100.68	3.0e+03	gb_pat:E29065	20	1	E29065	Mutant S182(Ps-1) gene	16.00	100.68	3.0e+03
gb_pat:AR016001	20	1	AR016001	Sequence 21 from Patent	16.00	100.68	3.0e+03	gb_pat:E33607	20	1	E33607	Novel prokaryotic poly	16.00	100.68	3.0e+03
gb_pat:AR026504	20	1	AR026504	Sequence 11 from Patent	16.00	100.68	3.0e+03	gb_pat:E36060	20	1	E36060	Higher-order structure	16.00	100.68	3.0e+03
gb_pat:AR042393	20	1	AR042393	Sequence 13 from Patent	16.00	100.68	3.0e+03	gb_pat:E36060	20	1	E36060	Higher-order structure	16.00	100.68	3.0e+03
gb_pat:AR050226	20	1	AR050226	Sequence 32 from Patent	16.00	100.68	3.0e+03	gb_pat:E36664	20	1	E36664	DNA and plasmid contai	16.00	100.68	3.0e+03
gb_pat:AR062036	20	1	AR062036	Sequence 115 from Patent	16.00	100.68	3.0e+03	gb_pat:E51768	20	1	E51768	Promoter of melon ethy	16.00	100.68	3.0e+03
gb_pat:AR082042	20	1	AR082042	Sequence 21 from Patent	16.00	100.68	3.0e+03	gb_pat:E58612	20	1	E58612	Thermotolerant esteras	16.00	100.68	3.0e+03
gb_pat:AR082552	20	1	AR082552	Sequence 2 from Patent	16.00	100.68	3.0e+03	gb_pat:E59328	20	1	E59328	Method for purifying o	16.00	100.68	3.0e+03
gb_pat:AR088161	20	1	AR088161	Sequence 51 from Patent	16.00	100.68	3.0e+03	gb_pat:E16848	20	1	E16848	Sequence 13 from Patent	16.00	100.68	3.0e+03
gb_pat:AR087161	20	1	AR087161	Sequence 31 from Patent	16.00	100.68	3.0e+03	gb_pat:E123825	20	1	E123825	Sequence 4 from Patent	16.00	100.68	3.0e+03
gb_pat:AR087938	20	1	AR087938	Sequence 31 from Patent	16.00	100.68	3.0e+03	gb_pat:E125376	20	1	E125376	Sequence 13 from Patent	16.00	100.68	3.0e+03
gb_pat:AR089398	20	1	AR089398	Sequence 157 from Patent	16.00	100.68	3.0e+03	gb_pat:E136544	20	1	E136544	Sequence 13 from Patent	16.00	100.68	3.0e+03
gb_pat:AR089580	20	1	AR089580	Sequence 40 from Patent	16.00	100.68	3.0e+03	gb_pat:E149616	20	1	E149616	Sequence 31 from Patent	16.00	100.68	3.0e+03
gb_pat:AR092979	20	1	AR092979	Sequence 74 from Patent	16.00	100.68	3.0e+03	gb_pat:E149616	20	1	E149616	Sequence 31 from Patent	16.00	100.68	3.0e+03
gb_pat:AR093063	20	1	AR093063	Sequence 158 from Patent	16.00	100.68	3.0e+03	gb_sy:AB069479	20	1	AB069479	Synthetic construct	16.00	100.68	3.0e+03
gb_pat:AR093598	20	1	AR093598	Sequence 157 from Patent	16.00	100.68	3.0e+03	em_pat:E09534	20	1	E09534	Synthetic DNA. 9/2000	16.00	100.68	3.0e+03
gb_pat:AR093676	20	1	AR093676	Sequence 51 from Patent	16.00	100.68	3.0e+03	gb_pat:E09785	20	1	E09785	DNA fragment for ligat	16.00	100.68	3.0e+03
gb_pat:AR096477	20	1	AR096477	Sequence 6 from Patent	16.00	100.68	3.0e+03	gb_om:DOGP2101	20	1	DOGP2101	Dog (Clone: CXX.21) pr	16.00	100.35	3.2e+03
gb_pat:AR096479	20	1	AR096479	Sequence 4 from Patent	16.00	100.68	3.0e+03	gb_om:DOGP41401	20	1	DOGP41401	Dog (Clone: CXX.414) p	16.00	100.35	3.2e+03
gb_pat:AR098294	20	1	AR098294	Sequence 11 from Patent	16.00	100.68	3.0e+03	gb_om:DOGP48902	20	1	DOGP48902	Dog (Clone: CXX.489) p	16.00	100.35	3.2e+03
gb_pat:AR100615	20	1	AR100615	Sequence 4 from Patent	16.00	100.68	3.0e+03	gb_pat:A23687	20	1	A23687	L. monocytogenes HlyA	16.00	100.35	3.2e+03
gb_pat:AR101034	20	1	AR101034	Sequence 10 from Patent	16.00	100.68	3.0e+03	gb_pat:AX35600	20	1	AX35600	Sequence 5 from Patent	16.00	100.35	3.2e+03
gb_pat:AR101049	20	1	AR101049	Sequence 19 from Patent	16.00	100.68	3.0e+03	gb_pat:AX35956	20	1	AX35956	Sequence 25 from Patent	16.00	100.35	3.2e+03
gb_pat:AR105641	20	1	AR105641	Sequence 3 from Patent	16.00	100.68	3.0e+03	gb_pat:AX151562	20	1	AX151562	Sequence 89 from Patent	16.00	100.35	3.2e+03
gb_pat:AR118958	20	1	AR118958	Sequence 84 from Patent	16.00	100.68	3.0e+03	gb_pat:AR000177	20	1	AR000177	Sequence 8 from Patent	16.00	100.35	3.2e+03
gb_pat:AR118959	20	1	AR118959	Sequence 85 from Patent	16.00	100.68	3.0e+03	gb_pat:AR016251	20	1	AR016251	Sequence 5 from Patent	16.00	100.35	3.2e+03
gb_pat:AR121076	20	1	AR121076	Sequence 97 from Patent	16.00	100.68	3.0e+03	gb_pat:AR066940	20	1	AR066940	Sequence 288 from Pat	16.00	100.35	3.2e+03
gb_pat:AR121615	20	1	AR121615	Sequence 12 from Patent	16.00	100.68	3.0e+03	gb_pat:AR100526	20	1	AR100526	Sequence 3 from Patent	16.00	100.35	3.2e+03
gb_pat:AR122236	20	1	AR122236	Sequence 82 from Patent	16.00	100.68	3.0e+03	gb_pat:AR103576	20	1	AR103576	Sequence 100 from Pat	16.00	100.35	3.2e+03
gb_pat:AR122473	20	1	AR122473	Sequence 27 from Patent	16.00	100.68	3.0e+03	gb_pat:AR118155	20	1	AR118155	Sequence 23 from Pat	16.00	100.35	3.2e+03
gb_pat:AR131210	20	1	AR131210	Sequence 82 from Patent	16.00	100.68	3.0e+03	gb_pat:AR142678	20	1	AR142678	Sequence 8 from Patent	16.00	100.35	3.2e+03
gb_pat:AR142339	20	1	AR142339	Sequence 21 from Patent	16.00	100.68	3.0e+03	gb_pat:AR153849	20	1	AR153849	Sequence 2 from Patent	16.00	100.35	3.2e+03
gb_pat:AR142340	20	1	AR142340	Sequence 22 from Patent	16.00	100.68	3.0e+03	gb_pat:AX023419	20	1	AX023419	Sequence 34 from Pat	16.00	100.35	3.2e+03
gb_pat:AR142341	20	1	AR142341	Sequence 23 from Patent	16.00	100.68	3.0e+03	gb_pat:AX111720	20	1	AX111720	Sequence 17 from Pat	16.00	100.35	3.2e+03
gb_pat:AR142342	20	1	AR142342	Sequence 24 from Patent	16.00	100.68	3.0e+03	gb_pat:AX111723	20	1	AX111723	Sequence 20 from Pat	16.00	100.35	3.2e+03
gb_pat:AR143169	20	1	AR143169	Sequence 62 from Patent	16.00	100.68	3.0e+03	gb_pat:AX119910	20	1	AX119910	Sequence 18 from Pat	16.00	100.35	3.2e+03
gb_pat:AR144624	20	1	AR144624	Sequence 169 from Patent	16.00	100.68	3.0e+03	gb_pat:AX119911	20	1	AX119911	Sequence 19 from Pat	16.00	100.35	3.2e+03
gb_pat:AR149897	20	1	AR149897	Sequence 4 from Patent	16.00	100.68	3.0e+03	gb_pat:AX133303	20	1	AX133303	Sequence 4521 from P	16.00	100.35	3.2e+03
gb_pat:AR167071	20	1	AR167071	Sequence 88 from Patent	16.00	100.68	3.0e+03	gb_pat:AX154158	20	1	AX154158	Sequence 286 from Pat	16.00	100.35	3.2e+03
gb_pat:AR167072	20	1	AR167072	Sequence 89 from Patent	16.00	100.68	3.0e+03	gb_pat:AX288083	20	1	AX288083	Sequence 28 from Pat	16.00	100.35	3.2e+03
gb_pat:AR167073	20	1	AR167073	Sequence 90 from Patent	16.00	100.68	3.0e+03	gb_pat:E08958	20	1	E08958	Probe of Stb-gene. 9/1	16.00	100.35	3.2e+03
gb_pat:AR167074	20	1	AR167074	Sequence 91 from Patent	16.00	100.68	3.0e+03	gb_pat:E28097	20	1	E28097	Method for analyzing D	16.00	100.35	3.2e+03
gb_pat:AR167077	20	1	AR167077	Sequence 94 from Patent	16.00	100.68	3.0e+03	gb_pat:E29379	20	1	E29379	Oligonucleotide and re	16.00	100.35	3.2e+03
gb_pat:AR173877	20	1	AR173877	Sequence 75 from Patent	16.00	100.68	3.0e+03	gb_pat:E29379	20	1	E29379	Oligonucleotide and re	16.00	100.35	3.2e+03
gb_pat:AX076462	20	1	AX076462	Sequence 76 from Patent	16.00	100.68	3.0e+03	gb_pat:130723	20	1	130723	Sequence 161 from Pat	16.00	100.35	3.2e+03
gb_pat:AX104239	20	1	AX104239	Sequence 431 from Patent	16.00	100.68	3.0e+03	gb_pat:130769	20	1	130769	Sequence 207 from Pat	16.00	100.35	3.2e+03
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gb_pat:AX104369	20	1	AX104369	Sequence 561 from Patent	16.00	100.68	3.0e+03	gb_pat:139871	20	1	139871	Sequence 1 from Patent	16.00	100.35	3.2e+03
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gb_in:DME421766	+	16.00	100.04	3.3e+03	22	AJ421766 Drosophila melanogaster	gb_pat:I26414	16.00	99.74	3.4e+03	23	I26414 Sequence 106 from patent
gb_pat:A42091	+	16.00	100.04	3.3e+03	22	A42091 Sequence 3 from Patent WO	gb_pat:I30437	16.00	99.74	3.4e+03	23	I30437 Sequence 24 from patent
gb_pat:A51385	+	16.00	100.04	3.3e+03	22	A51385 Sequence 1 from Patent WO	gb_pat:I32906	16.00	99.74	3.4e+03	23	I32906 Sequence 15 from patent
gb_pat:A51391	+	16.00	100.04	3.3e+03	22	A51391 Sequence 7 from Patent WO	gb_pat:I35681	16.00	99.74	3.4e+03	23	I35681 Sequence 24 from patent
gb_pat:A85577	-	16.00	100.04	3.3e+03	22	A85577 Sequence 6 from Patent WO	gb_pat:I79498	16.00	99.74	3.4e+03	23	I79498 Sequence 5 from patent
gb_pat:AR072065	+	16.00	100.04	3.3e+03	22	AR072065 Sequence 1 from patent	gb_pat:I79499	16.00	99.74	3.4e+03	23	I79499 Sequence 6 from patent
gb_pat:AR092325	+	16.00	100.04	3.3e+03	22	AR092325 Sequence 11 from patent	gb_pat:I79499	16.00	99.74	3.4e+03	23	I79499 Sequence 5 from patent
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gb_pat:AR176656	+	16.00	100.04	3.3e+03	22	AR176656 Sequence 3 from patent	gb_pat:I79499	16.00	99.74	3.4e+03	23	I79499 Sequence 5 from patent
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gb_pat:AX352315	-	16.00	100.04	3.3e+03	22	AX352315 Sequence 348 from Patent	gb_pat:AX352315	16.00	99.74	3.4e+03	23	AX352315 Sequence 348 from Patent
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gb_pat:E40156	+	16.00	100.04	3.3e+03	22	E40156 Genetic diagnosis method	gb_pat:E40156	16.00	99.74	3.4e+03	23	E40156 Genetic diagnosis method
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gb_pat:I47486	+	16.00	100.04	3.3e+03	22	I47486 Sequence 148 from patent	gb_pat:I47486	16.00	99.74	3.4e+03	23	I47486 Sequence 148 from patent
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gb_pat:I69408	+	16.00	100.04	3.3e+03	22	I69408 Sequence 2 from patent	gb_pat:I69408	16.00	99.74	3.4e+03	23	I69408 Sequence 2 from patent
gb_sy:AR069603	-	16.00	100.04	3.3e+03	22	AR069603 Synthetic construct	gb_sy:AR069603	16.00	99.74	3.4e+03	23	AR069603 Synthetic construct
gb_pat:AR91179	+	16.00	99.74	3.4e+03	23	AR91179 Sequence 13 from Patent	gb_pat:AR91179	16.00	99.74	3.4e+03	23	AR91179 Sequence 13 from Patent
gb_pat:AR014285	+	16.00	99.74	3.4e+03	23	AR014285 Sequence 17 from patent	gb_pat:AR014285	16.00	99.74	3.4e+03	23	AR014285 Sequence 17 from patent
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gb_pat:AR061895	+	16.00	99.74	3.4e+03	23	AR061895 Sequence 6 from patent	gb_pat:AR061895	16.00	99.74	3.4e+03	23	AR061895 Sequence 6 from patent
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gb_pat:AX183613	+	16.00	99.74	3.4e+03	23	AX183613 Sequence 1366 from Patent	gb_pat:AX183613	16.00	99.74	3.4e+03	23	AX183613 Sequence 1366 from Patent
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gb_pat:E14519	+	16.00	99.74	3.4e+03	23	E14519 PCR primer for gaining	gb_pat:E14519	16.00	99.74	3.4e+03	23	E14519 PCR primer for gaining
gb_pat:E16748	+	16.00	99.74	3.4e+03	23	E16748 Primer 7/1999	gb_pat:E16748	16.00	99.74	3.4e+03	23	E16748 Primer 7/1999
gb_pat:I00179	-	16.00	99.74	3.4e+03	23	I00179 Sequence 3 from Patent	gb_pat:I00179	16.00	99.74	3.4e+03	23	I00179 Sequence 3 from Patent
gb_pat:I00269	+	16.00	99.74	3.4e+03	23	I00269 Sequence 2 from Patent	gb_pat:I00269	16.00	99.74	3.4e+03	23	I00269 Sequence 2 from Patent

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gb_pat:ARX003409	16.00	99.19	3.7e+03	25	AX003409	Sequence 26	from patent
gb_pat:ARX007110	16.00	99.19	3.7e+03	25	AX007110	Sequence 10	from patent
gb_pat:ARX03469	16.00	99.19	3.7e+03	25	AX03469	Sequence 34	from patent
gb_pat:ARX04751	16.00	99.19	3.7e+03	25	AX04751	Sequence 943	from patent
gb_pat:ARX100892	16.00	99.19	3.7e+03	25	AX100892	Sequence 1625	from patent
gb_pat:ARX115660	16.00	99.19	3.7e+03	25	AX115660	Sequence 783	from patent
gb_pat:ARX115988	16.00	99.19	3.7e+03	25	AX115988	Sequence 1111	from patent
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gb_pat:ARX116396	16.00	99.19	3.7e+03	25	AX116396	Sequence 1519	from patent
gb_pat:ARX116440	16.00	99.19	3.7e+03	25	AX116440	Sequence 1563	from patent
gb_pat:ARX116671	16.00	99.19	3.7e+03	25	AX116671	Sequence 1794	from patent
gb_pat:ARX116811	16.00	99.19	3.7e+03	25	AX116811	Sequence 1934	from patent
gb_pat:ARX116840	16.00	99.19	3.7e+03	25	AX116840	Sequence 1963	from patent
gb_pat:ARX117208	16.00	99.19	3.7e+03	25	AX117208	Sequence 2331	from patent
gb_pat:ARX117788	16.00	99.19	3.7e+03	25	AX117788	Sequence 2911	from patent
gb_pat:ARX118212	16.00	99.19	3.7e+03	25	AX118212	Sequence 3335	from patent
gb_pat:ARX118336	16.00	99.19	3.7e+03	25	AX118336	Sequence 3459	from patent
gb_pat:ARX151163	16.00	99.19	3.7e+03	25	AX151163	Sequence 52	from patent
gb_pat:ARX155622	16.00	99.19	3.7e+03	25	AX155622	Sequence 34	from patent
gb_pat:ARX196867	16.00	99.19	3.7e+03	25	AX196867	Sequence 574	from patent
gb_pat:ARX196988	16.00	99.19	3.7e+03	25	AX196988	Sequence 695	from patent
gb_pat:ARX241161	16.00	99.19	3.7e+03	25	AX241161	Sequence 399	from patent
gb_pat:ARX113373	16.00	99.19	3.7e+03	25	AX113373	Sequence 24	from patent
gb_pat:ARX121975	16.00	99.19	3.7e+03	25	AX121975	Sequence 61	from patent
gb_pat:ARX145922	16.00	99.19	3.7e+03	25	AX145922	Sequence 10	from patent
gb_pat:ARX158716	16.00	99.19	3.7e+03	25	AX158716	H.sapiens primer 1 of STS	
gb_pat:ARX158363	16.00	99.19	3.7e+03	25	AX158363	H.sapiens dystrophin poly	
gb_pat:ARX158369	16.00	99.19	3.7e+03	25	AX158369	Sequence 8	from patent
gb_pat:ARX158347	16.00	99.19	3.7e+03	25	AX158347	Sequence 10	from patent
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gb_pat:ARX158347	16.00	99.19	3.7e+03	25	AX158347	Sequence 3086	from patent
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gb_pat:ARX158347	16.00	99.19	3.7e+03	25	AX158347	Sequence 1553	from patent
gb_pat:ARX158347	16.00	99.19	3.7e+03	25	AX158347	Sequence 393	from patent
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gb_pat:ARX158347	16.00	99.19	3.7e+03	25	AX158347	Sequence 23	from patent
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gb_pat:ARX158347	16.00	99.19	3.7e+03	25	AX158347	Thermotolerant esterase	
gb_pat:ARX158347	16.00	99.19	3.7e+03	25	AX158347	Stress-responsive gene	
gb_pat:ARX158347	16.00	99.19	3.7e+03	25	AX158347	Glucose dehydrogenase	
gb_pat:ARX158347	16.00	99.19	3.7e+03	25	AX158347	Probe for detecting oligo	

gb_pat:187998	-	16.00	98.43	4.0e+03	28	I 187998	Sequence 9 from patent US	gb_pat:AR138576	-	16.00	97.96	4.3e+03	30	I AR138576	Sequence 101 from pa
gb_pat:A57879	-	16.00	98.19	4.2e+03	29	I A57879	Sequence 2 from Patent EP	gb_pat:AR138579	-	16.00	97.96	4.3e+03	30	I AR138579	Sequence 104 from pa
gb_pat:A68962	-	16.00	98.19	4.2e+03	29	I A68962	Sequence 34 from Patent EP	gb_pat:AR138591	-	16.00	97.96	4.3e+03	30	I AR138591	Sequence 116 from pa
gb_pat:A69264	-	16.00	98.19	4.2e+03	29	I A69264	Sequence 3 from Patent WC	gb_pat:AR138594	+	16.00	97.96	4.3e+03	30	I AR138594	Sequence 119 from pa
gb_pat:A71416	-	16.00	98.19	4.2e+03	29	I A71416	Sequence 27 from Patent WC	gb_pat:AR138615	-	16.00	97.96	4.3e+03	30	I AR138615	Sequence 140 from pa
gb_pat:A71941	-	16.00	98.19	4.2e+03	29	I A71941	Sequence 3 from Patent WC	gb_pat:AR138645	-	16.00	97.96	4.3e+03	30	I AR138645	Sequence 170 from pa
gb_pat:A76894	-	16.00	98.19	4.2e+03	29	I A76894	Sequence 26 from Patent WC	gb_pat:AR138654	-	16.00	97.96	4.3e+03	30	I AR138654	Sequence 179 from pa
gb_pat:AR094999	+	16.00	98.19	4.2e+03	29	I AR094999	Sequence 37 from patent	gb_pat:AR138662	-	16.00	97.96	4.3e+03	30	I AR138662	Sequence 187 from pa
gb_pat:AR095000	+	16.00	98.19	4.2e+03	29	I AR095000	Sequence 38 from patent	gb_pat:AR138674	-	16.00	97.96	4.3e+03	30	I AR138674	Sequence 199 from pa
gb_pat:AR098149	-	16.00	98.19	4.2e+03	29	I AR098149	Sequence 25 from patent	gb_pat:AR138676	-	16.00	97.96	4.3e+03	30	I AR138676	Sequence 201 from pa
gb_pat:AR098648	-	16.00	98.19	4.2e+03	29	I AR098648	Sequence 6 from patent	gb_pat:AX028510	+	16.00	97.96	4.3e+03	30	I AX028510	Sequence 13 from Pat
gb_pat:AR101056	-	16.00	98.19	4.2e+03	29	I AR101056	Sequence 32 from patent	gb_pat:AX032823	-	16.00	97.96	4.3e+03	30	I AX032823	Sequence 1 from Pat
gb_pat:AR101062	-	16.00	98.19	4.2e+03	29	I AR101062	Sequence 26 from patent	gb_pat:AX060497	-	16.00	97.96	4.3e+03	30	I AX060497	Sequence 32 from Pat
gb_pat:AR101064	-	16.00	98.19	4.2e+03	29	I AR101064	Sequence 34 from patent	gb_pat:AX098446	+	16.00	97.96	4.3e+03	30	I AX098446	Sequence 18 from Pat
gb_pat:AR116621	-	16.00	98.19	4.2e+03	29	I AR116621	Sequence 25 from patent	gb_pat:AX100424	-	16.00	97.96	4.3e+03	30	I AX100424	Sequence 64 from Pat
gb_pat:AR139188	-	16.00	98.19	4.2e+03	29	I AR139188	Sequence 40 from patent	gb_pat:AX116662	-	16.00	97.96	4.3e+03	30	I AX116662	Sequence 1785 from P
gb_pat:AR147129	-	16.00	98.19	4.2e+03	29	I AR147129	Sequence 3 from patent	gb_pat:AX117042	-	16.00	97.96	4.3e+03	30	I AX117042	Sequence 2165 from P
gb_pat:AR162080	-	16.00	98.19	4.2e+03	29	I AR162080	Sequence 8 from patent	gb_pat:AX280450	-	16.00	97.96	4.3e+03	30	I AX280450	Sequence 73 from Pat
gb_pat:AR166605	-	16.00	98.19	4.2e+03	29	I AR166605	Sequence 8 from patent	gb_pat:AX288069	+	16.00	97.96	4.3e+03	30	I AX288069	Sequence 14 from Pat
gb_pat:AR176110	-	16.00	98.19	4.2e+03	29	I AR176110	Sequence 96 from patent	gb_pat:AX288076	-	16.00	97.96	4.3e+03	30	I AX288076	Sequence 21 from Pat
gb_pat:AX011029	-	16.00	98.19	4.2e+03	29	I AX011029	Sequence 16 from Patent	gb_pat:AX351705	-	16.00	97.96	4.3e+03	30	I AX351705	Sequence 1 from Pat
gb_pat:AX016303	-	16.00	98.19	4.2e+03	29	I AX016303	Sequence 6 from Patent	gb_pat:AX351706	-	16.00	97.96	4.3e+03	30	I AX351706	Sequence 2 from Pat
gb_pat:AX048408	-	16.00	98.19	4.2e+03	29	I AX048408	Sequence 7 from Patent	gb_pat:AX351707	-	16.00	97.96	4.3e+03	30	I AX351707	Sequence 3 from Pat
gb_pat:AX048409	-	16.00	98.19	4.2e+03	29	I AX048409	Sequence 8 from Patent	gb_pat:AX351708	-	16.00	97.96	4.3e+03	30	I AX351708	Sequence 4 from Pat
gb_pat:AX052989	-	16.00	98.19	4.2e+03	29	I AX052989	Sequence 5 from Patent	gb_pat:AX351710	-	16.00	97.96	4.3e+03	30	I AX351710	Sequence 6 from Pat
gb_pat:AX052994	-	16.00	98.19	4.2e+03	29	I AX052994	Sequence 10 from Patent	gb_pat:AX351711	-	16.00	97.96	4.3e+03	30	I AX351711	Sequence 7 from Pat
gb_pat:AX078918	-	16.00	98.19	4.2e+03	29	I AX078918	Sequence 4 from Patent	gb_pat:AX352051	-	16.00	97.96	4.3e+03	30	I AX352051	Sequence 347 from Pa
gb_pat:AX078919	-	16.00	98.19	4.2e+03	29	I AX078919	Sequence 5 from Patent	gb_pat:BD008891	+	16.00	97.96	4.3e+03	30	I BD008891	High level expressio
gb_pat:AX268782	-	16.00	98.19	4.2e+03	29	I AX268782	Sequence 4 from Patent	gb_pat:BD05835	-	16.00	97.96	4.3e+03	30	I BD05835	DNA sequences of fragm
gb_pat:AX286501	-	16.00	98.19	4.2e+03	29	I AX286501	Sequence 8 from Patent	gb_pat:EI3629	-	16.00	97.96	4.3e+03	30	I EI3629	A part of polyribonuc
gb_pat:AX297747	-	16.00	98.19	4.2e+03	29	I AX297747	Sequence 9509 from Pat	gb_pat:EI3951	-	16.00	97.96	4.3e+03	30	I EI3951	Method for transformin
gb_pat:AX304639	-	16.00	98.19	4.2e+03	29	I AX304639	Sequence 153 from Pat	gb_pat:ES9120	-	16.00	97.96	4.3e+03	30	I ES9120	Recombinant subunit va
gb_pat:AX351955	-	16.00	98.19	4.2e+03	29	I AX351955	Sequence 251 from Pat	gb_pat:EI12382	-	16.00	97.96	4.3e+03	30	I EI12382	Sequence 5 from patent
gb_pat:AX353685	-	16.00	98.19	4.2e+03	29	I AX353685	Sequence 5 from Patent	gb_pat:EI14394	-	16.00	97.96	4.3e+03	30	I EI14394	Sequence 18 from patent
gb_pat:BD006075	-	16.00	98.19	4.2e+03	29	I BD006075	Poly nucleotide vaccine	gb_pat:EI14394	-	16.00	97.96	4.3e+03	30	I EI14394	Sequence 18 from patent
gb_pat:BD009817	-	16.00	98.19	4.2e+03	29	I BD009817	Avian polynucleotide va	gb_pat:EI39988	+	16.00	97.96	4.3e+03	30	I EI39988	Sequence 41 from patent
gb_pat:EI65795	-	16.00	98.19	4.2e+03	29	I EI65795	Sequence 13 from patent	gb_pat:EI49601	-	16.00	97.96	4.3e+03	30	I EI49601	Sequence 43 from patent
gb_pat:A36778	-	16.00	97.96	4.3e+03	30	I A36778	Oligonucleotide GP67-SC.1	gb_pat:EI59848	+	16.00	97.96	4.3e+03	30	I EI59848	Sequence 85 from patent
gb_pat:A38144	-	16.00	97.96	4.3e+03	30	I A38144	Sequence 6 from Patent	gb_pat:EI75175	-	16.00	97.96	4.3e+03	30	I EI75175	Sequence 85 from patent
gb_pat:A39182	-	16.00	97.96	4.3e+03	30	I A39182	Sequence 16 from Patent	gb_pat:EI91906	-	16.00	97.96	4.3e+03	30	I EI91906	Sequence 4 from patent
gb_pat:A83875	+	16.00	97.96	4.3e+03	30	I A83875	Sequence 10 from Patent W	gb_pat:MHNSND6M	-	16.00	97.96	4.3e+03	30	I A84433	H.sapiens mitochondria
gb_pat:A83876	+	16.00	97.96	4.3e+03	30	I A83876	Sequence 11 from Patent W	gb_pat:A04979	-	16.00	97.74	4.4e+03	31	I A04979	Artificial sequence fo
gb_pat:A93586	-	16.00	97.96	4.3e+03	30	I A93586	Sequence 16 from Patent W	gb_pat:A04980	-	16.00	97.74	4.4e+03	31	I A04980	Artificial sequence fo
gb_pat:AR000059	-	16.00	97.96	4.3e+03	30	I AR000059	Sequence 7 from patent	gb_pat:A08914	-	16.00	97.74	4.4e+03	31	I A08914	H.sapiens (haplotype 3
gb_pat:AR016018	-	16.00	97.96	4.3e+03	30	I AR016018	Sequence 50 from patent	gb_pat:A74270	+	16.00	97.74	4.4e+03	31	I A74270	Sequence 26 from Paten
gb_pat:AR016018	-	16.00	97.96	4.3e+03	30	I AR016018	Sequence 5 from patent	gb_pat:AR028224	-	16.00	97.74	4.4e+03	31	I AR028224	Sequence 73 from pat
gb_pat:AR020878	+	16.00	97.96	4.3e+03	30	I AR020878	Sequence 85 from patent	gb_pat:AR029622	-	16.00	97.74	4.4e+03	31	I AR029622	Sequence 7 from pat
gb_pat:AR023796	+	16.00	97.96	4.3e+03	30	I AR023796	Sequence 28 from patent	gb_pat:AR063949	-	16.00	97.74	4.4e+03	31	I AR063949	Sequence 48 from pat
gb_pat:AR027201	+	16.00	97.96	4.3e+03	30	I AR027201	Sequence 85 from patent	gb_pat:AR079777	-	16.00	97.74	4.4e+03	31	I AR079777	Sequence 101 from pa
gb_pat:AR028168	-	16.00	97.96	4.3e+03	30	I AR028168	Sequence 17 from patent	gb_pat:AR081307	-	16.00	97.74	4.4e+03	31	I AR081307	Sequence 101 from pa
gb_pat:AR028174	-	16.00	97.96	4.3e+03	30	I AR028174	Sequence 23 from patent	gb_pat:AR091411	-	16.00	97.74	4.4e+03	31	I AR091411	Sequence 1 from pat
gb_pat:AR028176	-	16.00	97.96	4.3e+03	30	I AR028176	Sequence 25 from patent	gb_pat:AR125616	-	16.00	97.74	4.4e+03	31	I AR125616	Sequence 1 from pat
gb_pat:AR028188	-	16.00	97.96	4.3e+03	30	I AR028188	Sequence 37 from patent	gb_pat:AR138627	-	16.00	97.74	4.4e+03	31	I AR138627	Sequence 152 from pa
gb_pat:AR028191	-	16.00	97.96	4.3e+03	30	I AR028191	Sequence 40 from patent	gb_pat:AR149549	-	16.00	97.74	4.4e+03	31	I AR149549	Sequence 101 from pa
gb_pat:AR028212	-	16.00	97.96	4.3e+03	30	I AR028212	Sequence 61 from patent	gb_pat:AR170667	+	16.00	97.74	4.4e+03	31	I AR170667	Sequence 101 from pa
gb_pat:AR028251	-	16.00	97.96	4.3e+03	30	I AR028251	Sequence 91 from patent	gb_pat:AX069293	-	16.00	97.74	4.4e+03	31	I AX069293	Sequence 5 from Pat
gb_pat:AR028251	-	16.00	97.96	4.3e+03	30	I AR028251	Sequence 100 from Pat	gb_pat:AX100366	-	16.00	97.74	4.4e+03	31	I AX100366	Sequence 6 from Pat
gb_pat:AR028271	-	16.00	97.96	4.3e+03	30	I AR028271	Sequence 108 from patent	gb_pat:AX113882	-	16.00	97.74	4.4e+03	31	I AX113882	Sequence 30 from Pat
gb_pat:AR028271	-	16.00	97.96	4.3e+03	30	I AR028271	Sequence 122 from patent	gb_pat:AX115915	-	16.00	97.74	4.4e+03	31	I AX115915	Sequence 1038 from Pa
gb_pat:AR038488	-	16.00	97.96	4.3e+03	30	I AR038488	Sequence 85 from patent	gb_pat:AX159660	-	16.00	97.74	4.4e+03	31	I AX159660	Sequence 203 from Pat
gb_pat:AR064630	-	16.00	97.96	4.3e+03	30	I AR064630	Sequence 85 from patent	gb_pat:AX221242	-	16.00	97.74	4.4e+03	31	I AX221242	Sequence 69 from Pat
gb_pat:AR064882	-	16.00	97.96	4.3e+03	30	I AR064882	Sequence 7 from patent	gb_pat:AX221248	-	16.00	97.74	4.4e+03	31	I AX221248	Sequence 6684 from Pa
gb_pat:AR064925	+	16.00	97.96	4.3e+03	30	I AR064925	Sequence 50 from patent	gb_pat:AX223359	-	16.00	97.74	4.4e+03	31	I AX223359	Sequence 8801 from Pa
gb_pat:AR067555	-	16.00	97.96	4.3e+03	30	I AR067555	Sequence 85 from patent	gb_pat:AX223469	-	16.00	97.74	4.4e+03	31	I AX223469	Sequence 8911 from Pa
gb_pat:AR082883	-	16.00	97.96	4.3e+03	30	I AR082883	Sequence 16 from patent	gb_pat:AX232350	-	16.00	97.74	4.4e+03	31	I AX232350	Sequence 8942 from Pa
gb_pat:AR084895	-	16.00	97.96	4.3e+03	30	I AR084895	Sequence 40 from patent	gb_pat:AX248129	-	16.00	97.74	4.4e+03	31	I AX248129	Sequence 208 from Pa
gb_pat:AR103197	-	16.00	97.96	4.3e+03	30	I AR103197	Sequence 91 from patent	gb_pat:AX248178	-	16.00	97.74	4.4e+03	31	I AX248178	Sequence 257 from Pa
gb_pat:AR110027	-	16.00	97.96	4.3e+03	30	I AR110027	Sequence 28 from patent	gb_pat:AX248235	+	16.00	97.74	4.4e+03	31	I AX248235	Sequence 314 from Pa
gb_pat:AR134337	-	16.00	97.96	4.3e+03	30	I AR134337	Sequence 20 from patent	gb_pat:AX249293	-	16.00	97.74	4.4e+03	31	I AX249293	Sequence 1372 from Pa
gb_pat:AR138571	-	16.00	97.96	4.3e+03	30	I AR138571	Sequence 96 from patent	gb_pat:AX252349	+	16.00	97.74	4.4e+03	31	I AX252349	Sequence 18 from Pa
gb_pat:AR138571	-	16.00	97.96	4.3e+03	30	I AR138571	Sequence 96 from patent	gb_pat:AX252350	+	16.00	97.74	4.4e+03	31	I AX252350	Sequence 19 from Pa

gb_pat:BD002609	+	16.00	97.74	4.4e+03	31	BD002609	Gene composition and me	gb_pat:AX007104	+	16.00	97.32	4.7e+03	33	AX007104	Sequence 4 from Pat
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gb_pat:AR76289	+	16.00	97.53	4.5e+03	32	AR76289	Sequence 12 from Patent W	gb_pat:BD008459	+	16.00	97.32	4.7e+03	33	BD008459	Targeting adenovirus
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gb_pat:AR020449	-	16.00	97.53	4.5e+03	32	AR020449	Sequence 1 from patent	gb_pat:I45569	+	16.00	97.32	4.7e+03	33	I45569	Sequence 4 from patent
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gb_pat:I16939	-	16.00	97.53	4.5e+03	32	I16939	Sequence 8 from Patent US	gb_pat:AR162956	-	16.00	97.12	4.8e+03	34	AR162956	Sequence 11 from Patent
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gb_pat:I121848	-	16.00	97.53	4.5e+03	32	I121848	Sequence 3 from Patent US	gb_pat:AX068844	-	16.00	97.12	4.8e+03	34	AX068844	Sequence 4 from Patent
gb_pat:I21982	+	16.00	97.53	4.5e+03	32	I21982	Sequence 68 from Patent US	gb_pat:AX100352	+	16.00	97.12	4.8e+03	34	AX100352	Sequence 35 from Patent
gb_pat:I45733	+	16.00	97.53	4.5e+03	32	I45733	Sequence 8 from Patent US	gb_pat:AX180829	+	16.00	97.12	4.8e+03	34	AX180829	Sequence 6 from Patent
gb_pat:I51731	-	16.00	97.53	4.5e+03	32	I51731	Sequence 52 from Patent US	gb_pat:AX183973	+	16.00	97.12	4.8e+03	34	AX183973	Sequence 1726 from P
gb_pat:I60422	-	16.00	97.53	4.5e+03	32	I60422	Sequence 9 from Patent US	gb_pat:AX202205	+	16.00	97.12	4.8e+03	34	AX202205	Sequence 10 from Patent
gb_pat:I74482	+	16.00	97.53	4.5e+03	32	I74482	Sequence 61 from Patent US	gb_pat:AX350106	+	16.00	97.12	4.8e+03	34	AX350106	Sequence 629 from Patent
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gb_pat:I75246	+	16.00	97.53	4.5e+03	32	I75246	Sequence 18 from Patent US	gb_pat:AX351961	+	16.00	97.12	4.8e+03	34	AX351961	Sequence 257 from Patent
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 gb_pat:AR037793 - 16.00 96.93 4.9e+03 35 1 AR037793 Sequence 11 from patent
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 gb_pat:AR043620 - 16.00 96.93 4.9e+03 35 1 AR043620 Sequence 5 from patent
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DEFINITION Sequence 2 from patent US 6008400.

ACCESSION AR096851

VERSION AR096851.1 GI:10026020

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 10)

AUTHORS Scaringe,S. and Caruthers,M.H.

TITLE Orthoester reagents for use as protecting groups in oligonucleotide

JOURNAL synthesis

FEATURES Patent: US 6008400-A 2 28-DEC-1999;

source Location/Qualifiers

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seq_documentation_block:
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DEFINITION Sequence 3 from patent US 6008400.

ACCESSION AR096852

VERSION AR096852.1 GI:10026022

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 10)

AUTHORS Scaringe,S. and Caruthers,M.H.

TITLE Orthoester reagents for use as protecting groups in oligonucleotide

JOURNAL synthesis

FEATURES Patent: US 6008400-A 3 28-DEC-1999;

source Location/Qualifiers

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DEFINITION Sequence 110 from Patent WO0185941.

ACCESSION AX301396

VERSION AX301396.1 GI:17382479

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Versteeg,R. and Caron,H.N.

TITLE Myc targets

JOURNAL Patent: WO 0185941-A 110 15-NOV-2001;

Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)

FEATURES Location/Qualifiers

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LOCUS AX301521 10 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 235 from Patent WO0185941.

ACCESSION AX301521

VERSION AX301521.1 GI:17382604

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Versteeg,R. and Caron,H.N.

TITLE Myc targets

JOURNAL Patent: WO 0185941-A 235 15-NOV-2001;

Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)

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DEFINITION Sequence 54 from Patent WO0100816.
ACCESSION AX061320
VERSION AX061320.1 GI:12406455
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 11)
AUTHORS Lexow,P.
TITLE Methods of cloning and producing fragment chains with readable
information content
JOURNAL Patent: WO 0100816-A 54 04-JAN-2001;
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DEFINITION Sequence 3 from Patent WO0121833.
ACCESSION AX100363
VERSION AX100363.1 GI:13619379
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 11)
AUTHORS Bayliffe,A.I., Docter,E., Kelly,S.J. and Robertson,N.H.
TITLE Assay for detection of human cfr allele variants using specific
diagnostic primers
JOURNAL Patent: WO 0121833-A 3 29-MAR-2001;
Astrazeneca AB (SE)
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DEFINITION Sequence 13 from Patent WO9641812.
ACCESSION AS8733
VERSION AS8733.1 GI:3714275
KEYWORDS
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ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Brownlee,G.G., Lowe,G. and Fodor,E.
TITLE OLIGONUCLEOTIDE PHOSPHORYLATION METHOD AND PRODUCTS
JOURNAL Patent: WO 9641812-A 13 27-DEC-1996;
ISIS INNOVATION (GB)
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/db_xref="taxon:32644"
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ORIGIN
alignment_scores:
  Quality:      16.00      Length:      3
  Ratio:        5.333      Gaps:      0
  Percent Similarity: 100.000      Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x AS8733/rev ..
Align seg 1/1 to reverse of: AS8733 from: 1 to: 12
1 LysLysAsn 3
9 AAAAAAAAAAC 1
seq_name: gb_pat:AR162081
seq_documentation_block:
LOCUS AR162081 12 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 9 from patent US 6258558.
ACCESSION AR162081
VERSION AR162081.1 GI:16229145
KEYWORDS
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Szostak,J.W., Roberts,R.W. and Liu,R.
TITLE Method for selection of proteins using RNA-protein fusions
JOURNAL Patent: US 6258558-A 9 10-JUL-2001;
FEATURES Location/Qualifiers
source 1..12
BASE COUNT 10 a 2 c 0 g 0 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AR162081 ..
Align seg 1/1 to: AR162081 from: 1 to: 12

1 LysLysAsn 3
|||||
3 AAAAAAAC 11

seq_name: gb_pat:AR166606

seq_documentation_block:
LOCUS AR166606 12 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 9 from patent US 6281344.
ACCESSION AR166606
VERSION AR166606.1 GI:16241998
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Szostak,J.W., Roberts,R.W. and Liu,R.
TITLE Nucleic acid-protein fusion molecules and libraries
JOURNAL Patent: US 6281344-A 9 28-AUG-2001;
FEATURES Location/Qualifiers
source 1..12
BASE COUNT 10 a 2 c 0 g 0 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AR166606 ..
Align seg 1/1 to: AR166606 from: 1 to: 12

1 LysLysAsn 3
|||||
3 AAAAAAAC 11

seq_name: gb_pat:AX175319

seq_documentation_block:
LOCUS AX175319 12 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 83 from Patent WO0144465.
ACCESSION AX175319
VERSION AX175319.1 GI:14598687
KEYWORDS
SOURCE synthetic construct.

ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 12)
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 83 21-JUN-2001;
FEATURES Location/Qualifiers
source 1..12
BASE COUNT 0 a 0 c 2 g 10 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AX175319/rev ..
Align seg 1/1 to reverse of: AX175319 from: 1 to: 12

1 LysLysAsn 3
|||||
11 AAAAAAAC 3

seq_name: gb_pat:AR012701

seq_documentation_block:
LOCUS AR012701 13 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5763591.
ACCESSION AR012701
VERSION AR012701.1 GI:3971019
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Toyoda,H. and Formby,B.
TITLE Polynucleic acid sequences that are functionally associated with
the development of autoimmune disease
JOURNAL Patent: US 5763591-A 3 09-JUN-1998;
FEATURES Location/Qualifiers
source 1..13
BASE COUNT 1 a 1 c 0 g 11 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AR012701/rev ..
Align seg 1/1 to reverse of: AR012701 from: 1 to: 13

1 LysLysAsn 3
|||||
10 AAAAAAAT 2

seq_name: gb_pat:AR029782

seq_documentation_block:
LOCUS AR029782 13 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5861242.
ACCESSION AR029782
VERSION AR029782.1 GI:5942996


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seq_name: gb_pat:A88063
seq_documentation_block:
LOCUS A88063 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 211 from Patent WO9833904.
ACCESSION A88063
VERSION A88063.1 GI:6736633
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 211 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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1 t
BASE COUNT 10 a 2 c 1 g 1 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x A88063 ..
Align seg 1/1 to: A88063 from: 1 to: 14

1 LysLysAsn 3
|||||
2 AAAAAAAC 10

seq_name: gb_pat:A88065
seq_documentation_block:
LOCUS A88065 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 213 from Patent WO9833904.
ACCESSION A88065
VERSION A88065.1 GI:6736635
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 213 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
1..14
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/db_xref="taxon:32644"
1 t
BASE COUNT 10 a 2 c 1 g 1 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x A88065 ..
Align seg 1/1 to: A88065 from: 1 to: 14

1 LysLysAsn 3
|||||
2 AAAAAAAC 10

seq_name: gb_pat:A88107
seq_documentation_block:
LOCUS A88107 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 255 from Patent WO9833904.
ACCESSION A88107
VERSION A88107.1 GI:6736677
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 255 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
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/db_xref="taxon:32644"
1 t
BASE COUNT 10 a 2 c 1 g 1 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x A88107 ..
Align seg 1/1 to: A88107 from: 1 to: 14

1 LysLysAsn 3
|||||
2 AAAAAAAC 10

seq_name: gb_pat:A88110
seq_documentation_block:
LOCUS A88110 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 258 from Patent WO9833904.
ACCESSION A88110
VERSION A88110.1 GI:6736680
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 258 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
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/db_xref="taxon:32644"
2 t
BASE COUNT 9 a 2 c 1 g 2 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x A88110 ..
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Align seg 1/1 to: A88110 from: 1 to: 14

1 LysLysAsn 3
|||||
6 AAAAAAAC 14

seq_name: gb_pat:A90030

seq_documentation_block:

LOCUS A90030 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 211 from Patent EP0856579.
ACCESSION A90030
VERSION A90030.1 GI:6738544

KEYWORDS
SOURCE
ORGANISM

unidentified.

unclassified.

REFERENCE 1 (bases 1 to 14)

AUTHORS Brysch,W.D. and Schlingensiepen,K.D.

TITLE An antisense oligonucleotide preparation method

JOURNAL Patent: EP 0856579-A 211 05-AUG-1998;

KEYWORDS BIOGNOSTIK GES (DE)

FEATURES Location/Qualifiers

source

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/db_xref="taxon:32644"

BASE COUNT 10 a 2 c 1 g 1 t

ORIGIN

alignment_scores:

Quality: 16.00 Length: 3

Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x A90030 ..

Align seg 1/1 to: A90030 from: 1 to: 14

1 LysLysAsn 3
|||||
2 AAAAAAAC 10

seq_name: gb_pat:A90032

seq_documentation_block:

LOCUS A90032 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 213 from Patent EP0856579.
ACCESSION A90032
VERSION A90032.1 GI:6738546

KEYWORDS

SOURCE

unidentified.

unclassified.

REFERENCE 1 (bases 1 to 14)

AUTHORS Brysch,W.D. and Schlingensiepen,K.D.

TITLE An antisense oligonucleotide preparation method

JOURNAL Patent: EP 0856579-A 213 05-AUG-1998;

KEYWORDS BIOGNOSTIK GES (DE)

FEATURES Location/Qualifiers

source

1..14

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/db_xref="taxon:32644"

BASE COUNT 10 a 2 c 1 g 1 t

ORIGIN

alignment_scores:

Quality: 16.00 Length: 3

Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x A90032 ..

Align seg 1/1 to: A90032 from: 1 to: 14

1 LysLysAsn 3
|||||
4 AAAAAAAC 12

seq_name: gb_pat:A90074

seq_documentation_block:

LOCUS A90074 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 255 from Patent EP0856579.
ACCESSION A90074
VERSION A90074.1 GI:6738588

KEYWORDS

SOURCE

unidentified.

unclassified.

REFERENCE 1 (bases 1 to 14)

AUTHORS Brysch,W.D. and Schlingensiepen,K.D.

TITLE An antisense oligonucleotide preparation method

JOURNAL Patent: EP 0856579-A 255 05-AUG-1998;

KEYWORDS BIOGNOSTIK GES (DE)

FEATURES Location/Qualifiers

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/db_xref="taxon:32644"

BASE COUNT 10 a 2 c 1 g 1 t

ORIGIN

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Quality: 16.00 Length: 3

Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x A90074 ..

Align seg 1/1 to: A90074 from: 1 to: 14

1 LysLysAsn 3
|||||
2 AAAAAAAC 10

seq_name: gb_pat:A90077

seq_documentation_block:

LOCUS A90077 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 258 from Patent EP0856579.
ACCESSION A90077
VERSION A90077.1 GI:6738591

KEYWORDS

SOURCE

unidentified.

unclassified.

REFERENCE 1 (bases 1 to 14)

AUTHORS Brysch,W.D. and Schlingensiepen,K.D.

TITLE An antisense oligonucleotide preparation method

JOURNAL Patent: EP 0856579-A 258 05-AUG-1998;

KEYWORDS BIOGNOSTIK GES (DE)

FEATURES Location/Qualifiers

source

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/db_xref="taxon:32644"

BASE COUNT 9 a 2 c 1 g 2 t

ORIGIN

alignment_scores:

Quality: 16.00 Length: 3

Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x A90077 ..

Align seg 1/1 to: A90077 from: 1 to: 14

1 LysLysAsn 3
|||||
6 AAAAAAGAAC 14

seq_name: gb_pat:AR031685

seq_documentation_block:

LOCUS AR031685 14 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5866395.
ACCESSION AR031685
VERSION AR031685.1 GI:5945974
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Mathur,E.J.
TITLE Purified thermostable pyrococcus furiosus DNA polymerase I
JOURNAL Patent: US 5866395-A 5 02-FEB-1999;
FEATURES
source 1..14
BASE COUNT 6 a 0 c 2 t 4 others
ORIGIN

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AR031685 ..

Align seg 1/1 to: AR031685 from: 1 to: 14

1 LysLysAsn 3
|||||
4 AAAAAAAY 12

seq_name: gb_pat:AR031686

seq_documentation_block:

LOCUS AR031686 14 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5866395.
ACCESSION AR031686
VERSION AR031686.1 GI:5945975
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Mathur,E.J.
TITLE Purified thermostable pyrococcus furiosus DNA polymerase I
JOURNAL Patent: US 5866395-A 6 02-FEB-1999;
FEATURES
source 1..14
BASE COUNT 2 a 2 c 0 g 6 t 4 others
ORIGIN

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AR031686/rev ..

Align seg 1/1 to reverse of: AR031686 from: 1 to: 14

1 LysLysAsn 3
|||||
11 AAAAAAAY 3

seq_name: gb_pat:AR051240

seq_documentation_block:

LOCUS AR051240 14 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5830558.
ACCESSION AR051240
VERSION AR051240.1 GI:5974604
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
macromolecular structures
JOURNAL Patent: US 5830658-A 8 03-NOV-1998;
FEATURES
source 1..14
BASE COUNT 12 a 2 c 0 g 0 t
ORIGIN

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AR051240 ..

Align seg 1/1 to: AR051240 from: 1 to: 14

1 LysLysAsn 3
|||||
6 AAAAAAAY 14

seq_name: gb_pat:AR072886

seq_documentation_block:

LOCUS AR072886 14 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 5 from patent US 5948663.
ACCESSION AR072886
VERSION AR072886.1 GI:9999649
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Mathur,E.J.
TITLE Purified thermostable pyrococcus furiosus DNA polymerase I
JOURNAL Patent: US 5948663-A 5 07-SEP-1999;
FEATURES
source 1..14
BASE COUNT 6 a 0 c 2 g 2 t 4 others
ORIGIN

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AR072886 ..

Align seg 1/1 to: AR072886 from: 1 to: 14

1 LysLysAsn 3
|||||
4 AARARAAAY 12

seq_name: gb_pat:AR072887

seq_documentation_block:

LOCUS AR072887 14 bp DNA linear PAT 28-AUG-2000

DEFINITION Sequence 6 from patent US 5948663.

ACCESSION AR072887

VERSION AR072887.1 GI:9999650

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 14)

AUTHORS Mathur,E.J.

TITLE Purified thermostable pyrococcus furiosus DNA polymerase I

JOURNAL Patent: US 5948663-A 6 07-SEP-1999;

FEATURES Location/Qualifiers

1..14

BASE COUNT 2 a 2 c 0 g 6 t 4 others

ORIGIN

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AR072887/rev ..

Align seg 1/1 to reverse of: AR072887 from: 1 to: 14

1 LysLysAsn 3
|||||
11 AARARAAAY 3

seq_name: gb_pat:AR074714

seq_documentation_block:

LOCUS AR074714 14 bp DNA linear PAT 28-AUG-2000

DEFINITION Sequence 11 from patent US 5955276.

ACCESSION AR074714

VERSION AR074714.1 GI:10001467

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 14)

AUTHORS Morgante,M. and Vogel,J.Marie.

TITLE Compound microsatellite primers for the detection of genetic

polymorphisms

JOURNAL Patent: US 5955276-A 11 21-SEP-1999;

FEATURES Location/Qualifiers

1..14

BASE COUNT 0 a 2 c 2 g 10 t

ORIGIN

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AR074714/rev ..

Align seg 1/1 to reverse of: AR074714 from: 1 to: 14

1 LysLysAsn 3
|||||
12 AAAAAAAC 4

seq_name: gb_pat:AR119038

seq_documentation_block:

LOCUS AR119038 14 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 164 from patent US 6150092.

ACCESSION AR119038

VERSION AR119038.1 GI:14100948

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 14)

AUTHORS Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.

TITLE Antisense nucleic acid compound targeted to VEGF

JOURNAL Patent: US 6150092-A 164 21-NOV-2000;

FEATURES Location/Qualifiers

1..14

BASE COUNT 2 a 3 c 1 g 8 t

ORIGIN

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AR119038/rev ..

Align seg 1/1 to reverse of: AR119038 from: 1 to: 14

1 LysLysAsn 3
|||||
11 AAGAAAAAT 3

seq_name: gb_pat:AR127787

seq_documentation_block:

LOCUS AR127787 14 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 8 from patent US 6180777.

ACCESSION AR127787

VERSION AR127787.1 GI:14114382

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 14)

AUTHORS Horn,T.

TITLE Synthesis of branched nucleic acids

JOURNAL Patent: US 6180777-A 8 30-JAN-2001;

FEATURES Location/Qualifiers

1..14

BASE COUNT 12 a 2 c 0 g 0 t

ORIGIN

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000


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alignment_block:
US-09-528-682-2 x AR127787 ..
Align seg 1/1 to: AR127787 from: 1 to: 14

1 LysLysAsn 3
|||||
6 AAAAAAAC 14

seq_name: gb_pat:124766

seq_documentation_block:
LOCUS 124766 14 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 5 from patent US 5545552.
ACCESSION 124766
VERSION 124766.1 GI:1604636
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Mathur,E.J.
TITLE Purified thermostable pyrococcus furiosus DNA polymerase I
JOURNAL Patent: US 5545552-A 5 13-AUG-1996;
FEATURES
Location/Qualifiers
1..14
source
BASE COUNT 6 a 2 c 4 g 2 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x 124766 ..
Align seg 1/1 to: 124766 from: 1 to: 14

1 LysLysAsn 3
|||||
4 AAGAAGAAC 12

seq_name: gb_pat:124767

seq_documentation_block:
LOCUS 124767 14 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 6 from patent US 5545552.
ACCESSION 124767
VERSION 124767.1 GI:1604637
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Mathur,E.J.
TITLE Purified thermostable pyrococcus furiosus DNA polymerase I
JOURNAL Patent: US 5545552-A 6 13-AUG-1996;
FEATURES
Location/Qualifiers
1..14
source
BASE COUNT 2 a 4 c 2 g 6 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x I24767/rev ..
Align seg 1/1 to reverse of: I24767 from: 1 to: 14

1 LysLysAsn 3
|||||
11 AAGAAGAAC 3

seq_name: gb_pat:128369

seq_documentation_block:
LOCUS 128369 14 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 8 from patent US 5571677.
ACCESSION 128369
VERSION 128369.1 GI:1819145
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Gryznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
macromolecular structures
JOURNAL Patent: US 5571677-A 8 05-NOV-1996;
FEATURES
Location/Qualifiers
1..14
source
BASE COUNT 12 a 2 c 0 g 0 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x I28369 ..
Align seg 1/1 to: I28369 from: 1 to: 14

1 LysLysAsn 3
|||||
6 AAAAAAAC 14

seq_name: gb_pat:A65238

seq_documentation_block:
LOCUS A65238 15 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 2 from Patent WO9735869.
ACCESSION A65238
VERSION A65238.1 GI:4531033
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Baxter,A.D., Baylis,E.K., Collingwood,S., Paul, Fairhurst,R.A. and
Taylor,R.J.
TITLE DINUCLEOTIDE AND OLIGONUCLEOTIDE ANALOGUES
JOURNAL Patent: WO 9735869-A 2 02-OCT-1997;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 2103197 19971017.
FEATURES
Location/Qualifiers
1..15
source
BASE COUNT 0 a 2 c 4 g 9 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x A65238/rev ..

Align seg 1/1 to reverse of: A65238 from: 1 to: 15

1 LysLysAsn 3
|||||
11 AAAAAAAC 3

seq_name: gb_pat:A88106

seq_documentation_block:

LOCUS A88106 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 254 from Patent WO9833904.
ACCESSION A88106
VERSION A88106.1 GI:6736676

KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
unclassified.

REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 254 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)

FEATURES
source
1..15
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 11 a 2 c 1 g 1 t
ORIGIN

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x A88106 ..

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2 AAAAAAAC 10

seq_name: gb_pat:A88108

seq_documentation_block:

LOCUS A88108 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 256 from Patent WO9833904.
ACCESSION A88108
VERSION A88108.1 GI:6736678

KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
unclassified.

REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 256 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)

FEATURES
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alignment_block:

US-09-528-682-2 x A88108 ..

Align seg 1/1 to: A88108 from: 1 to: 15

1 LysLysAsn 3
|||||
5 AAAAAAAC 13

seq_name: gb_pat:A90073

seq_documentation_block:

LOCUS A90073 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 254 from Patent EP0856579.
ACCESSION A90073
VERSION A90073.1 GI:6738587

KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
unclassified.

REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 254 05-AUG-1998;
BIOGNOSTIK GES (DE)

FEATURES
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Location/Qualifiers
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/db_xref="taxon:32644"

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ORIGIN

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Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x A90073 ..

Align seg 1/1 to: A90073 from: 1 to: 15

1 LysLysAsn 3
|||||
2 AAAAAAAC 10

seq_name: gb_pat:A90075

seq_documentation_block:

LOCUS A90075 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 256 from Patent EP0856579.
ACCESSION A90075
VERSION A90075.1 GI:6738589

KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
unclassified.

REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 256 05-AUG-1998;
BIOGNOSTIK GES (DE)

FEATURES
source
1..15
Location/Qualifiers
/organism="unidentified"

FEATURES Location/Qualifiers
1..15
source 1 a 0 c 1 g 13 t
BASE COUNT
ORIGIN

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Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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11 AAAAAAAT 3

seq_name: gb_pat:AR056155

seq_documentation_block:

LOCUS AR056155 15 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 359 from patent US 5837542.

ACCESSION AR056155

VERSION AR056155.1 GI:5981732

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 15)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.

TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes

JOURNAL Patent: US 5837542-A 359 17-NOV-1998;

FEATURES Location/Qualifiers

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source

/organism="unknown"

BASE COUNT 1 a 0 c 1 g 13 t

ORIGIN

alignment_scores:
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Percent Similarity: 100.000 Percent Identity: 100.000

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10 AAAAAAAT 2

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seq_documentation_block:

LOCUS AR056156 15 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 360 from patent US 5837542.

ACCESSION AR056156

VERSION AR056156.1 GI:5981733

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 15)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.

TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes

JOURNAL Patent: US 5837542-A 360 17-NOV-1998;
FEATURES Location/Qualifiers
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source 1 a 0 c 0 g 14 t
BASE COUNT
ORIGIN

alignment_scores:
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Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AR056156/rev ..

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9 AAAAAAAT 1

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seq_documentation_block:

LOCUS AR079608 15 bp DNA linear PAT 31-AUG-2000

DEFINITION Sequence 3 from patent US 5965721.

ACCESSION AR079608

VERSION AR079608.1 GI:10006352

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 15)

AUTHORS Cook,P.Dan, Sanghvi,Y.Shantilal, Vasseur,J.Jacques and Debart,F.
TITLE Backbone modified oligonucleotide analogues

JOURNAL Patent: US 5965721-A 3 12-OCT-1999;

FEATURES Location/Qualifiers

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/organism="unknown"

BASE COUNT 0 a 2 c 3 g 10 t

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alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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11 AAAAAAAC 3

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seq_documentation_block:

LOCUS AR113909 15 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 355 from patent US 6132967.

ACCESSION AR113909

VERSION AR113909.1 GI:14094231

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 15)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.

TITLE Ribozyme treatment of diseases or conditions related to levels of

intercellular adhesion molecule-1 (ICAM-1)
Patent: US 6132967-A 355 17-OCT-2000;
Location/Qualifiers
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Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AR113909/rev ..

Align seg 1/1 to reverse of: AR113909 from: 1 to: 15

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|||||
14 AAAAAAAT 6

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seq_documentation_block:
LOCUS AR113910 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 356 from patent US 6132967.
ACCESSION AR113910
VERSION AR113910.1 GI:14094232

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.

TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)

JOURNAL Patent: US 6132967-A 356 17-OCT-2000;

FEATURES
Location/Qualifiers
1. .15
/organism="unknown"

BASE COUNT 1 a 0 c 1 g 13 t
ORIGIN

alignment_scores:
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Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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|||||
13 AAAAAAAT 5

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LOCUS AR113911 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 357 from patent US 6132967.
ACCESSION AR113911
VERSION AR113911.1 GI:14094233

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 357 17-OCT-2000;
FEATURES
Location/Qualifiers
1. .15
source

BASE COUNT 1 a 0 c 1 g 13 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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|||||
12 AAAAAAAT 4

seq_name: gb_pat:AR113912

seq_documentation_block:
LOCUS AR113912 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 358 from patent US 6132967.
ACCESSION AR113912
VERSION AR113912.1 GI:14094234

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.

TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)

JOURNAL Patent: US 6132967-A 358 17-OCT-2000;

FEATURES
Location/Qualifiers
1. .15
source

BASE COUNT 1 a 0 c 1 g 13 t
ORIGIN

alignment_scores:
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Ratio: 5.333 Gaps: 0
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11 AAAAAAAT 3

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Date: Jun 18, 2002 7:39 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH71052	+	16.00	101.07	2.8e+03
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/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH71292	+	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH71359	+	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH71401	+	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH71441	+	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH71442	-	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH71473	+	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH71622	-	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH71699	-	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH72193	+	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH72249	+	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH72262	-	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH72306	+	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH72500	+	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH72501	-	16.00	101.07	2.8e+03
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH72568	-	16.00	101.07	2.8e+03

/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABC56537 + 16.00 100.49 3.0e+03
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABC56950 - 16.00 100.49 3.0e+03
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABC56951 + 16.00 100.49 3.0e+03
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABC57548 - 16.00 100.49 3.0e+03
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABC57549 + 16.00 100.49 3.0e+03
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABC57630 - 16.00 100.49 3.0e+03
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABC57631 + 16.00 100.49 3.0e+03
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABC57956 - 16.00 100.49 3.0e+03
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABC57957 + 16.00 100.49 3.0e+03
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABC58202 - 16.00 100.49 3.0e+03
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABC58203 + 16.00 100.49 3.0e+03

seq_name: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:AAV50073

seq_documentation_block:

ID AAV50073 standard; DNA; 10 BP.

XX AAV50073;

DT 21-OCT-1998 (first entry)

XX Yeast tag for highly expressed gene PYK1.

XX Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle;

KW regulation; eukaryotic cell; antifungal; SAGE tag; gene expression;

XX serial analysis of gene expression; probe; ss.

OS Saccharomyces cerevisiae.

OS Synthetic.

XX WO9832847-A2.

XX 30-JUL-1998.

XX 22-JAN-1998; 98WO-US01216.

XX 23-JAN-1997; 97US-0035917.

XX (UWJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Kinzler KW, Velculescu VE, Vogelstein B;

XX WPI; 1998-427943/36.

XX Yeast transcriptome - useful for modulating eukaryotic cell, for
PT screening antifungal agents, and for identifying genes in cell cycle
PT progression

XX Claim 11; Page 21; 44pp; English.

XX Yeast transcriptome is encoded by a DNA molecule comprising a yeast
CC gene involved in cell cycle progression selected from the group of
CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC tags for highly expressed genes and NORF genes are given in AAV50051 to
CC AAV50345. The present invention describes: (1) a method of using yeast
CC genes to modulate the cell cycle which comprises administering to a cell
CC an isolated DNA molecule comprising a yeast gene which is involved in
CC cell cycle progression selected from differentially expressed genes
CC (SAGE tags given in AAV50051 to AAV50345); (2) a method for screening
CC candidate antifungal drugs which comprises contacting a test substance
CC with a yeast cell and monitoring expression of a yeast gene which is
CC involved in cell cycle progression; (3) a method of identifying human
CC genes which are involved in cell cycle progression which comprises
CC hybridizing a probe comprising at least 10 contiguous nucleotides of a
CC yeast gene which is differentially expressed between at least 2 phases
CC selected from the log phase, the S phase and the G2/M phase; and (4) a
CC probe for ascertaining the phase in the cell cycle, where the probe
CC comprises at least 14 contiguous nucleotides of a NORF gene (SAGE tags
CC given in AAV50051 to AAV50345), or as an array of probes on a solid
CC support.

XX Sequence 10 BP; 0 A; 1 C; 1 G; 8 T; 0 other;

50

alignment_scores:

Quality: 16.00 Length: 3

Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AAV50073/rev ..

Align seg 1/1 to reverse of: AAV50073 from: 1 to: 10

1 LysLysAsn 3

|||||

9 AAGAAAAAC 1

seq_name: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAZ86504

seq_documentation_block:

ID AAZ86504 standard; DNA; 10 BP.

XX AAZ86504;

DT 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #5738.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

XX antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

XX WO9965928-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US13647.

XX 19-JUN-1998; 98US-0089853.

XX 19-JUN-1998; 98US-0089997.

XX 19-JUN-1998; 98US-0090039.

XX 19-JUN-1998; 98US-0090040.

XX 19-JUN-1998; 98US-0090041.

XX (GENZ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

XX WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic
CC and non-metastatic breast cancer cells, useful for diagnosis,
CC prevention and treatment of cancer -
PS Claim 1; Page 210; 219pp; English.

XX AAZ80767 to AAZ83941 represent tags corresponding to distinct
CC transcripts that are preferentially transcribed in the metastatic breast
CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the primary or non-metastatic
CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
CC cells). These transcripts can be used for diagnosis, prognosis, metastatic
CC monitoring and treatment of breast cancer, particularly where metastatic.
CC diagnosis is by standard immunoassays or hybridisation/amplification
CC reactions. Compounds that modulate expression of the transcripts are
CC potentially useful for treatment of (metastatic) breast cancer, while
CC promoters from the transcripts are used to direct expression, in selected
CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
CC sequences), particularly an antigen-encoding sequence for use in gene or
CC cell-based vaccines. Polypeptides encoded by the transcripts are also

CC useful in vaccines; for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.

XX Sequence 10 BP; 2 A; 1 C; 0 G; 7 T; 0 other;

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-528-682-2 x AA286504/rev ..

Align seg 1/1 to reverse of: AA286504 from: 1 to: 10

1 LysLysasn 3
 |||||
 9 AAAAAGAT 1

seq_name: /SID85/gcgdata/geneseq/geneseq-emb1/NA286504.DAT:AAF29870

seq_documentation_block:
 ID AAF29870 standard; DNA; 10 BP.

XX AC AAF29870;
 XX DT 03-APR-2001 (first entry)
 XX DE Starting 1 fragment #3.
 XX KW Cloning; exon shuffling; store; adapter; ss.

XX OS Unidentified.

XX PN WO200100816-A1.

XX PD 04-JAN-2001.

XX PF 27-JUN-2000; 2000WO-GB02512.

XX PR 28-JUN-1999; 99NO-0001325.

XX PR 20-JUN-2000; 2000NO-0003190.

XX PR 20-JUN-2000; 2000NO-0003191.

XX (COMP-) COMPLETE GENOMICS AS.

XX PA (JONE/) JONES E L.

XX PI Lexow P;

XX WPI; 2001-123006/13.

XX Attaching fragments of first nucleic acids to second nucleic acids by
 PT use of adapters complementary to first single stranded regions on the
 PT first molecules but which have a different single stranded region at
 PT the other terminus -

PS Disclosure; Fig 2; 100pp; English.

XX The present invention relates to attaching a fragment of first and
 CC second nucleic acid molecules involves use of an adapter molecule
 CC which is complementary to a single stranded region generated on the
 CC target but which has a different single stranded region at its
 CC other terminus and therefore modifies single stranded regions
 CC presented for binding by the target. Attaching first and second
 CC nucleic acid molecules may be used in cloning. The method can
 CC also be used for exon shuffling other recombinations that are
 CC relevant in connection with artificial evolutionary systems.
 CC The fragment chains may be used to store information.

XX Sequence 10 BP; 9 A; 1 C; 0 G; 0 U; 0 other;

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-528-682-2 x AAF29870 ..

Align seg 1/1 to: AAF29870 from: 1 to: 10

1 LysLysasn 3
 |||||
 2 AAAAAAAC 10

seq_name: /SID85/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAF33290

seq_documentation_block:
 ID AAF33290 standard; DNA; 10 BP.

XX AC AAF33290;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast highly expressed gene SAGE tag oligonucleotide SEQ ID NO:29.

XX KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US16223.

XX PR 16-JUN-1999; 99US-0335032.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis
 PT of gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle -

XX Example; Page 21; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a
 CC yeast cell; and (b) monitoring expression of a NORF gene whose
 CC expression varies as in M1, where a test substance which modifies the
 CC expression of the yeast gene is a candidate antifungal drug; (3) a method
 CC (M3) for identifying human genes which are involved in cell cycle
 CC progression comprising contacting human DNA with a probe which comprises
 CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
 CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
 CC member of a class of drugs having a characteristic effect on gene

CC expression in a yeast cell comprising contacting a yeast cell with a
 CC candidate drug and monitoring expression in the yeast cell of at least 1
 CC NORF gene whose expression is affected by the class of drugs. The NORF
 CC genes may be used to study, monitor and affect phases of the cell cycle,
 CC the differentially expressed genes may be used as markers of phases of
 CC the cell cycle. The methods may be used to identify candidate drugs which
 CC affect the cell cycle and for identification of antifungal drugs.
 CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
 CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
 CC primers used in the SAGE method, in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 10 BP; 0 A; 1 C; 1 G; 8 T; 0 other;

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000
 alignment_block:
 US-09-528-682-2 x AAF33290/rev ..

Align seg 1/1 to reverse of: AAF33290 from: 1 to: 10

1 LysLysAsn 3
 |||||
 9 AAGAAAC 1

seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF34095

seq_documentation_block:
 ID AAF34095 standard; DNA; 10 BP.

XX AAF34095;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:834.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US16223.

XX 16-JUN-1999; 99US-0335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis
 PT of gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle -

XX Example; Page 29; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a
 CC yeast cell; and (b) monitoring expression of a NORF gene whose
 CC expression varies as in M1, where a test substance which modifies the
 CC expression of the yeast gene is a candidate antifungal drug; (3) a method
 CC (M3) for identifying human genes which are involved in cell cycle
 CC progression comprising contacting human DNA with a probe which comprises
 CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
 CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
 CC member of a class of drugs having a characteristic effect on gene
 CC expression in a yeast cell comprising contacting a yeast cell with a
 CC candidate drug and monitoring expression in the yeast cell of at least 1
 CC NORF gene whose expression is affected by the class of drugs. The NORF
 CC genes may be used to study, monitor and affect phases of the cell cycle,
 CC the differentially expressed genes may be used as markers of phases of
 CC the cell cycle. The methods may be used to identify candidate drugs which
 CC affect the cell cycle and for identification of antifungal drugs.
 CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
 CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
 CC primers used in the SAGE method, in the exemplification of the present
 CC invention.
 XX

SQ Sequence 10 BP; 0 A; 1 C; 1 G; 8 T; 0 other;

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-528-682-2 x AAF34095/rev ..

Align seg 1/1 to reverse of: AAF34095 from: 1 to: 10

1 LysLysAsn 3
 |||||
 9 AAGAAAC 1

seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF34588

seq_documentation_block:
 ID AAF34588 standard; DNA; 10 BP.

XX AAF34588;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1327.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US16223.

XX 16-JUN-1999; 99US-0335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis

PT of gene expression (SAGE) tags, useful for studying, monitoring and
 PF affecting phases of the cell cycle -
 PS Example; Page 47; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a
 CC yeast cell; and (b) monitoring expression of a NORF gene whose
 CC expression varies as in M1, where a test substance which modifies the
 CC expression of the yeast gene is a candidate antifungal drug; (3) a method
 CC (M3) for identifying human genes which are involved in cell cycle
 CC progression comprising contacting human DNA with a probe which comprises
 CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
 CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
 CC member of a class of drugs having a characteristic effect on gene
 CC expression in a yeast cell comprising contacting a yeast cell with a
 CC candidate drug and monitoring expression in the yeast cell of at least 1
 CC NORF gene whose expression is affected by the class of drugs. The NORF
 CC genes may be used to study, monitor and affect phases of the cell cycle,
 CC the differentially expressed genes may be used as markers of phases of
 CC the cell cycle. The methods may be used to identify candidate drugs which
 CC affect the cell cycle and for identification of antifungal drugs.
 CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
 CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
 CC primers used in the SAGE method, in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 0 G; 6 T; 0 other;

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-528-682-2 x AAF34588/rev ..

Align seg 1/1 to reverse of: AAF34588 from: 1 to: 10

1 LysLysAsn 3
 |||||
 10 AAGAAGAAT 2

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAF35488

seq_documentation_block:
 ID AAF35488 standard; DNA; 10 BP.
 XX
 AC AAF35488;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2227.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX

PF 14-JUN-2000; 2000WO-US16223.
 XX
 PR 16-JUN-1999; 99US-0335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Veiculescu V, Vogelstein B, Kinzler K;
 XX
 DR WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis
 PT of gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle -
 PS Example; Page 79; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a
 CC yeast cell; and (b) monitoring expression of a NORF gene whose
 CC expression varies as in M1, where a test substance which modifies the
 CC expression of the yeast gene is a candidate antifungal drug; (3) a method
 CC (M3) for identifying human genes which are involved in cell cycle
 CC progression comprising contacting human DNA with a probe which comprises
 CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
 CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
 CC member of a class of drugs having a characteristic effect on gene
 CC expression in a yeast cell comprising contacting a yeast cell with a
 CC candidate drug and monitoring expression in the yeast cell of at least 1
 CC NORF gene whose expression is affected by the class of drugs. The NORF
 CC genes may be used to study, monitor and affect phases of the cell cycle,
 CC the differentially expressed genes may be used as markers of phases of
 CC the cell cycle. The methods may be used to identify candidate drugs which
 CC affect the cell cycle and for identification of antifungal drugs.
 CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
 CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
 CC primers used in the SAGE method, in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 other;

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-528-682-2 x AAF35488/rev ..

Align seg 1/1 to reverse of: AAF35488 from: 1 to: 10

1 LysLysAsn 3
 |||||
 10 AAGAAGAAT 2

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAF36874

seq_documentation_block:
 ID AAF36874 standard; DNA; 10 BP.
 XX
 AC AAF36874;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3613.
 XX

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US16223.
XX
XX 16-JUN-1999; 99US-0335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
XX Example; Page 129; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
XX Sequence 10 BP; 9 A; 1 C; 0 G; 0 U; 0 other;

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AAF36874 ..

Align seg 1/1 to: AAF36874 from: 1 to: 10

1 LysLysAsn 3
|||||
2 AAAAAAAC 10

seq_name: /STDS5/gcdata/geneseq/geneseq-embl/NA2001A.DAT:AAF37316
seq_documentation_block:
ID AAF37316 standard; DNA; 10 BP.
XX
XX AAF37316;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4055.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX WO200077214-A2.
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US16223.
XX
XX 16-JUN-1999; 99US-0335032.
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
XX Example; Page 144; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
XX Sequence 10 BP; 1 A; 0 C; 0 G; 9 T; 0 other;

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AAF37316/rev ..

Align seg 1/1 to reverse of: AAF37316 from: 1 to: 10

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1 LysLysAsn 3
|||||
9 AAAAAAAT 1

```

seq_name: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF38396

seq_documentation_block:

ID AAF38396 standard; DNA; 10 BP.

XX AC AAF38396;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5135.

XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US16223.

XX PR 16-JUN-1999; 99US-0335032.

XX PA (UVJO) UNIV JOHNS HOPKINS.

XX PI Velculescu V, Vogelstein B, Kinzler K;

XX DR WPT; 2001-061874/07.

XX PT Yeast gene coding sequences comprising NORF genes with serial analysis
 PT of gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle -

XX PS Example; Page 183; 419pp; English.

XX CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a
 CC yeast cell; and (b) monitoring expression of a NORF gene whose
 CC expression varies as in M1, where a test substance which modifies the
 CC (M3) for identifying human genes which are involved in cell cycle
 CC progression comprising contacting human DNA with a probe which comprises
 CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
 CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
 CC member of a class of drugs having a characteristic effect on gene
 CC expression in a yeast cell comprising contacting a yeast cell with a
 CC candidate drug and monitoring expression in the yeast cell of at least 1
 CC NORF gene whose expression is affected by the class of drugs. The NORF
 CC genes may be used to study, monitor and affect phases of the cell cycle,
 CC the differentially expressed genes may be used as markers of phases of
 CC the cell cycle. The methods may be used to identify candidate drugs which
 CC affect the cell cycle and for identification of antifungal drugs.

CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
 CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
 CC primers used in the SAGE method, in the exemplification of the present
 CC invention.

XX SQ Sequence 10 BP; 9 A; 0 C; 0 G; 1 T; 0 other;

alignment_scores:

Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AAF38396 ..

Align seg 1/1 to: AAF38396 from: 1 to: 10

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1 LysLysAsn 3
|||||
2 AAAAAAAT 10

```

seq_name: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF38397

seq_documentation_block:

ID AAF38397 standard; DNA; 10 BP.

XX AC AAF38397;

XX DT 23-MAR-2001 (first entry)

XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5136.

XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.

XX PN WO200077214-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-US16223.

XX PR 16-JUN-1999; 99US-0335032.

XX PA (UVJO) UNIV JOHNS HOPKINS.

XX PI Velculescu V, Vogelstein B, Kinzler K;

XX DR WPT; 2001-061874/07.

XX PT Yeast gene coding sequences comprising NORF genes with serial analysis
 PT of gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle -

XX PS Example; Page 183; 419pp; English.

XX CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a
 CC yeast cell; and (b) monitoring expression of a NORF gene whose
 CC expression varies as in M1, where a test substance which modifies the
 CC expression of the yeast gene is a candidate antifungal drug; (3) a method
 CC (M3) for identifying human genes which are involved in cell cycle

CC progression comprising contacting human DNA with a probe which comprises
 CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
 CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
 CC member of a class of drugs having a characteristic effect on gene
 CC expression in a yeast cell comprising contacting a yeast cell with a
 CC candidate drug and monitoring expression in the yeast cell of at least 1
 CC NORF gene whose expression is affected by the class of drugs. The NORF
 CC genes may be used to study, monitor and affect phases of the cell cycle,
 CC the differentially expressed genes may be used as markers of phases of
 CC the cell cycle. The methods may be used to identify candidate drugs which
 CC affect the cell cycle and for identification of antifungal drugs.
 CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
 CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
 CC primers used in the SAGE method, in the exemplification of the present
 CC invention.
 CC XX
 CC SQ Sequence 10 BP; 8 A; 1 C; 0 G; 1 T; 0 other;

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-528-682-2 x AAF38397 ..

Align seg 1/1 to: AAF38397 from: 1 to: 10

1 LysLysAsn 3
 ||||||||
 1 AAAAAAAT 9

seq_name: /SID5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF38535

seq_documentation_block:
 ID AAF38535 standard; DNA; 10 BP.

AC AAF38535;
 XX
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5274.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

XX

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US16223.

XX 16-JUN-1999; 99US-0335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis
 PT of gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle -

XX Example; Page 188; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a
 CC yeast cell; and (b) monitoring expression of a NORF gene whose
 CC expression varies as in M1, where a test substance which modifies the
 CC expression of the yeast gene is a candidate antifungal drug; (3) a method
 CC (M3) for identifying human genes which are involved in cell cycle
 CC progression comprising contacting human DNA with a probe which comprises
 CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
 CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
 CC member of a class of drugs having a characteristic effect on gene
 CC expression in a yeast cell comprising contacting a yeast cell with a
 CC candidate drug and monitoring expression in the yeast cell of at least 1
 CC NORF gene whose expression is affected by the class of drugs. The NORF
 CC genes may be used to study, monitor and affect phases of the cell cycle,
 CC the differentially expressed genes may be used as markers of phases of
 CC the cell cycle. The methods may be used to identify candidate drugs which
 CC affect the cell cycle and for identification of antifungal drugs.
 CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
 CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
 CC primers used in the SAGE method, in the exemplification of the present
 CC invention.
 CC XX
 CC SQ Sequence 10 BP; 7 A; 1 C; 2 G; 0 U; 0 other;

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-528-682-2 x AAF38535 ..

Align seg 1/1 to: AAF38535 from: 1 to: 10

1 LysLysAsn 3
 ||||||||
 2 AAGAAGAAC 10

seq_name: /SID5/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF40328

seq_documentation_block:
 ID AAF40328 standard; DNA; 10 BP.

XX

XX AAF40328;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7067.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US16223.

XX 16-JUN-1999; 99US-0335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;


```
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 252; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF4064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33282 to AAF3267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
XX Sequence 10 BP; 1 A; 1 C; 0 G; 8 T; 0 other;
SQ
alignment_scores:
    Quality: 16.00 Length: 3
    Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x AAF40328/rev ..
Align seg 1/1 to reverse of: AAF40328 from: 1 to: 10
    1 LysLysAsn 3
    9 AAAAAAAT 1
seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAF40495
seq_documentation_block:
ID AAF40495 standard; DNA; 10 BP.
XX
XX AAF40495;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO: 7234.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
```

```
PN WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US16223.
XX
XX 16-JUN-1999; 99US-0335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Veiculescu V, Vogelstein B, Kinzler K;
PI WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 258; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF4064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33282 to AAF3267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
CC invention.
XX
XX Sequence 10 BP; 7 A; 1 C; 1 G; 1 T; 0 other;
SQ
alignment_scores:
    Quality: 16.00 Length: 3
    Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x AAF40495 ..
Align seg 1/1 to: AAF40495 from: 1 to: 10
    1 LysLysAsn 3
    2 AAGAAAAAT 10
seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAF41776
seq_documentation_block:
ID AAF41776 standard; DNA; 10 BP.
XX
XX AAF41776;
XX
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DT 23-MAR-2001 (first entry)
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8515.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US16223.
XX
XX 16-JUN-1999; 99US-0335032.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
XX Example; Page 304; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
XX invention.
XX
XX Sequence 10 BP; 6 A; 1 C; 3 G; 0 U; 0 other;
SQ

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AAF41776 ..
Align seg 1/1 to: AAF41776 from: 1 to: 10

1 LyslysAsn 3
|||||||
2 AAGAAGRAC 10
seq_name: /STD5/gcdata/geneseq/geneseq-emb1/NA2001A.DAT:AAF42242
seq_documentation_block:
ID AAF42242 standard; DNA; 10 BP.
XX
XX AC AAF42242;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8981.
XX
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US16223.
XX
XX 16-JUN-1999; 99US-0335032.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
XX Example; Page 320; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
XX invention.
XX
XX Sequence 10 BP; 1 A; 1 C; 1 G; 7 T; 0 other;
SQ

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AAF42242/rev ..

Align seg 1/1 to reverse of: AAF42242 from: 1 to: 10

1 LysLysAsn 3
|||||
10 AAGAAAAAT 2

seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH19036

seq_documentation_block:
ID AAH19036 standard; DNA; 11 BP.

XX
AC AAH19036;
XX
DT 26-JUN-2001 (first entry)
XX
DE Diagnostic variant primer #3.
XX
KW CTER; cystic fibrosis transmembrane conductance regulator; 5T; 7T;
KW 9T; ss.
XX
OS Homo sapiens.
XX
PN WO200121833-A2.
XX
PD 29-MAR-2001.

XX
PF 19-SEP-2000; 2000WO-GB03597.

XX
PR 24-SEP-1999; 99GB-0022527.

XX
PA (ASTR) ASTRAZENECA AB.

XX
PA (ASTR) ASTRAZENECA UK LTD.

XX
PI Bayliffe AI, Docter E, Kelly SJ, Robertson NH;

XX
WPI: 2001-308093/32.

XX
PT Detecting 5T, 7T and 9T alleles in intron 8 of the human cystic
PT fibrosis transmembrane conductance regulator comprises contacting a
PT nucleic acid sample with a multiplex of diagnostic primers comprising
PT 5T, 7T and 9T variant primers -

XX
PS Disclosure; Page 6; 73pp; English.

XX
CC The present invention relates to detecting 5T, 7T and 9T alleles in
CC intron 8 of the human cystic fibrosis transmembrane conductance
CC regulator (CFTR) gene. The method involves a multiplex of
CC diagnostic primers comprising 5T, 7T and 9T variant primers.
CC The invention is useful for simultaneous detection of variable length
CC polythymidine (polyT) tract alleles in the CFTR gene that are
CC associated with the phenotypic modulation of selected CFTR mutations.
CC The present sequence is a primer used in the invention.

XX
SQ Sequence 11 BP; 8 A; 1 C; 0 G; 1 T; 1 other;

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AAH19036 ..

Align seg 1/1 to: AAH19036 from: 1 to: 11

1 LysLysAsn 3
|||||
2 AAAAAAAT 10

seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF29873

seq_documentation_block:

ID AAF29873 standard; DNA; 11 BP.

XX
AC AAF29873;
XX
DT 03-APR-2001 (first entry)
XX
DE Starting 1 fragment #6.
XX
KW Cloning; exon shuffling; store; adapter; ss.
XX
OS Unidentified.
XX
PN WO200100816-A1.
XX
PD 04-JAN-2001.

XX
PF 27-JUN-2000; 2000WO-GB02512.

XX
PR 28-JUN-1999; 99NO-0001325.

XX
PR 20-JUN-2000; 2000NO-0003190.

XX
PR 20-JUN-2000; 2000NO-0003191.

XX
PA (COMP-) COMPLETE GENOMICS AS.

XX
PA (JONE/) JONES E L.

XX
PI Lexow P;

XX
WPI: 2001-123006/13.

XX
PT Attaching fragments of first nucleic acids to second nucleic acids by
PT use of adapters complementary to first single stranded regions on the
PT first molecules but which have a different single stranded region at
PT the other terminus -

XX
PS Disclosure; Fig 2; 100pp; English.

XX
CC The present invention relates to attaching a fragment of first and
CC second nucleic acid molecules involves use of an adapter molecule
CC which is complementary to a single stranded region generated on the
CC target but which has a different single stranded region at its
CC other terminus and therefore modifies single stranded regions
CC presented for binding by the target. Attaching first and second
CC nucleic acid molecules may be used in cloning. The method can
CC also be used for exon shuffling other recombinations that are
CC relevant in connection with artificial evolutionary systems.
CC The fragment chains may be used to store information.

XX
SQ Sequence 11 BP; 0 A; 1 C; 2 G; 8 T; 0 other;

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AAF29873/rev ..

Align seg 1/1 to reverse of: AAF29873 from: 1 to: 11

1 LysLysAsn 3
|||||
11 AAAAAAAC 3

seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:AAT73560

seq_documentation_block:

ID AAT73560 standard; RNA; 12 BP.

XX AC AAT73560;

XX DT 29-AUG-1997 (first entry)

XX DE Antiviral capped short oligonucleotide 2.

XX KW antiviral; diphosphate; triphosphate; capped; guanylyl transferase;
XX KW large scale synthesis; influenza RNA polymerase; inhibit; cap-dependent;
XX KW transcription; in vitro; study; transcription; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

FT /note= "m7G"

FT modified_base 2

FT /*tag= b

FT /note= "pppU"

XX WO9641812-A1.

XX PD 27-DEC-1996.

XX PF 07-JUN-1996; 96WO-GB01360.

XX PR 09-JUN-1995; 95GB-0011720.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PI Brownlee GG, Fodor E, Lowe G;

XX DR WPI; 1997-065418/06.

XX PT Oligo:nucleotide phosphorylation process - for prepn. of
XX PT oligo:nucleotide(s) having 5'-terminal di- or triphosphate gp.,
XX PT which are useful in influenza virus transcription studies

XX PS Claim 11; Page 26; 35pp; English.

XX CC A novel process comprises reacting an oligonucleotide, having a 5'
XX CC -terminal -OH gp., with a phosphorylating or phosphorylating agent,
XX CC then with a phosphate or pyrophosphate and recovering an
XX CC oligonucleotide, having a 5'-terminal di- or triphosphate group. The
XX CC recovered oligonucleotides (AAT73560-63) are then capped by reaction with
XX CC guanylyl transferase. The process is useful for the large scale synthesis
XX CC of short-capped oligonucleotides. The short-capped oligonucleotides are
XX CC potential antiviral agents as they can bind to influenza RNA polymerase,
XX CC and specifically inhibit cap-dependent transcription in vitro. The
XX CC prods. may also be useful for the study of influenza virus
XX CC transcription.

SQ Sequence 12 BP; 0 A; 0 C; 1 G; 11 U; 0 other;

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AAT73560/rev ..

Align seg 1/1 to reverse of: AAT73560 from: 1 to: 12

1 LysLysAsn 3

|||||||

9 AAAAAAAC 1

seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:AAA94316

seq_documentation_block:

ID AAA94316 standard; DNA; 12 BP.

XX AC AAA94316;

XX DT 11-JAN-2001 (first entry)

XX DE RNA-protein fusion oligonucleotide 13-P.

XX KW RNA-protein fusion; protein library; protein isolation; gene cloning; ss.
XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 12

FT /*tag= a

FT /mod_base= OTHER

FT /note= "attached to puromycin, a peptide acceptor"

XX WO200047775-A1.

XX PD 17-AUG-2000.

XX PF 01-FEB-2000; 2000WO-US02589.

XX PR 09-FEB-1999; 99US-0247190.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PI Szostak JW, Roberts RW, Liu R;

XX DR WPI; 2000-533022/48.

XX PT Producing protein or DNA libraries which are useful for improving
XX PT existing proteins, by in vitro translating protein coding sequences to
XX PT produce RNA-protein fusions and incubating these protein fusions under
XX PT high salt conditions -

XX PS Disclosure; Page 43; 121pp; English.

XX CC The present sequence is one of a number of oligonucleotides which were
XX CC used for the generation of RNA-protein fusions, including fusions having
XX CC a myc epitope tag. The RNA-protein fusions comprise a protein covalently
XX CC linked to the 3' end of its own mRNA. This is accomplished by synthesis
XX CC and in vitro or in situ translation of an mRNA molecule with a peptide
XX CC acceptor attached to its 3' end. The RNA-protein fusions are incubated
XX CC under high salt conditions to produce a protein library. This method is
XX CC useful for improving or altering existing proteins, as well as for
XX CC isolating new proteins and nucleic acid or small molecule targets. It may
XX CC also be used to improve human or humanised single-chain antibodies for
XX CC the treatment of a number of diseases. The method is useful for the
XX CC isolation of proteins with specific binding properties, for screening
XX CC cDNA libraries and cloning new genes on the basis of protein-protein
XX CC interactions. Unlike prior art, the new method does not rely on
XX CC maintaining the integrity of an mRNA:ribosome:nascent chain ternary
XX CC complex, which is very fragile and is therefore of limited use. The
XX CC method does not rely on topological links between the protein and the
XX CC nucleic acid so that the information of the protein is retained and can
XX CC be recovered in readable, nucleic acid form.

SQ Sequence 12 BP; 10 A; 2 C; 0 G; 0 U; 0 other;

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AAA94316 ..

Align seg 1/1 to: AAA94316 from: 1 to: 12

1 LysLysAsn 3
|||||
3 AAAAAAAC 11

seq_name: /SIDS5/gcgdata/geneseq/geneseq-embl/NA2000.DAT:AAA10356

seq_documentation_block:

ID AAA10356 standard; DNA; 12 BP.

AC AAA10356;

DT 03-JUL-2000 (first entry)

DE DNA ligand binding assay competitor oligonucleotide, SEQ ID NO:39.

KW Nucleic acid ligand binding assay; duplex formation; stability;
KW detectable signal; competition assay; competitor oligonucleotide; ds.
XX
OS Synthetic.

XX WO200015848-A1.

XX 23-MAR-2000.

XX 10-SEP-1999; 99WO-US20719.

XX 11-SEP-1998; 98US-0151890.

XX (GENE-) GENELABS TECHNOLOGIES INC.

XX Schroth GP, Bruice TW, Suh YJ;

XX WPT; 2000-271478/23.

XX Determining binding affinity of a ligand to an oligonucleotide sequence
PT in double stranded form, comprises measuring the effect of adding
PT increasing amounts of a ligand on a signal generated by two indicator
PT oligonucleotides of the duplex -

XX Examples 7-8; Page 20; 78pp; English.

XX The invention relates to new methods of determining the binding affinity
CC of a ligand to an oligonucleotide sequence, particularly to a duplex.
CC The ligand is typically a metal ion, a small organic or inorganic
CC molecule, a protein or a multi-protein complex. The methods comprise
CC measuring the effect of adding increasing amounts of a ligand on a signal
CC generated by two indicator oligonucleotides of the duplex. In the absence
CC of ligand, conditions are such that the oligonucleotides exist primarily
CC in single-stranded form; binding of ligand to double-stranded nucleic
CC acids stabilises the duplexes, such that duplex formation is favoured.
CC One of the indicator oligonucleotides contains a first group capable of
CC producing a detectable signal, while the other indicator oligonucleotide
CC contains a second group that on hybridisation of the two indicator
CC molecules, will detectably alter the signal produced by the first group.
CC The signal may be increased or decreased on hybridisation. For example,
CC the pairs of signalling groups used could be a radioactive group and a
CC scintillant (where an increase in signal intensity indicates that
CC hybridisation has taken place) or a fluorophore and a fluorescence
CC quencher (where a reduction in signal intensity indicates that
CC hybridisation has occurred). Other methods of the invention comprise a
CC strand displacement assay, where the ability of an unlabelled
CC strand to displace one of the oligonucleotides in the duplex
CC assay, where an unlabelled single or double-stranded competitor
CC oligonucleotide is added to the ligand-bound indicator duplex, and the
CC effect on the signal produced from the indicator duplex determined. The
CC methods are useful for determining the binding affinity of a ligand to
CC an oligonucleotide sequence. They are particularly useful for
CC determining relative binding affinities of various ligands to various
CC oligonucleotide sequences, particularly double-stranded oligonucleotide

CC sequences. The assays allow rapid and convenient determination of nucleic
CC acid binding specificities. Sequences AAA10342-A10391 represent
CC competitor oligonucleotides used in competition assays in
CC exemplifications of the present invention.

XX Sequence 12 BP; 8 A; 4 C; 0 G; 0 U; 0 other;

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AAA10356 ..

Align seg 1/1 to: AAA10356 from: 1 to: 12

1 LysLysAsn 3
|||||
3 AAAAAAAC 11

seq_name: /SIDS5/gcgdata/geneseq/geneseq-embl/NA2001A.DAT:AAH46026

seq_documentation_block:

ID AAH46026 standard; DNA; 12 BP.

XX AC AAH46026;

XX 12-SEP-2001 (first entry)

XX Mycobacterium phlei murA oligonucleotide 3.

XX Synthetic oligonucleotide; dinucleotide repeat; cytostatic; apoptosis;
KW cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;
KW tumour necrosis factor; TNF; cancer; carcinoma; sarcoma; leukemia;
KW lymphoma; ss; murA.

XX OS Mycobacterium phlei.
XX OS Synthetic.

XX WO200144465-A2.

XX 21-JUN-2001.

XX 12-DEC-2000; 2000WO-CA01467.

XX 13-DEC-1999; 99US-0170325.

XX 29-AUG-2000; 2000US-0228925.

XX (BION-) BIONICHE LIFE SCI INC.

XX Phillips NC, Fillion MC;

XX WPT; 2001-398150/42.

XX Composition comprising synthetic oligonucleotides which comprise
PT multiple repeats of dinucleotides such as GT, TG useful for treating
PT cancer by inducing cell cycle arrest, inhibiting proliferation,
PT activating caspases -

XX Claim 5; Page 41; 77pp; English.

XX The present sequence is that of a synthetic Mycobacterium phlei murA
CC derived oligonucleotide useful to the invention. The invention relates to
CC a composition, comprising a 2 to 20 base 3'-OH, 5'-OH synthetic
CC oligonucleotide which comprises multiple repeats of dinucleotides such as
CC GT, TG, etc., according to specific formula and having cytostatic
CC activity. The oligonucleotide compositions are useful for inducing cell
CC cycle arrest, inhibition of proliferation, activation of caspases and
CC induction of apoptosis or production of cytokines such as interleukin
CC (IL)-1-beta, IL-6, IL-10, IL-12 and tumour necrosis factor (TNF)-alpha by
CC immune system cells, in an animal having cancer such as primary

CC carcinoma, secondary carcinoma, primary sarcoma and secondary sarcoma
CC such as, leukemia, lymphoma, breast, prostate, colorectal, ovarian or
CC bone cancer. The compositions induce apoptosis independent of Fas,
CC p53/p21, p21/waf-1/CIP, p15(ink4B), p16(ink4), drug resistance,
CC caspase 3, transforming growth factor (TGF)-beta 1 receptor and hormone
CC dependence.
XX
SQ Sequence 12 BP; 0 A; 0 C; 2 G; 10 T; 0 other;

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AAH46026/rev ..

Align seg 1/1 to reverse of: AAH46026 from: 1 to: 12

1 LysLysAsn 3
|||||
11 AAAAAAAC 3

seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:ABH67135

seq_documentation_block:

ID_ ABH67135 standard; DNA; 12 BP.

XX AC ABH67135;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 267112 for detecting SNP TSC00000016.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single nucleotide polymorphisms and cytosine
methylation status

Claim 1; SEQ ID 267112; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
ABI00010-ABI82073 represent the oligomers described in the invention.
NOTE: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 12 BP; 2 A; 0 C; 0 G; 10 T; 0 other;
alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x ABH67135/rev ..

Align seg 1/1 to reverse of: ABH67135 from: 1 to: 12

1 LysLysAsn 3
|||||
9 AAAAAAA 1

seq_name: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:ABH67157

seq_documentation_block:

ID_ ABH67157 standard; DNA; 12 BP.

XX AC ABH67157;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 267134 for detecting SNP TSC00000024.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single nucleotide polymorphisms and cytosine
methylation status

Claim 1; SEQ ID 267134; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligonucleotides are also used for detecting cell type differentiation.
ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
ABI00010-ABI82073 represent the oligomers described in the invention.
NOTE: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 other;

alignment_scores:
Quality: 16.00 Length: 3

Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH67157/rev ..

Align seg 1/1 to reverse of: ABH67157 from: 1 to: 12

1 LysLysAsn 3
|||||
10 AAAAAAAC 4

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH67218

seq_documentation_block:

ID ABH67218 standard; DNA; 12 BP.

XX

AC ABH67218;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 267195 for detecting SNP TSC00000048.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

XX

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.

XX

PR 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single nucleotide polymorphisms and cytosine

PT methylation status

XX

XX Claim 1; SEQ ID 267195; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABT00010-ABT2073 represent the oligomers described in the invention.

Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH67218/rev ..

Align seg 1/1 to reverse of: ABH67157 from: 1 to: 12

1 LysLysAsn 3
|||||
12 AAAAAAAC 4

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH67218

seq_documentation_block:

ID ABH67218 standard; DNA; 12 BP.

XX

AC ABH67218;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 267195 for detecting SNP TSC00000048.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

XX

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.

XX

PR 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single nucleotide polymorphisms and cytosine

PT methylation status

XX

XX Claim 1; SEQ ID 267195; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABT00010-ABT2073 represent the oligomers described in the invention.

Align seg 1/1 to reverse of: ABH67218 from: 1 to: 12

1 LysLysAsn 3
|||||
10 AAAAAAAC 2

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH67278

seq_documentation_block:

ID ABH67278 standard; DNA; 12 BP.

XX

AC ABH67278;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 267255 for detecting SNP TSC00000067.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

XX

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.

XX

PR 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single nucleotide polymorphisms and cytosine

PT methylation status

XX

XX Claim 1; SEQ ID 267255; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABT00010-ABT2073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format from WIPO at

Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH67157/rev ..

Align seg 1/1 to reverse of: ABH67157 from: 1 to: 12

1 LysLysAsn 3
|||||
12 AAAAAAAC 4

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH67218

seq_documentation_block:

ID ABH67218 standard; DNA; 12 BP.

XX

AC ABH67218;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 267195 for detecting SNP TSC00000048.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

XX

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.

XX

PR 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single nucleotide polymorphisms and cytosine

PT methylation status

XX

XX Claim 1; SEQ ID 267195; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABT00010-ABT2073 represent the oligomers described in the invention.

Align seg 1/1 to reverse of: ABH67218 from: 1 to: 12

1 LysLysAsn 3
|||||
10 AAAAAAAC 2

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH67278

seq_documentation_block:

ID ABH67278 standard; DNA; 12 BP.

XX

AC ABH67278;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 267255 for detecting SNP TSC00000067.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

XX

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.

XX

PR 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single nucleotide polymorphisms and cytosine

PT methylation status

XX

XX Claim 1; SEQ ID 267255; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABT00010-ABT2073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format from WIPO at

Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH67157/rev ..

Align seg 1/1 to reverse of: ABH67157 from: 1 to: 12

1 LysLysAsn 3
|||||
12 AAAAAAAC 4

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH67218

seq_documentation_block:

ID ABH67218 standard; DNA; 12 BP.

XX

AC ABH67218;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 267195 for detecting SNP TSC00000048.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

XX

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.

XX

PR 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single nucleotide polymorphisms and cytosine

PT methylation status

XX

XX Claim 1; SEQ ID 267195; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The

CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABT00010-ABT2073 represent the oligomers described in the invention.

Align seg 1/1 to reverse of: ABH67218 from: 1 to: 12

1 LysLysAsn 3
|||||
10 AAAAAAAC 2

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH67278

seq_documentation_block:

ID ABH67278 standard; DNA; 12 BP.

XX

AC ABH67278;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 267255 for detecting SNP TSC00000067.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

XX

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.

XX

PR 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single nucleotide polymorphisms and cytosine

seq_name: /SIDS5/gcgdata/geneseq/geneseq-embl/NA2001B.DAT:ABH67354

seq_documentation_block:

ID ABH67354 standard; DNA; 12 BP.

XX AC ABH67354;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 267331 for detecting SNP TSC0000112.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN W0200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPi; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX Claim 1; SEQ ID 267331; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 12 BP; 0 A; 0 C; 4 G; 8 T; 0 other;

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH67354/rev ..

Align seg 1/1 to reverse of: ABH67354 from: 1 to: 12

1 LysLysAsn 3

|||||

12 AAAAAAAC 4

seq_name: /SIDS5/gcgdata/geneseq/geneseq-embl/NA2001B.DAT:ABH67386

seq_documentation_block:

ID ABH67386 standard; DNA; 12 BP.

XX AC ABH67386;

XX

DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 267363 for detecting SNP TSC0000141.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN W0200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPi; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -
XX Claim 1; SEQ ID 267363; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABI00010-ABI82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 12 BP; 10 A; 0 C; 0 G; 2 T; 0 other;

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH67386 ..

Align seg 1/1 to: ABH67386 from: 1 to: 12

1 LysLysAsn 3

|||||

4 AAAAAAAT 12

seq_name: /SIDS5/gcgdata/geneseq/geneseq-embl/NA2001B.DAT:ABH67427

seq_documentation_block:

ID ABH67427 standard; DNA; 12 BP.

XX AC ABH67427;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 267404 for detecting SNP TSC0000178.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.

XX

XX WO200177384-A2.

XX

XX 18-OCT-2001.

XX

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -

XX

XX Claim 1; SEQ ID 267404; 29pp + Sequence Listing; German.

XX

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and

CC ABT00010-ABT82073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 12 BP; 1 A; 0 C; 0 G; 11 T; 0 other;

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH67427/rev ..

Align seg 1/1 to reverse of: ABH67427 from: 1 to: 12

1 LysLysAsn 3

|||||||
10 AAAAAAAAAA 2

seq_name: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:ABH67458

seq_documentation_block:

ID ABH67458 standard; DNA; 12 BP.

XX

AC ABH67458;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 267435 for detecting SNP TSC0000225.

XX

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB00713.

XX 07-APR-2000; 2000DE-1019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -

XX

XX Claim 1; SEQ ID 267435; 29pp + Sequence Listing; German.

XX

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and

CC ABT00010-ABT82073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 12 BP; 1 A; 0 C; 1 G; 10 T; 0 other;

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH67458/rev ..

Align seg 1/1 to reverse of: ABH67458 from: 1 to: 12

1 LysLysAsn 3

|||||||
11 AAAAAAAAAA 3

seq_name: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:ABH67482

seq_documentation_block:

ID ABH67482 standard; DNA; 12 BP.

XX

AC ABH67482;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 267459 for detecting SNP TSC0000264.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX

XX WO200177384-A2.

XX

PD 18-OCT-2001.

XX

XX 06-APR-2001; 2001WO-IB00713.

XX

XX 07-APR-2000; 2000DE-1019173.


```

XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status
XX
XX Claim 1; SEQ ID 267459; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABI00010-ABI82073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 other;

alignment_scores:
    Quality: 16.00      Length: 3
    Ratio: 5.333        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x ABH67482/rev ..
    1 LysLysAsn 3
    |||||
    9 AAAAAAAC 1

Align seg 1/1 to reverse of: ABH67482 from: 1 to: 12

seq_name: /SIDS5/gcgdata/geneseq/geneseq-n-emb1/NA2001B.DAT:ABH67505

seq_documentation_block:
ID_ ABH67505 standard; DNA; 12 BP.
XX
XX AC ABH67505;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 267482 for detecting SNP TSC0000294.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN W0200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB00713.
XX
XX PR 07-APR-2000; 2000DE-1019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status
XX
XX Claim 1; SEQ ID 267459; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABI00010-ABI82073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 other;

alignment_scores:
    Quality: 16.00      Length: 3
    Ratio: 5.333        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x ABH67482/rev ..
    1 LysLysAsn 3
    |||||
    9 AAAAAAAC 1

Align seg 1/1 to reverse of: ABH67482 from: 1 to: 12

seq_name: /SIDS5/gcgdata/geneseq/geneseq-n-emb1/NA2001B.DAT:ABH67505

seq_documentation_block:
ID_ ABH67505 standard; DNA; 12 BP.
XX
XX AC ABH67505;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 267482 for detecting SNP TSC0000294.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN W0200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB00713.
XX
XX PR 07-APR-2000; 2000DE-1019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status
XX
XX Claim 1; SEQ ID 267459; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation.
XX CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX CC ABI00010-ABI82073 represent the oligomers described in the invention.
XX CC NOTE: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 12 BP; 0 A; 0 C; 1 G; 11 T; 0 other;

alignment_scores:
    Quality: 16.00      Length: 3
    Ratio: 5.333        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x ABH67505/rev ..
    1 LysLysAsn 3
    |||||
    10 AAAAAAAC 2

Align seg 1/1 to reverse of: ABH67505 from: 1 to: 12

seq_name: /SIDS5/gcgdata/geneseq/geneseq-n-emb1/NA2001B.DAT:ABH67640

seq_documentation_block:
ID_ ABH67640 standard; DNA; 12 BP.
XX
XX AC ABH67640;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 267617 for detecting SNP TSC0000400.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN W0200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB00713.
XX
XX PR 07-APR-2000; 2000DE-1019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single nucleotide polymorphisms and cytosine
XX PT methylation status
XX
XX Claim 1; SEQ ID 267617; 29pp + Sequence Listing; German.

```


XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABT00010-ABT82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 1 A; 0 C; 1 G; 10 T; 0 other;

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH67640/rev ..

Align seg 1/1 to reverse of: ABH67640 from: 1 to: 12

1 LysLysAsn 3
|||||||
9 AAAAAAAC 1

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.ABH67643

seq_documentation_block:

ID ABH67643 standard; DNA; 12 BP.

XX AC ABH67643;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 267620 for detecting SNP TSC0000401.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB00713.

XX PR 07-APR-2000; 2000DE-1019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -

XX Claim 1; SEQ ID 267620; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABT00010-ABT82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 12 BP; 10 A; 1 C; 0 G; 1 T; 0 other;

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH67643 ..

Align seg 1/1 to: ABH67643 from: 1 to: 12

1 LysLysAsn 3
|||||||
4 AAAAAAAC 12

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.ABH67751

seq_documentation_block:

ID ABH67751 standard; DNA; 12 BP.

XX AC ABH67751;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 267728 for detecting SNP TSC0000491.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB00713.

XX PR 07-APR-2000; 2000DE-1019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -

XX Claim 1; SEQ ID 267728; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABT00010-ABT82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at


```
CC ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 12 BP; 2 A; 0 C; 1 G; 9 T; 0 other;
SQ

alignment_scores:
  Quality: 16.00 Length: 3
  Ratio: 5.333 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
  US-09-528-682-2 x ABH67751/rev ..

  Align seg 1/1 to reverse of: ABH67751 from: 1 to: 12

    1 LysLysAsn 3
    |||||
    10 AAAAAAAC 2

seq_name: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH67810

seq_documentation_block:
  ID ABH67810 standard; DNA; 12 BP.
  XX
  AC ABH67810;
  XX
  DT 22-FEB-2002 (first entry)
  XX
  DE Oligonucleotide primer SEQ ID NO 267787 for detecting SNP TSC0000529.
  XX
  KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
  KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
  KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
  XX
  OS Homo sapiens.
  XX
  PN WO200177384-A2.
  XX
  PD 18-OCT-2001.
  XX
  PF 06-APR-2001; 2001WO-IB00713.
  XX
  PR 07-APR-2000; 2000DE-1019173.
  XX
  PA (EPIG-) EPIGENOMICS AG.
  XX
  PI Olek A, Piepenbrock C, Berlin K;
  XX
  DR WPI; 2001-657177/75.
  XX
  PT Set of oligonucleotides, useful for diagnosis and cell typing, is
  PT designed to detect single nucleotide polymorphisms and cytosine
  PT methylation status
  XX
  PS Claim 1; SEQ ID 267787; 29pp + Sequence Listing; German.
  XX
  CC This invention describes novel oligonucleotide primers or peptide nucleic
  CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
  CC and cytosine methylation status in chemically pretreated genomic DNA. The
  CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
  CC range of diseases including immune system, gastrointestinal, respiratory,
  CC central nervous system, cardiovascular and metabolic disorders. The
  CC oligomers are also used for detecting cell type differentiation.
  CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
  CC ABI00010-ABI82073 represent the oligomers described in the invention.
  CC NOTE: The sequence data for this patent did not form part of the printed
  CC specification, but was obtained in electronic format from WIPO at
  CC ftp.wipo.int/pub/published_pct_sequences.
  XX
  SQ Sequence 12 BP; 10 A; 1 C; 0 G; 1 T; 0 other;

alignment_scores:
  Quality: 16.00 Length: 3
  Ratio: 5.333 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
  US-09-528-682-2 x ABH67912 ..

  Align seg 1/1 to: ABH67810 from: 1 to: 12

    1 LysLysAsn 3
    |||||
    3 AAAAAAAT 11

seq_name: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH67912

seq_documentation_block:
  ID ABH67912 standard; DNA; 12 BP.
  XX
  AC ABH67912;
  XX
  DT 22-FEB-2002 (first entry)
  XX
  DE Oligonucleotide primer SEQ ID NO 267889 for detecting SNP TSC0000635.
  XX
  KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
  KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
  KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
  XX
  OS Homo sapiens.
  XX
  PN WO200177384-A2.
  XX
  PD 18-OCT-2001.
  XX
  PF 06-APR-2001; 2001WO-IB00713.
  XX
  PR 07-APR-2000; 2000DE-1019173.
  XX
  PA (EPIG-) EPIGENOMICS AG.
  XX
  PI Olek A, Piepenbrock C, Berlin K;
  XX
  DR WPI; 2001-657177/75.
  XX
  PT Set of oligonucleotides, useful for diagnosis and cell typing, is
  PT designed to detect single nucleotide polymorphisms and cytosine
  PT methylation status
  XX
  PS Claim 1; SEQ ID 267889; 29pp + Sequence Listing; German.
  XX
  CC This invention describes novel oligonucleotide primers or peptide nucleic
  CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
  CC and cytosine methylation status in chemically pretreated genomic DNA. The
  CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
  CC range of diseases including immune system, gastrointestinal, respiratory,
  CC central nervous system, cardiovascular and metabolic disorders. The
  CC oligomers are also used for detecting cell type differentiation.
  CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
  CC ABI00010-ABI82073 represent the oligomers described in the invention.
  CC NOTE: The sequence data for this patent did not form part of the printed
  CC specification, but was obtained in electronic format from WIPO at
  CC ftp.wipo.int/pub/published_pct_sequences.
  XX
  SQ Sequence 12 BP; 9 A; 0 C; 1 G; 2 T; 0 other;

alignment_scores:
  Quality: 16.00 Length: 3
  Ratio: 5.333 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
  US-09-528-682-2 x ABH67912 ..
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Align seg 1/1 to: ABH67912 from: 1 to: 12

1 LysLysAsn 3
|||||
1 AAAAAAAT 9

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH67913

seq_documentation_block:

ID ABH67913 standard; DNA; 12 BP.

XX

AC ABH67913;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 267890 for detecting SNP TSC0000635.

XX

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB00713.

XX

PR 07-APR-2000; 2000DE-1019173.

XX

PA (EPIC-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

DR WPI; 2001-657177/75.

XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -

XX

PS Claim 1; SEQ ID 267890; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABI00010-ABI82073 represent the oligomers described in the invention.

CC NOTE: the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 12 BP; 10 A; 0 C; 0 G; 2 T; 0 other;

alignment_scores:

Quality: 16.00

Ratio: 5.333

Percent Similarity: 100.000

Length: 3

Gaps: 0

Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH67913 ..

Align seg 1/1 to: ABH67913 from: 1 to: 12

1 LysLysAsn 3
|||||
1 AAAAAAAT 9

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH67928

seq_documentation_block:

ID ABH67928 standard; DNA; 12 BP.

XX

AC ABH67928;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide primer SEQ ID NO 267905 for detecting SNP TSC0000655.

XX

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB00713.

XX

PR 07-APR-2000; 2000DE-1019173.

XX

PA (EPIC-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

DR WPI; 2001-657177/75.

XX

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -

XX

PS Claim 1; SEQ ID 267905; 29pp + Sequence Listing; German.

XX

CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.

CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

CC ABI00010-ABI82073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 other;

alignment_scores:

Quality: 16.00

Ratio: 5.333

Percent Similarity: 100.000

Length: 3

Gaps: 0

Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH67928/rev ..

Align seg 1/1 to reverse of: ABH67928 from: 1 to: 12

1 LysLysAsn 3
|||||
9 AAAAAAAC 1

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH68005

seq_documentation_block:

ID ABH68005 standard; DNA; 12 BP.

XX

AC ABH68005;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 267982 for detecting SNP TSC0000755.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB00713.
 XX
 XX 07-APR-2000; 2000DE-1019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX
 PS Claim 1; SEQ ID 267982; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC AB100010-AB182073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 12 BP; 2 A; 0 C; 0 G; 10 T; 0 other;

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-528-682-2 x ABH68005/rev ..
 Align seg 1/1 to reverse of: ABH68005 from: 1 to: 12

1 LysLysAsn 3
 |||||
 10 AAAAAAAAAAT 2

seq_name: /SIDS5/gcgdata/geneseq/geneseq-embl/NA2001B.DAT:ABH68036
 seq_documentation_block:
 ID ABH68036 standard; DNA; 12 BP.
 XX
 AC ABH68036;
 XX
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 268013 for detecting SNP TSC0000799.
 XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB00713.
 XX
 XX 07-APR-2000; 2000DE-1019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX
 PS Claim 1; SEQ ID 268013; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC AB100010-AB182073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 12 BP; 9 A; 2 C; 0 G; 1 T; 0 other;

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-528-682-2 x ABH68036 ..
 Align seg 1/1 to: ABH68036 from: 1 to: 12

1 LysLysAsn 3
 |||||
 2 AAAAAAAC 10

seq_name: /SIDS5/gcgdata/geneseq/geneseq-embl/NA2001B.DAT:ABH68090
 seq_documentation_block:
 ID ABH68090 standard; DNA; 12 BP.
 XX
 AC ABH68090;
 XX
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 268067 for detecting SNP TSC0000855.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX

PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX
 PS Claim 1; SEQ ID 268067; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 12 BP; 2 A; 0 C; 1 G; 9 T; 0 other;

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-528-682-2 x ABH68090/rev ..

Align seg 1/1 to reverse of: ABH68090 from: 1 to: 12

1 LysLysAsn 3
 |||||
 9 AAAAAAAAAAC 1

seq_name: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH68175

seq_documentation_block:
 ID ABH68175 standard; DNA; 12 BP.
 XX
 AC ABH68175;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 268152 for detecting SNP TSC0000930.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB00713.
 XX

PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX
 PS Claim 1; SEQ ID 268152; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 12 BP; 9 A; 2 C; 0 G; 1 T; 0 other;

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-528-682-2 x ABH68175 ..

Align seg 1/1 to: ABH68175 from: 1 to: 12

1 LysLysAsn 3
 |||||
 1 AAAAAAAAAAT 9

seq_name: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH68195

seq_documentation_block:
 ID ABH68195 standard; DNA; 12 BP.
 XX
 AC ABH68195;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 268172 for detecting SNP TSC0000936.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX


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DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
PS Claim 1; SEQ ID 268172; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABT00010-ABT82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 11 A; 1 C; 0 G; 0 U; 0 other;

alignment_scores:
    Quality: 16.00      Length: 3
    Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x ABH68195 ..
Align seg 1/1 to: ABH68195 from: 1 to: 12

    1 LysLysAsn 3
      |||||
      12 AAAAAAAC 4

seq_name: /SIDS5/gcgdata/geneseq/geneseq-embl/NA2001B.DAT:ABH68196
seq_documentation_block:
ID ABH68196 standard; DNA; 12 BP.
XX
XX AC ABH68196;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 268173 for detecting SNP TSC00000936.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN W0200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB00713.
XX
XX PR 07-APR-2000; 2000DE-1019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX

```

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PS Claim 1; SEQ ID 268173; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABT00010-ABT82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 0 A; 0 C; 1 G; 11 T; 0 other;

alignment_scores:
    Quality: 16.00      Length: 3
    Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x ABH68196/rev ..
Align seg 1/1 to reverse of: ABH68196 from: 1 to: 12

    1 LysLysAsn 3
      |||||
      12 AAAAAAAC 4

seq_name: /SIDS5/gcgdata/geneseq/geneseq-embl/NA2001B.DAT:ABH68217
seq_documentation_block:
ID ABH68217 standard; DNA; 12 BP.
XX
XX AC ABH68217;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 268194 for detecting SNP TSC00000959.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN W0200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB00713.
XX
XX PR 07-APR-2000; 2000DE-1019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status
XX
XX Claim 1; SEQ ID 268194; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABT00010-ABT82073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 0 A; 0 C; 1 G; 11 T; 0 other;

```


CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABT00010-ABT82073 represent the oligomers described in the invention.
CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 12 BP; 2 A; 0 C; 0 G; 10 T; 0 other;

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH68217/rev ..

Align seg 1/1 to reverse of: ABH68217 from: 1 to: 12

1 LysLysAsn 3
|||||||
12 AAAAAAAAAAT 4

seq_name: /SID55/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:ABH68243

seq_documentation_block:

ID ABH68243 standard; DNA; 12 BP.

AC ABH68243;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 268220 for detecting SNP TSC0000988.

XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.

PR 07-APR-2000; 2000DE-1019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -

PS Claim 1; SEQ ID 268220; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABT00010-ABT82073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 12 BP; 1 A; 2 C; 0 G; 9 T; 0 other;

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH68243/rev ..

Align seg 1/1 to reverse of: ABH68243 from: 1 to: 12

1 LysLysAsn 3
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11 AAGAAAAAT 3

seq_name: /SID55/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:ABH68246

seq_documentation_block:

ID ABH68246 standard; DNA; 12 BP.

AC ABH68246;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 268223 for detecting SNP TSC0000988.

XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB00713.

PR 07-APR-2000; 2000DE-1019173.

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single nucleotide polymorphisms and cytosine
PT methylation status -

PS Claim 1; SEQ ID 268223; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation.
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
CC ABT00010-ABT82073 represent the oligomers described in the invention.

CC NOTE: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 12 BP; 1 A; 0 C; 0 G; 11 T; 0 other;

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH68246/rev ..

Align seg 1/1 to reverse of: ABH68246 from: 1 to: 12

1 LysLysAsn 3
|||||
11 AAAAAAAT 3

seq_name: /SID5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH68268

seq_documentation_block:

ID ABH68268 standard; DNA; 12 BP.

XX AC ABH68268;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 268245 for detecting SNP TSC0001000.
XX KW SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PS WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status -

Claim 1: SEQ ID 268245; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 12 BP; 10 A; 0 C; 0 G; 2 T; 0 other;

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH68268 ..
Align seg 1/1 to: ABH68268 from: 1 to: 12

1 LysLysAsn 3
|||||
2 AAAAAAAT 10

seq_name: /SID5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABH68290

seq_documentation_block:

ID ABH68290 standard; DNA; 12 BP.

XX AC ABH68290;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 268267 for detecting SNP TSC0001028.
XX KW SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB00713.
XX PR 07-APR-2000; 2000DE-1019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX PS WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single nucleotide polymorphisms and cytosine methylation status -

Claim 1: SEQ ID 268267; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and

ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 12 BP; 10 A; 1 C; 0 G; 1 T; 0 other;

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x ABH68290 ..

Align seg 1/1 to: ABH68290 from: 1 to: 12

1 LysLysAsn 3
|||||

2 AAAAAAAAAAC 10

OM of: US-09-528-682-2 to: EST:* out_format : pfs

Date: Jun 18, 2002 6:25 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-O/cgn2_1/USPTO.spool/US09528682/runat_18062002_082443_7797/app_query.fasta_1.689
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCI=0.000 -LOOPEXT=0.000 -GAPOP=4.500
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-FGAEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=1000 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=50 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZ=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09528682@cgn1_1.5309
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-NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-528-682-2

Query length: 3

Database: EST:*

Database sequences: 13736207

Database length: -184157050

Search time (sec): 4056.470000

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gb_gss:AZ357587	+	89.48	9.7e+04	19	AZ357587 LM0099C15F Mouse 10kb F
gb_gss:AZ357587	+	89.48	9.7e+04	19	AZ357587 LM0099C15F Mouse 10kb F
gb_gss:AZ358099	+	89.48	9.7e+04	19	AZ358099 LM0100N12F Mouse 10kb F
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gb_gss:TA279B01P	+	16.00	88.36	1.1e+05	23	TA279B01P T. brucei sheared ge
gb_gss:TA328D05P	+	16.00	88.36	1.1e+05	23	TA328D05P T. brucei sheared ge

gb_gss:TA328D05P	-	16.00	88.36	1.1e+05	23	AL493117	T. brucei sheared genom	gb_gss:AX339270	16.00	87.41	1.3e+05	27	AZ339270	LM0070K10R	Mouse	10k		
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gb_gss:AZ330762	-	16.00	88.10	1.2e+05	24	AZ330762	LM0056L12F	Mouse	10k	gb_gss:BH011509	16.00	87.41	1.3e+05	27	BH011509	BG02453-3prime Droso		
gb_gss:AZ349008	-	16.00	88.10	1.2e+05	24	AZ349008	LM0085013R	Mouse	10k	gb_gss:TA252b10P	16.00	87.41	1.3e+05	27	TA252b10P	T. brucei sheared ge		
gb_gss:AZ396663	-	16.00	88.10	1.2e+05	24	AZ396663	LM0165C10R	Mouse	10k	gb_gss:TA287F07P	16.00	87.41	1.3e+05	27	TA287F07P	T. brucei sheared ge		
gb_gss:AZ3438069	-	16.00	88.10	1.2e+05	24	AZ38069	LM0228A10F	Mouse	10k	gb_gss:TA356D05P	16.00	87.41	1.3e+05	27	TA356D05P	T. brucei sheared ge		
gb_gss:AZ4581112	-	16.00	88.10	1.2e+05	24	AZ458112	LM0261E24R	Mouse	10k	gb_gss:TA70808P	16.00	87.41	1.3e+05	27	TA70808P	T. brucei sheared ge		
gb_gss:AZ510115	-	16.00	88.10	1.2e+05	24	AZ510115	LM0354G23F	Mouse	10k	gb_gss:TA70808P	16.00	87.41	1.3e+05	27	TA70808P	T. brucei sheared ge		
gb_gss:AZ513027	-	16.00	88.10	1.2e+05	24	AZ513027	LM0358P22R	Mouse	10k	gb_estl:AI093972	16.00	87.19	1.3e+05	28	AI093972	oxj04d07.s1 NCI_CGAP		
gb_gss:AZ5261257	-	16.00	88.10	1.2e+05	24	AZ5261257	LM0454E23F	Mouse	10k	gb_estl:AI130321	16.00	87.19	1.3e+05	28	AI130321	SMOVL3CAN17D09 Oncho		
gb_gss:AZ6267850	-	16.00	88.10	1.2e+05	24	AZ627850	LM0474N20F	Mouse	10k	gb_estl:AI241875	16.00	87.19	1.3e+05	28	AI241875	qu69e06.x1 NCI_CGAP		
gb_gss:AZ764496	-	16.00	88.10	1.2e+05	24	AZ764496	LM0560H02R	Mouse	10k	gb_estl:AI458838	16.00	87.19	1.3e+05	28	AI458838	tl74h07.x1 NCI_CGAP		
gb_gss:AZ764513	-	16.00	88.10	1.2e+05	24	AZ764513	LM0360D11R	Mouse	10k	gb_estl:AI588880	16.00	87.19	1.3e+05	28	AI588880	tg28g01.x1 NCI_CGAP		
gb_gss:AZ764519	-	16.00	88.10	1.2e+05	24	AZ764519	LM0560P11R	Mouse	10k	gb_estl:AI590364	16.00	87.19	1.3e+05	28	AI590364	ts09e12.x1 NCI_CGAP		
gb_gss:AZ782507	-	16.00	88.10	1.2e+05	24	AZ782507	LM0022L22R	Mouse	10k	gb_estl:AI678332	16.00	87.19	1.3e+05	28	AI678332	tu80g12.x1 NCI_CGAP		
gb_gss:AZ801201	-	16.00	88.10	1.2e+05	24	AZ801201	LM0059M02R	Mouse	10k	gb_estl:AI688906	16.00	87.19	1.3e+05	28	AI688906	tx22e03.x1 NCI_CGAP		
gb_gss:TA215C030	-	16.00	88.10	1.2e+05	24	AL479238	T. brucei sheared genom	gb_estl:AI690628	16.00	87.19	1.3e+05	28	AI690628	tx98g09.x1 NCI_CGAP				
gb_gss:TA356G08P	-	16.00	88.10	1.2e+05	24	AL497144	T. brucei sheared genom	gb_estl:AI758806	16.00	87.19	1.3e+05	28	AI758806	ty24f05.x1 NCI_CGAP				
gb_estl:AI903841	-	16.00	87.86	1.2e+05	25	AA903841	ok64e05.s1 NCI_CGAP_GC4	gb_estl:AI9171979	16.00	87.19	1.3e+05	28	AI9171979	wv30h06.x1 NCI_CGAP				
gb_estl:AI189662	-	16.00	87.86	1.2e+05	25	AI189662	qdl8h06.x1 Soares_place	gb_estl:AW332443	16.00	87.19	1.3e+05	28	AW332443	S8E7 AGS-1 Pneumocys				
gb_estl:AI1318195	-	16.00	87.86	1.2e+05	25	AI1318195	ta73e09.x1 NCI_CGAP_HSC	gb_estl:AW466587	16.00	87.19	1.3e+05	28	AW466587	ve20d12.r1 Soares mo				
gb_estl:AI433266	-	16.00	87.86	1.2e+05	25	AI433266	l132g02.x1 NCI_CGAP_Gas	gb_estl:AW56352	16.00	87.19	1.3e+05	28	AW56352	yb34c09.s1 Stratagene				
gb_estl:AI445764	-	16.00	87.86	1.2e+05	25	AI445764	tj09g10.x1 NCI_CGAP_Gas	gb_gss:AX3357605	16.00	87.19	1.3e+05	28	AX3357605	LM0099115F	Mouse	10k		
gb_estl:AI620546	-	16.00	87.86	1.2e+05	25	AI620546	tu95b04.x1 NCI_CGAP_Gas	gb_gss:AX357605	16.00	87.19	1.3e+05	28	AX357605	LM0099115F	Mouse	10k		
gb_estl:AI587648	-	16.00	87.86	1.2e+05	25	AL587648	AL587648 BP Chicken Bra	gb_gss:AX358038	16.00	87.19	1.3e+05	28	AX358038	LM0138A00F	Mouse	10k		
gb_estl:AI587718	-	16.00	87.86	1.2e+05	25	AL587718	AL587718 BP Chicken Bra	gb_gss:AX381403	16.00	87.19	1.3e+05	28	AX381403	LM0138A00F	Mouse	10k		
gb_estl:C02553	-	16.00	87.86	1.2e+05	25	C02553	HUMG0012453 Human adult	gb_gss:AX387839	16.00	87.19	1.3e+05	28	AX387839	LM0147H22R	Mouse	10k		
gb_estl:N33150	-	16.00	87.86	1.2e+05	25	N33150	yy06g01.s1 Soares melanoc	gb_gss:AX425633	16.00	87.19	1.3e+05	28	AX425633	LM0252807R	Mouse	10k		
gb_gss:AZ318035	-	16.00	87.86	1.2e+05	25	AZ318035	LM0036L12R	Mouse	10k	gb_gss:AX466214	16.00	87.19	1.3e+05	28	AX466214	LM0276E18R	Mouse	10k
gb_gss:AZ339378	-	16.00	87.86	1.2e+05	25	AZ339378	LM0071C09F	Mouse	10k	gb_gss:AX481286	16.00	87.19	1.3e+05	28	AX481286	LM0303124F	Mouse	10k
gb_gss:AZ3861039	-	16.00	87.86	1.2e+05	25	AZ3861039	LM0137N18F	Mouse	10k	gb_gss:AX4835060	16.00	87.19	1.3e+05	28	AX4835060	LM0129A11F	Mouse	10k
gb_gss:AZ386891	-	16.00	87.86	1.2e+05	25	AZ386891	LM0146A08F	Mouse	10k	gb_gss:AX4836072	16.00	87.19	1.3e+05	28	AX4836072	LM0130K08R	Mouse	10k
gb_gss:AZ393511	-	16.00	87.86	1.2e+05	25	AZ393511	LM0156B07R	Mouse	10k	gb_gss:AX4869547	16.00	87.19	1.3e+05	28	AX4869547	LM0181007R	Mouse	10k
gb_gss:AZ442170	-	16.00	87.86	1.2e+05	25	AZ442170	LM0234H18R	Mouse	10k	gb_gss:AX4924359	16.00	87.19	1.3e+05	28	AX4924359	LM0248K19F	Mouse	10k
gb_gss:AZ510128	-	16.00	87.86	1.2e+05	25	AZ510128	LM0354L23F	Mouse	10k	gb_gss:AX973999	16.00	87.19	1.3e+05	28	AX973999	LM0248K19F	Mouse	10k
gb_gss:AZ510144	-	16.00	87.86	1.2e+05	25	AZ510144	LM0354P24F	Mouse	10k	gb_gss:TA173D10P	16.00	87.19	1.3e+05	28	TA173D10P	T. brucei sheared ge		
gb_gss:AZ764498	-	16.00	87.86	1.2e+05	25	AZ764498	LM0360K04R	Mouse	10k	gb_gss:TA236A02P	16.00	87.19	1.3e+05	28	TA236A02P	T. brucei sheared ge		
gb_gss:AZ764498	-	16.00	87.86	1.2e+05	25	AZ764498	LM0360K04R	Mouse	10k	gb_gss:TA29A09P	16.00	87.19	1.3e+05	28	TA29A09P	T. brucei sheared ge		
gb_gss:AZ774476	-	16.00	87.86	1.2e+05	25	AZ774476	LM0004A01F	Mouse	10k	gb_gss:TA324H01Q	16.00	87.19	1.3e+05	28	TA324H01Q	T. brucei sheared ge		
gb_gss:AZ812604	-	16.00	87.86	1.2e+05	25	AZ812604	LM0079F23F	Mouse	10k	gb_gss:TA58F07P	16.00	86.99	1.3e+05	29	TA58F07P	AHUH bsst.dnc15.aa		
gb_gss:AZ855418	-	16.00	87.86	1.2e+05	25	AZ855418	LM0159M21F	Mouse	10k	gb_estl:AW059655	16.00	86.99	1.3e+05	29	AW059655	LM0065C06F	Mouse	10k
gb_gss:AZ867155	-	16.00	87.86	1.2e+05	25	AZ867155	LM0177F23R	Mouse	10k	gb_gss:AX335504	16.00	86.99	1.3e+05	29	AX335504	LM0080112F	Mouse	10k
gb_gss:TA154D03P	-	16.00	87.86	1.2e+05	25	AL472971	T. brucei sheared genom	gb_gss:AX492630	16.00	86.99	1.3e+05	29	AX492630	LM0236B22R	Mouse	10k		
gb_estl:AL587774	-	16.00	87.63	1.2e+05	26	AL587774	AL587774 BP Chicken Bra	gb_gss:AX492630	16.00	86.99	1.3e+05	29	AX492630	LM0236B22R	Mouse	10k		
gb_estl:AL588210	-	16.00	87.63	1.2e+05	26	AL588210	AL588210 BP Chicken Bra	gb_gss:AX492630	16.00	86.99	1.3e+05	29	AX492630	LM0236B22R	Mouse	10k		
gb_gss:AZ303994	-	16.00	87.63	1.2e+05	26	AZ303994	LM0003J22R	Mouse	10k	gb_gss:AX492630	16.00	86.99	1.3e+05	29	AX492630	LM0236B22R	Mouse	10k
gb_gss:AZ316353	-	16.00	87.63	1.2e+05	26	AZ316353	LM0034D09F	Mouse	10k	gb_gss:AX621725	16.00	86.99	1.3e+05	29	AX621725	LM0455C16F	Mouse	10k
gb_gss:AZ355083	-	16.00	87.63	1.2e+05	26	AZ355083	LM0094D14R	Mouse	10k	gb_gss:AX800642	16.00	86.99	1.3e+05	29	AX800642	LM0058G16R	Mouse	10k
gb_gss:AZ405677	-	16.00	87.63	1.2e+05	26	AZ405677	LM0174D07R	Mouse	10k	gb_gss:AX807660	16.00	86.99	1.3e+05	29	AX807660	LM0070G12R	Mouse	10k
gb_gss:AZ422541	-	16.00	87.63	1.2e+05	26	AZ422541	LM0201G14F	Mouse	10k	gb_gss:AX8119924	16.00	86.99	1.3e+05	29	AX8119924	LM0091A19R	Mouse	10k
gb_gss:AZ442116	-	16.00	87.63	1.2e+05	26	AZ442116	LM0203A10R	Mouse	10k	gb_gss:AX825156	16.00	86.99	1.3e+05	29	AX825156	LM02100N08R	Mouse	10k
gb_gss:AZ485624	-	16.00	87.63	1.2e+05	26	AZ485624	LM0313H11F	Mouse	10k	gb_gss:AX827060	16.00	86.99	1.3e+05	29	AX827060	LM0130F17F	Mouse	10k
gb_gss:AZ620113	-	16.00	87.63	1.2e+05	26	AZ620113	LM04512N08R	Mouse	10k	gb_gss:TA129F03P	16.00	86.99	1.3e+05	29	TA129F03P	T. brucei sheared ge		
gb_gss:AZ623156	-	16.00	87.63	1.2e+05	26	AZ623156	LM0460L01R	Mouse	10k	gb_gss:TA271F07P	16.00	86.99	1.3e+05	29	TA271F07P	T. brucei sheared ge		
gb_gss:AZ651828	-	16.00	87.63	1.2e+05	26	AZ651828	LM0522D14R	Mouse	10k	em_estl:HSN002002	16.00	86.79	1.4e+05	30	HSN002002	Homo sapiens mRNA; E		
gb_gss:AZ764502	-	16.00	87.63	1.2e+05	26	AZ764502	LM0360L03R	Mouse	10k	gb_estl:AW248759	16.00	86.79	1.4e+05	30	AW248759	2820825-3prime NIH_M		
gb_gss:AZ818035	-	16.00	87.63	1.2e+05	26	AZ818035	LM0087015R	Mouse	10k	gb_estl:BJ082112	16.00	86.79	1.4e+05	30	BJ082112	BJ082112 N1BB Moch1		
gb_gss:AZ818035	-	16.00	87.63	1.2e+05	26	AZ818035	LM0087015R	Mouse	10k	gb_gss:AX345551	16.00	86.79	1.4e+05	30	AX345551	LM0080E14F	Mouse	10k
gb_gss:AZ828616	-	16.00	87.63	1.2e+05	26	AZ828616	LM											

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gb_est1:AA924443 1.4e+05 86.59 16.00 + A924443 aJ60a11.s1 NCI CGAP GC4
gb_est1:AA934214 1.4e+05 86.59 16.00 + A934214 SWOVLCAN09C08 Onchocel
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gb_est1:AI000307 1.4e+05 86.59 16.00 - AI000307 an24b06.s1 Gessler Wilm
gb_est1:AI021969 1.4e+05 86.59 16.00 - AI021969 ox04e05.x1 Soares_fetal
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gb_est1:AI148887 1.4e+05 86.59 16.00 + AI148887 qd70d08.x1 Soares_place
gb_est1:AI189788 1.4e+05 86.59 16.00 + AI189788 qd33d03.x1 Soares_place
gb_est1:AI158302 1.4e+05 86.59 16.00 + AI158302 qv37c02.x1 NCI CGAP Ut2
gb_est1:AI164767 1.4e+05 86.59 16.00 + AI164767 qul8d02.x1 NCI CGAP Ut2
gb_est1:AI175457 1.4e+05 86.59 16.00 + AI175457 t183h01.x1 NCI CGAP Col
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gb_est1:AL588362 1.4e+05 86.59 16.00 - AL588362 AL588362 Bp Chicken Bra
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gb_est1:AU008906 1.4e+05 86.59 16.00 - AU008906 AU008906 Schizosacchar
gb_est1:AV672830 1.4e+05 86.59 16.00 - AV672830 AV672830 Nori Satoh unp
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gb_gss:AZ587554 1.4e+05 86.40 16.00 - gb_gss:AZ587554
gb_gss:AZ659027 1.4e+05 86.40 16.00 - gb_gss:AZ659027
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gb_gss:AZ869514 1.4e+05 86.40 16.00 - gb_gss:AZ869514
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gb_gss:AZ9292942 1.4e+05 86.40 16.00 - gb_gss:AZ9292942
gb_gss:TA230A08P 1.4e+05 86.40 16.00 + T. brucei sheared ge
gb_gss:TA346D11P 1.4e+05 86.40 16.00 + AL494229 T. brucei sheared ge
em_esthum:HSM01806 1.4e+05 86.22 16.00 + AL037475 Homo sapiens mRNA: E
gb_est1:AV857609 1.5e+05 86.22 16.00 - AV857609 AV857609 Bp Chicken
gb_est1:AV857567 1.5e+05 86.22 16.00 - AV857567 AV857567 Nori Satoh
gb_est1:AW698829 1.5e+05 86.22 16.00 - AW698829 r436 non-glandular-h
gb_est2:BJ152241 1.5e+05 86.22 16.00 - BJ152241 602917653F1 NCI CGAP
gb_est2:BJ032135 1.5e+05 86.22 16.00 - BJ032135 BJ032135 NIBB Mochill
gb_est2:BJ033449 1.5e+05 86.22 16.00 - BJ033449 BJ033449 NIBB Mochill
gb_est2:BJ039102 1.5e+05 86.22 16.00 - BJ039102 BJ039102 NIBB Mochill
gb_est2:BJ058881 1.5e+05 86.22 16.00 - BJ058881 BJ058881 NIBB Mochill
gb_est2:BJ063093 1.5e+05 86.22 16.00 - BJ063093 BJ063093 NIBB Mochill
gb_est2:BJ066158 1.5e+05 86.22 16.00 - BJ066158 BJ066158 NIBB Mochill
gb_est2:BJ078868 1.5e+05 86.22 16.00 - BJ078868 BJ078868 NIBB Mochill
gb_est2:BJ0826144 1.5e+05 86.22 16.00 - BJ0826144 1(2)s1878 Drosophilla
gb_gss:AQ073226 1.5e+05 86.22 16.00 - AQ073226 EP(X)1507-Sprime Dro
gb_gss:AZ2311457 1.5e+05 86.22 16.00 - AZ2311457 1M0026121R Mouse 10k
gb_gss:AZ344777 1.5e+05 86.22 16.00 - AZ344777 1M0079801F Mouse 10k
gb_gss:AZ345453 1.5e+05 86.22 16.00 - AZ345453 1M0080K09F Mouse 10k
gb_gss:AZ345517 1.5e+05 86.22 16.00 - AZ345517 1M0080K04F Mouse 10k
gb_gss:AZ426849 1.5e+05 86.22 16.00 - AZ426849 1M0082114F Mouse 10k
gb_gss:AZ420776 1.5e+05 86.22 16.00 - AZ420776 1M0170C16F Mouse 10k
gb_gss:AZ411435 1.5e+05 86.22 16.00 - AZ411435 1M0184C05R Mouse 10k
gb_gss:AZ417833 1.5e+05 86.22 16.00 - AZ417833 1M0193J10R Mouse 10k
gb_gss:AZ4249331 1.5e+05 86.22 16.00 - AZ4249331 1M0214H08F Mouse 10k
gb_gss:AZ484838 1.5e+05 86.22 16.00 - AZ484838 1M0311005R Mouse 10k
gb_gss:AZ475946 1.5e+05 86.22 16.00 - AZ475946 1M053P07F Mouse 10k
gb_gss:AZ7714759 1.5e+05 86.22 16.00 - AZ7714759 2M0004A05F Mouse 10k
gb_gss:AZ828695 1.5e+05 86.22 16.00 - AZ828695 2M0105N18R Mouse 10k
gb_gss:TA356C03P 1.5e+05 86.22 16.00 - AL497114 T. brucei sheared ge
gb_gss:TA356C03P 1.5e+05 86.22 16.00 - AL497114 T. brucei sheared ge
gb_est1:AA890011 1.5e+05 86.05 16.00 - AA890011 aJ89h12.s1 Soares_pa
gb_est1:AA946688 1.5e+05 86.05 16.00 - AA946688 ot45f09.s1 NCI CGAP_
gb_est1:AA994607 1.5e+05 86.05 16.00 - AA994607 ot44c08.s1 Soares_te
gb_est1:AI000150 1.5e+05 86.05 16.00 - AI000150 os43f01.s1 NCI CGAP_
gb_est1:AI020751 1.5e+05 86.05 16.00 - AI020751 os52a05.x1 Soares_pa
gb_est1:AI096142 1.5e+05 86.05 16.00 - AI096142 SWOVLC3CAN20D08 Oncho
gb_est1:AI537371 1.5e+05 86.05 16.00 - AI537371 TJ73c05.x1 NCI CGAP_
gb_est1:AI538434 1.5e+05 86.05 16.00 - AI538434 td06b12.x1 NCI CGAP_
gb_est1:AI539675 1.5e+05 86.05 16.00 - AI539675 tp71f03.x1 NCI CGAP_
gb_est1:AI620541 1.5e+05 86.05 16.00 - AI620541 tu95a08.x1 NCI CGAP_
gb_est1:AI654467 1.5e+05 86.05 16.00 - AI654467 tq91c04.x1 NCI CGAP_
gb_est1:AI689593 1.5e+05 86.05 16.00 - AI689593 tx84q11.x1 NCI CGAP_
gb_est1:AI761474 1.5e+05 86.05 16.00 - AI761474 wh98f05.x1 NCI CGAP_
gb_est1:AV831490 1.5e+05 86.05 16.00 - AV831490 AV831490 Dictyostell
gb_est1:AV831490 1.5e+05 86.05 16.00 - AV831490 AV831490 K. Sato unp
gb_est1:AV831490 1.5e+05 86.05 16.00 - AV831490 AV831490 K. Sato unp
gb_est1:AV833489 1.5e+05 86.05 16.00 - AV833489 AV833489 K. Sato unp
gb_est1:AV857665 1.5e+05 86.05 16.00 - AV857665 AV857665 Nori Satoh
gb_est1:AW250804 1.5e+05 86.05 16.00 - AW250804 2822479.3prime NIH_M
gb_est2:BG6112023 1.5e+05 86.05 16.00 - BG6112023 602613924F1 NIH_MGC_
gb_est2:BJ029498 1.5e+05 86.05 16.00 - BJ029498 BJ029498 NIBB Mochill
gb_est2:BJ031262 1.5e+05 86.05 16.00 - BJ031262 BJ031262 NIBB Mochill
gb_est2:BJ031887 1.5e+05 86.05 16.00 - BJ031887 BJ031887 NIBB Mochill
gb_est2:BJ034690 1.5e+05 86.05 16.00 - BJ034690 BJ034690 NIBB Mochill
gb_est2:BJ037684 1.5e+05 86.05 16.00 - BJ037684 BJ037684 NIBB Mochill
gb_est2:BJ037907 1.5e+05 86.05 16.00 - BJ037907 BJ037907 NIBB Mochill
gb_est2:BJ038644 1.5e+05 86.05 16.00 - BJ038644 BJ038644 NIBB Mochill
gb_est2:BJ038988 1.5e+05 86.05 16.00 - BJ038988 BJ038988 NIBB Mochill
gb_est2:BJ041115 1.5e+05 86.05 16.00 - BJ041115 BJ041115 NIBB Mochill
gb_est2:BJ041405 1.5e+05 86.05 16.00 - BJ041405 BJ041405 NIBB Mochill
gb_est2:BJ051533 1.5e+05 86.05 16.00 - BJ051533 BJ051533 NIBB Mochill

gb_est2:B0052720	+	16.00	86.05	1.5e+05	34	! B0052720	B0052720	N1BB	Mochli	nd	gb_est1:AA938016	+	16.00	85.55	1.6e+05	37	! AA938016	0078f06.s1	NCI_CGAP_
gb_est2:B0057525	-	16.00	86.05	1.5e+05	34	! B0057525	B0057525	N1BB	Mochli	nd	gb_est1:AA939321	+	16.00	85.55	1.6e+05	37	! AA939321	0197f07.s1	NCI_CGAP_
gb_est2:B0058673	-	16.00	86.05	1.5e+05	34	! B0058673	B0058673	N1BB	Mochli	nd	gb_est1:AA939894	+	16.00	85.55	1.6e+05	37	! AA939894	0175h03.s1	Soares_NF
gb_est2:B0061790	-	16.00	86.05	1.5e+05	34	! B0061790	B0061790	N1BB	Mochli	nd	gb_est1:AA947987	+	16.00	85.55	1.6e+05	37	! AA947987	0q58e02.s1	NCI_CGAP_
gb_est2:B0061960	-	16.00	86.05	1.5e+05	34	! B0061960	B0061960	N1BB	Mochli	nd	gb_est1:AA961907	+	16.00	85.55	1.6e+05	37	! AA961907	0r68d10.s1	NCI_CGAP_
gb_est2:B0062401	-	16.00	86.05	1.5e+05	34	! B0062401	B0062401	N1BB	Mochli	nd	gb_est1:AA961907	+	16.00	85.55	1.6e+05	37	! AA961907	0r68d10.s1	NCI_CGAP_
gb_est2:B0064029	-	16.00	86.05	1.5e+05	34	! B0064029	B0064029	N1BB	Mochli	nd	gb_est1:AA972505	+	16.00	85.55	1.6e+05	37	! AA972505	0r15c01.s1	NCI_CGAP_
gb_est2:B0064541	-	16.00	86.05	1.5e+05	34	! B0064541	B0064541	N1BB	Mochli	nd	gb_est1:AI01000163	+	16.00	85.55	1.6e+05	37	! AI01000163	0s44d06.s1	NCI_CGAP_
gb_est2:B0065805	-	16.00	86.05	1.5e+05	34	! B0065805	B0065805	N1BB	Mochli	nd	gb_est1:AI0180668	+	16.00	85.55	1.6e+05	37	! AI0180668	0v64f01.s1	Soares_te
gb_est2:B0066776	-	16.00	86.05	1.5e+05	34	! B0066776	B0066776	N1BB	Mochli	nd	gb_est1:AI037939	+	16.00	85.55	1.6e+05	37	! AI037939	0x53b01.x1	Soares
gb_est2:B0067181	-	16.00	86.05	1.5e+05	34	! B0067181	B0067181	N1BB	Mochli	nd	gb_est1:AI149322	+	16.00	85.55	1.6e+05	37	! AI149322	0q76f08.x1	Soares_pl
gb_est2:DH20157	-	16.00	86.05	1.5e+05	34	! DH20157	HM0005258	Liver	HepG2	ce	gb_est1:AI174610	+	16.00	85.55	1.6e+05	37	! AI174610	an47c11.s1	Gessler_W
gb_est2:DH30031	-	16.00	86.05	1.5e+05	34	! DH30031	YP047e10.s1	Soares	retina	ce	gb_est1:AI267150	+	16.00	85.55	1.6e+05	37	! AI267150	aq36b12.x1	Stanley_F
gb_gss:AZ322675	+	16.00	86.05	1.5e+05	34	! AZ322675	1M0043D10R	Mouse	10kb	F	gb_est1:AI351618	+	16.00	85.55	1.6e+05	37	! AI351618	qr05g04.x1	Soares
gb_gss:AZ322675	+	16.00	86.05	1.5e+05	34	! AZ322675	1M0043D10R	Mouse	10kb	F	gb_est1:AI379566	+	16.00	85.55	1.6e+05	37	! AI379566	tc52g07.x1	Soares_Nh
gb_gss:AZ345609	+	16.00	86.05	1.5e+05	34	! AZ345609	1M0080C22F	Mouse	10kb	F	gb_est1:AI413136	+	16.00	85.55	1.6e+05	37	! AI413136	ar55e07.x1	Barstead
gb_gss:AZ475648	+	16.00	86.05	1.5e+05	34	! AZ475648	1M0093G05R	Mouse	10kb	F	gb_est1:AI435659	+	16.00	85.55	1.6e+05	37	! AI435659	th53a09.x1	NCI_CGAP_
gb_gss:AZ4803210	+	16.00	86.05	1.5e+05	34	! AZ4803210	2M0063C02R	Mouse	10kb	F	gb_est1:AI440016	+	16.00	85.55	1.6e+05	37	! AI440016	tl98e08.x1	NCI_CGAP_
gb_gss:AZ4803210	+	16.00	86.05	1.5e+05	34	! AZ4803210	2M0063C02R	Mouse	10kb	F	gb_est1:AI440016	+	16.00	85.55	1.6e+05	37	! AI440016	tl98e08.x1	NCI_CGAP_
gb_gss:AZ480416	+	16.00	86.05	1.5e+05	34	! AZ480416	2M0136P19R	Mouse	10kb	F	gb_est1:AI474144	+	16.00	85.55	1.6e+05	37	! AI474144	tm05h10.x1	NCI_CGAP_
gb_gss:CN5006ML	-	16.00	86.05	1.5e+05	34	! AL065757	Drosophila	melanogaster			gb_est1:AI475428	+	16.00	85.55	1.6e+05	37	! AI475428	tl83c09.x1	NCI_CGAP_
gb_gss:TA222809P	+	16.00	86.05	1.5e+05	34	! AL480722	T. brucei	sheared	genom		gb_est1:AI498217	+	16.00	85.55	1.6e+05	37	! AI498217	tm85b04.x1	NCI_CGAP_
gb_gss:TA222809P	+	16.00	86.05	1.5e+05	34	! AL480722	T. brucei	sheared	genom		gb_est1:AI500674	+	16.00	85.55	1.6e+05	37	! AI500674	tn95b01.x1	NCI_CGAP_
gb_gss:TA68D10P	-	16.00	86.05	1.5e+05	34	! AL457502	T. brucei	sheared	genom		gb_est1:AI508475	+	16.00	85.55	1.6e+05	37	! AI508475	fb79f06.x1	Zebrafish
gb_est1:AL641482	-	16.00	85.88	1.5e+05	35	! AL641482	AL641482	XGC-neurula	SI		gb_est1:AL641545	+	16.00	85.55	1.6e+05	37	! AL641545	fc15e11.x1	Zebrafish
gb_est1:AV836236	-	16.00	85.88	1.5e+05	35	! AV836236	AV836236	K. Sato	unpubl		gb_est1:AL653824	+	16.00	85.55	1.6e+05	37	! AL653824	ty01n06.x1	NCI_CGAP_
gb_est1:AV850856	+	16.00	85.88	1.5e+05	35	! AV850856	AV850856	Nori	Sato	unpubl	gb_est1:AL671076	+	16.00	85.55	1.6e+05	37	! AL671076	tz17g12.x1	NCI_CGAP_
gb_est1:AV850856	+	16.00	85.88	1.5e+05	35	! AV850856	AV850856	Nori	Sato	unpubl	gb_est1:AL679350	+	16.00	85.55	1.6e+05	37	! AL679350	tu73e08.x1	NCI_CGAP_
gb_est1:BG496638	+	16.00	85.88	1.5e+05	35	! BG496638	602537978F1	N1H_MGC	59		gb_est1:AI718104	+	16.00	85.55	1.6e+05	37	! AI718104	as49b08.x1	Barstead
gb_est2:BG569185	+	16.00	85.88	1.5e+05	35	! BG569185	602588454F1	N1H_MGC	76		gb_est1:AI741717	+	16.00	85.55	1.6e+05	37	! AI741717	wq22b07.x1	Soares
gb_est2:BG032028	+	16.00	85.88	1.5e+05	35	! BG032028	B0032028	N1BB	Mochli	nd	gb_est1:AI801336	+	16.00	85.55	1.6e+05	37	! AI801336	to88a01.x1	NCI_CGAP_
gb_est2:BG045059	+	16.00	85.88	1.5e+05	35	! BG045059	B0045059	N1BB	Mochli	nd	gb_est1:AI802260	+	16.00	85.55	1.6e+05	37	! AI802260	tj36g07.x1	NCI_CGAP_
gb_est2:BG080323	+	16.00	85.88	1.5e+05	35	! BG080323	B0080323	N1BB	Mochli	nd	gb_est1:AI803262	+	16.00	85.55	1.6e+05	37	! AI803262	tc38h12.x1	Soares
gb_est2:BG080509	+	16.00	85.88	1.5e+05	35	! BG080509	B0080509	N1BB	Mochli	nd	gb_est1:AI813747	+	16.00	85.55	1.6e+05	37	! AI813747	wk79a02.x1	NCI_CGAP_
gb_est2:TS0295	+	16.00	85.88	1.5e+05	35	! TS0295	ybl6g12.s1	Stratagene	fet		gb_est1:AI918824	+	16.00	85.55	1.6e+05	37	! AI918824	tn09a03.x1	NCI_CGAP_
gb_gss:AZ351309	+	16.00	85.88	1.5e+05	35	! AZ351309	1M0098K13F	Mouse	10kb	F	gb_est1:AL962222	+	16.00	85.55	1.6e+05	37	! AL962222	zp98b06.r1	Stratagen
gb_gss:AZ4365817	+	16.00	85.88	1.5e+05	35	! AZ4365817	1M0112G18R	Mouse	10kb	F	gb_est1:AV832716	+	16.00	85.55	1.6e+05	37	! AV832716	AV832716	K. Sato
gb_gss:AZ4410442	+	16.00	85.88	1.5e+05	35	! AZ4410442	1M0112G18R	Mouse	10kb	F	gb_est1:AV852302	+	16.00	85.55	1.6e+05	37	! AV852302	AV852302	Nori
gb_gss:AZ4469855	+	16.00	85.88	1.5e+05	35	! AZ4469855	1M0283B07R	Mouse	10kb	F	gb_est1:AV858269	+	16.00	85.55	1.6e+05	37	! AV858269	AV858269	Nori
gb_gss:AZ475373	+	16.00	85.88	1.5e+05	35	! AZ475373	1M0293E11R	Mouse	10kb	F	gb_est1:AW254247	+	16.00	85.55	1.6e+05	37	! AW254247	2820028.3prime	N1H_M
gb_gss:AZ785657	+	16.00	85.88	1.5e+05	35	! AZ785657	2M0029F17R	Mouse	10kb	F	gb_est1:AW332808	+	16.00	85.55	1.6e+05	37	! AW332808	13D3 AGS-1	Pneumocy
gb_gss:AZ785657	+	16.00	85.88	1.5e+05	35	! AZ785657	2M0029F17R	Mouse	10kb	F	gb_est1:BG175511	+	16.00	85.55	1.6e+05	37	! BG175511	602334778F2	NCI_CGAP_
gb_gss:AZ825655	+	16.00	85.88	1.5e+05	35	! AZ825655	2M0100P23R	Mouse	10kb	F	gb_est2:BG430173	+	16.00	85.55	1.6e+05	37	! BG430173	602495159F1	N1H_MGC
gb_est1:AL587891	+	16.00	85.71	1.6e+05	36	! AL587891	AL587891	XP	Chicken	bra	gb_est2:BG569157	+	16.00	85.55	1.6e+05	37	! BG569157	602588418F1	N1H_MGC
gb_est1:AL6339933	+	16.00	85.71	1.6e+05	36	! AL6339933	AL6339933	BC	neurula	SI	gb_est2:BJ073798	+	16.00	85.55	1.6e+05	37	! BJ073798	BJ073798	N1BB
gb_est1:AV673131	+	16.00	85.71	1.6e+05	36	! AV673131	mz91a02.r1	Soares	mouse		gb_est2:BJ073988	+	16.00	85.55	1.6e+05	37	! BJ073988	BJ073988	N1BB
gb_est1:AV832415	+	16.00	85.71	1.6e+05	36	! AV832415	AV832415	K. Sato	unpubl		gb_est2:BJ040638	+	16.00	85.55	1.6e+05	37	! BJ040638	BJ040638	N1BB
gb_est1:AV832705	+	16.00	85.71	1.6e+05	36	! AV832705	AV832705	K. Sato	unpubl		gb_est2:BJ053161	+	16.00	85.55	1.6e+05	37	! BJ053161	BJ053161	N1BB
gb_est1:AV833605	+	16.00	85.71	1.6e+05	36	! AV833605	AV833605	K. Sato	unpubl		gb_est2:BJ054011	+	16.00	85.55	1.6e+05	37	! BJ054011	BJ054011	N1BB
gb_est1:AW335193	+	16.00	85.71	1.6e+05	36	! AW335193	S44C8 AGS-1	Pneumocy	st		gb_est2:BJ066419	+	16.00	85.55	1.6e+05	37	! BJ066419	BJ066419	N1BB
gb_est2:BJ000288	+	16.00	85.71	1.6e+05	36	! BJ000288	BJ000288	MF01SSA	CDNA	C	gb_est2:DL18712	+	16.00	85.55	1.6e+05	37	! DL18712	MUSGS01774	Mouse
gb_est2:BJ015573	+	16.00	85.71	1.6e+05	36	! BJ015573	BJ015573	MF01SSA	CDNA	C	gb_est2:R27442	+	16.00	85.55	1.6e+05	37	! R27442	YH53a06.s1	Soares
gb_est2:BJ045088	+	16.00	85.71	1.6e+05	36	! BJ045088	BJ045088	N1BB	Mochli	nd	gb_est2:R20234	+	16.00	85.55	1.6e+05	37	! R20234	HSAAABQV.p1	Human
gb_est2:BJ062811	+	16.00	85.71	1.6e+05	36	! BJ062811	BJ062811	N1BB	Mochli	nd	gb_est2:BF180013	+	16.00	85.55	1.6e+05	37	! BF180013	601806360F1	NCI_CGAP_
gb_est2:BJ064992	+	16.00	85.71	1.6e+05	36	! BJ064992	BJ064992	N1BB	Mochli	nd	gb_gss:AZ453377	+	16.00	85.55	1.6e+05	37	! AZ453377	1M0292C17F	Mouse
gb_est2:BJ0688	+	16.00	85.71	1.6e+05	36	! BJ0688	HUMGS01664	Human	promyel	nd	gb_gss:AZ442522	+	16.00	85.55	1.6e+05	37	! AZ442522	1M0326D07R	Mouse
gb_est2:BE894682	+	16.00	85.71	1.6e+05	36	! BE894682	601435925F1	N1H_MGC	72		gb_gss:AZ442522	+	16.00	85.55	1.6e+05	37	! AZ442522	1M0326D07R	Mouse
gb_gss:AZ338246	+	16.00	85.71	1.6e+05	36	! AZ338246	1M0069C17F	Mouse	10kb	F	gb_gss:AZ595102	+	16.00	85.55	1.6e+05	37	! AZ595102	1M0407R03R	Mouse
gb_gss:AZ446375	+	16.00	85.71	1.6e+05	36	! AZ446375	1M0242G15R	Mouse	10kb	F	gb_gss:AZ595102	+	16.00	85.55	1.6e+05	37	! AZ595102	1M0407R03R	Mouse
gb_gss:AZ446375	+	16.00	85.71	1.6e+05	36	! AZ446375	1M0242G15R	Mouse	10kb	F	gb_gss:AZ595102	+	16.00	85.55					

gb_est1:A1524768	16.00	84.66	1.8e+05	43	A1524768	tc36g01.x1	NCI_CGAP_Ut4	gb_gss:A7776615	16.00	84.52	1.8e+05	44	AZ7776615	2M0010K23F	Mouse 10k
gb_est1:A1571023	16.00	84.66	1.8e+05	43	A1571023	tc25f03.x1	NCI_CGAP_Ut2	gb_gss:A2856367	16.00	84.52	1.8e+05	44	AZ856367	2M0160F15R	Mouse 10k
gb_est1:A1583078	16.00	84.66	1.8e+05	43	A1583078	ts30g05.x1	NCI_CGAP_Par	gb_gss:A2950525	16.00	84.52	1.8e+05	44	AZ950525	2M0220O31R	Mouse 10k
gb_est1:A1591196	16.00	84.66	1.8e+05	43	A1591196	tu12g05.x1	NCI_CGAP_Brd	gb_gss:A2969520	16.00	84.52	1.8e+05	44	AZ969520	2M0242M15F	Mouse 10k
gb_est1:A1597934	16.00	84.66	1.8e+05	43	A1597934	tu92c06.x1	NCI_CGAP_Gas	gb_gss:AL587540	16.00	84.39	1.9e+05	45	AL587540	AL587540	BP Chicken
gb_est1:A1610394	16.00	84.66	1.8e+05	43	A1610394	tp19d11.x1	NCI_CGAP_Gas	gb_est1:AL587734	16.00	84.39	1.9e+05	45	AL587734	AL587734	BP Chicken
gb_est1:A1669398	16.00	84.66	1.8e+05	43	A1669398	ty31h08.x1	NCI_CGAP_Ut2	gb_est1:AV848952	16.00	84.39	1.9e+05	45	AV848952	AV848952	Nori Satoh
gb_est1:A1687191	16.00	84.66	1.8e+05	43	A1687191	tp85a11.x1	NCI_CGAP_Ut3	gb_est1:AV851415	16.00	84.39	1.9e+05	45	AV851415	AV851415	Nori Satoh
gb_est1:A1700134	16.00	84.66	1.8e+05	43	A1700134	tg10h04.x1	NCI_CGAP_Ut3	gb_est1:AV853684	16.00	84.39	1.9e+05	45	AV853684	AV853684	Nori Satoh
gb_est1:A1758314	16.00	84.66	1.8e+05	43	A1758314	ty06c01.x1	NCI_CGAP_Ut3	gb_est1:AV854173	16.00	84.39	1.9e+05	45	AV854173	AV854173	Nori Satoh
gb_est1:A1799404	16.00	84.66	1.8e+05	43	A1799404	tu56a07.x1	NCI_CGAP_Ut3	gb_est1:AW249952	16.00	84.39	1.9e+05	45	AW249952	2821663.3prime	NIH_M
gb_est1:A18003919	16.00	84.66	1.8e+05	43	A18003919	tp76009.x1	NCI_CGAP_Ut4	gb_est2:BJ230882	16.00	84.39	1.9e+05	45	BJ230882	602891270F1	NCI_CGAP
gb_est1:A1814142	16.00	84.66	1.8e+05	43	A1814142	wk63a10.x1	NCI_CGAP_Par	gb_est2:BJ000444	16.00	84.39	1.9e+05	45	BJ000444	B0000444	MFOISSA CDN
gb_est1:A1857884	16.00	84.66	1.8e+05	43	A1857884	AL587884	BP Chicken	gb_est2:BJ000124	16.00	84.39	1.9e+05	45	BJ001124	B0001124	MFOISSA CDN
gb_est1:A18636541	16.00	84.66	1.8e+05	43	A18636541	AL636541	XGC-Neurenla	gb_est2:BJ003431	16.00	84.39	1.9e+05	45	BJ003431	B003431	NIBB Mochii
gb_est1:A18758314	16.00	84.66	1.8e+05	43	A18758314	ty06c01.x1	NCI_CGAP_Ut3	gb_est2:BJ0048121	16.00	84.39	1.9e+05	45	BJ0048121	B0048121	NIBB Mochii
gb_est1:A19014529	16.00	84.66	1.8e+05	43	A19014529	AU014529	Schizosacchar	gb_est2:BJ005780	16.00	84.39	1.9e+05	45	BJ005780	B005780	NIBB Mochii
gb_est1:A1932522	16.00	84.66	1.8e+05	43	A1932522	AV832522	K. K. Sato unpubl	gb_est2:BJ007340	16.00	84.39	1.9e+05	45	BJ007340	B007340	NIBB Mochii
gb_est1:A19832677	16.00	84.66	1.8e+05	43	A19832677	AV832677	K. K. Sato unpubl	gb_est2:BJ0060342	16.00	84.39	1.9e+05	45	BJ0060342	B0060342	NIBB Mochii
gb_est1:A19833807	16.00	84.66	1.8e+05	43	A19833807	AV833807	K. K. Sato unpubl	gb_est2:BJ007566	16.00	84.39	1.9e+05	45	BJ007566	mps v260	The blue guys
gb_est1:A19837712	16.00	84.66	1.8e+05	43	A19837712	AV837712	Nori Satoh unpubl	gb_est2:BJ007566	16.00	84.39	1.9e+05	45	BJ007566	mps v260	The blue guys
gb_est1:A19837712	16.00	84.66	1.8e+05	43	A19837712	AV837712	Nori Satoh unpubl	gb_est2:BJ007566	16.00	84.39	1.9e+05	45	BJ007566	mps v260	The blue guys

gb_gss:AZ588250	16.00	84.26	1.9e+05	46	! A2588250	1M0396020F	Mouse	10kb	gb_est1:AL643698	-	16.00	83.89	2.0e+05	49	! AL643698	AL643698	XGC-gastrul	
gb_gss:AZ779739	16.00	84.26	1.9e+05	46	! A27766403	1M0563023R	Mouse	10kb	gb_est1:AL649742	+	16.00	83.89	2.0e+05	49	! AL649742	AL649742	XGC-gastrul	
gb_gss:AZ779739	16.00	84.26	1.9e+05	46	! A2777939	2M0012M18R	Mouse	10kb	gb_est1:AL668512	+	16.00	83.89	2.0e+05	49	! AL668512	AL668512	directional	
gb_gss:AZ779739	16.00	84.26	1.9e+05	46	! A2778586	2M0013N16R	Mouse	10kb	gb_est1:AU053904	+	16.00	83.89	2.0e+05	49	! AU053904	AU053904	Dictyostell	
gb_gss:AZ806877	16.00	84.26	1.9e+05	46	! A2806877	2M006914F	Mouse	10kb	gb_est1:AV832408	+	16.00	83.89	2.0e+05	49	! AV832408	AV832408	K. Sato unp	
gb_gss:AZ240H03P	16.00	84.26	1.9e+05	46	! A240H03P	T. brucei	sheared genom		gb_est1:AV832408	+	16.00	83.89	2.0e+05	49	! AV832408	AV832408	K. Sato unp	
gb_est1:AL6427881	16.00	84.13	1.9e+05	47	! A6427881	AL627881	XGC-gastrula	sl	gb_est1:AV832225	+	16.00	83.89	2.0e+05	49	! AV832225	AV832225	K. Sato unp	
gb_est1:AL642997	16.00	84.13	1.9e+05	47	! A642997	AL642997	XGC-neurula	sl	gb_est1:AV860511	+	16.00	83.89	2.0e+05	49	! AV860511	AV860511	Nori Satoh	
gb_est1:AV675259	16.00	84.13	1.9e+05	47	! AV675259	AV675259	Nori Satoh	unp	gb_est1:AW432278	+	16.00	83.89	2.0e+05	49	! AW432278	sh2h02.y1 Gm-cl016		
gb_est2:BJ036309	16.00	84.13	1.9e+05	47	! BJ036309	BJ036309	NIBB	Mochil	nc	gb_est1:AA432254	+	16.00	83.89	2.0e+05	49	! AA432254	vf14c02.y1 NCICGAP_	
gb_est2:BJ043514	16.00	84.13	1.9e+05	47	! BJ043514	BJ043514	NIBB	Mochil	nc	gb_est1:AA515410	+	16.00	83.89	2.0e+05	49	! AA515410	nf68a09.s1 NCICGAP_	
gb_est2:BJ047667	16.00	84.13	1.9e+05	47	! BJ047667	BJ047667	NIBB	Mochil	nc	gb_est1:AA519644	+	16.00	83.89	2.0e+05	49	! AA519644	Tg5Strz2k2h05.s1 TgME	
gb_est2:BJ053798	16.00	84.13	1.9e+05	47	! BJ053798	BJ053798	NIBB	Mochil	nc	gb_est1:AA589132	+	16.00	83.89	2.0e+05	49	! AA589132	Y153g09.r1 Beddingto	
gb_est2:BJ078279	16.00	84.13	1.9e+05	47	! BJ078279	BJ078279	NIBB	Mochil	nc	gb_est1:BG409010	+	16.00	83.89	2.0e+05	49	! BG409010	gb85d05.y1 Moss EST	
gb_est2:C01236	16.00	84.13	1.9e+05	47	! C01236	HUMGS0007957	Human	adult	gb_est2:BJ049272	+	16.00	83.89	2.0e+05	49	! BJ049272	gb82f08.y1 Moss EST		
gb_est2:C12178	16.00	84.13	1.9e+05	47	! C12178	HUMGS0002592	Human	3'-direct	gb_est2:BJ030140	+	16.00	83.89	2.0e+05	49	! BJ030140	NTBB	Mochil	
gb_est2:D18780	16.00	84.13	1.9e+05	47	! D18780	HUMGS000496	Mouse	3'-direct	gb_est2:BJ031525	+	16.00	83.89	2.0e+05	49	! BJ031525	BJ031525	NIBB	Mochil
gb_est2:BE72251	16.00	84.13	1.9e+05	47	! BE72251	601568096F1	NIH_MGC_21		gb_est2:BJ040992	+	16.00	83.89	2.0e+05	49	! BJ040992	BJ040992	NIBB	Mochil
gb_est2:BF026945	16.00	84.13	1.9e+05	47	! BF026945	601671082F1	NIH_MGC_20		gb_est2:BJ050675	+	16.00	83.89	2.0e+05	49	! BJ050675	BJ050675	NIBB	Mochil
gb_est2:BF107886	16.00	84.13	1.9e+05	47	! BF107886	601823895R1	NIH_MGC_79		gb_est2:BJ062980	+	16.00	83.89	2.0e+05	49	! BJ062980	BJ062980	NIBB	Mochil
gb_est2:BF143912	16.00	84.13	1.9e+05	47	! BF143912	601786439F1	NCI_CGAP_Lu		gb_est2:BJ066390	+	16.00	83.89	2.0e+05	49	! BJ066390	BJ066390	NIBB	Mochil
gb_est2:BF573075	16.00	84.13	1.9e+05	47	! BF573075	602078712F2	NIH_MGC_52		gb_est2:BJ066390	+	16.00	83.89	2.0e+05	49	! BJ066390	BJ066390	NIBB	Mochil
gb_gss:AQ025310	16.00	84.13	1.9e+05	47	! AQ025310	EP33513	5-prime	Drosoph	gb_est2:BJ083898	+	16.00	83.89	2.0e+05	49	! BJ083898	BJ083898	NIBB	Mochil
gb_gss:AZ345567	16.00	84.13	1.9e+05	47	! AZ345567	1M0800116F	Mouse	10kb	gb_est2:BM283646	+	16.00	83.89	2.0e+05	49	! BM283646	k150c05.y1 Ascaris s		
gb_gss:AZ433989	16.00	84.13	1.9e+05	47	! AZ433989	1M0220307F	Mouse	10kb	gb_est2:BM283646	+	16.00	83.89	2.0e+05	49	! BM283646	50071-2-9-B10.f.1 Ch		
gb_gss:AZ588937	16.00	84.13	1.9e+05	47	! AZ588937	1M0397M06R	Mouse	10kb	gb_est2:BM395447	+	16.00	83.89	2.0e+05	49	! BM395447	50072-2-9-B10.f.1 Ch		
gb_gss:AZ823735	16.00	84.13	1.9e+05	47	! AZ823735	2M0097N19R	Mouse	10kb	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84.01	2.0e+05	48	! AI004570	0t54h05.s1	Soares	testi	gb_est2:D19180	+	16.00	83.89	2.0e+05	49	! D19180	MUSGS000493	Mouse	3'-di
gb_est1:AI004570	16.00	84																


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gb_est1:AUI04913      + 16.00  83.77  2.0e+05  50  ! AUI04913 AUI04913 Sugano Homo sa
gb_est1:AUI05362      - 16.00  83.77  2.0e+05  50  ! AUI05362 AUI05362 Sugano Homo sa
gb_est1:AUI05386      - 16.00  83.77  2.0e+05  50  ! AUI05386 AUI05386 Sugano Homo sa
gb_est1:AUI05390      - 16.00  83.77  2.0e+05  50  ! AUI05390 AUI05390 Sugano Homo sa
gb_est1:AUI05562      - 16.00  83.77  2.0e+05  50  ! AUI05562 AUI05562 Sugano Homo sa
gb_est1:AUI05572      + 16.00  83.77  2.0e+05  50  ! AUI05572 AUI05572 Sugano Homo sa
gb_est1:AUI05643      + 16.00  83.77  2.0e+05  50  ! AUI05643 AUI05643 Sugano Homo sa
gb_est1:AUI06026      - 16.00  83.77  2.0e+05  50  ! AUI06026 AUI06026 Sugano Homo sa
gb_est1:AUI06451      - 16.00  83.77  2.0e+05  50  ! AUI06451 AUI06451 Sugano Homo sa
gb_est1:AUI06514      + 16.00  83.77  2.0e+05  50  ! AUI06514 AUI06514 Sugano Homo sa
gb_est1:AUI06582      - 16.00  83.77  2.0e+05  50  ! AUI06582 AUI06582 Sugano Homo sa

```

seq_name: gb_est1:AW245664

```

seq_documentation_block:
LOCUS      AW245664              17 bp  mRNA  linear  EST 07-JAN-2000
DEFINITION 2822994.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822994 3',
            mRNA sequence.
ACCESSION  AW245664
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens

```

```

REFERENCE  1 (bases 1 to 17)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Other_ESTs: 2822994.5prime
          Contact: Robert Strausberg, Ph.D.
          Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
          Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
          Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
          project Clone distribution: MGC clone distribution information can
          be found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
          Scores: PHRED from University of Washington Genome Center. Vector
          Trimming: cross_match from University of Washington Genome Center
          PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
          Drosophila Genome Project. University of Washington Genome Center:
          http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
          PHRED high quality bases following vector sequence. Very Low
          Quality Sequence: Trace file contained 17 contiguous distinct peaks
          following vector sequence.
          Plate: LCM10 row: N column: 19.

```

```

FEATURES             Location/Qualifiers
     source            1..17
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822994"
                     /clone_lib="NIH_MGC_7"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"

```

```

     note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
     EcoRI; cDNA made by oligo-dT priming. Directionally
     cloned into EcoRI/XhoI sites using the following 5',
     adaptor: GGCACGAG(G). Size-selected >500bp for average
     insert size 1.8kb. Library constructed by Ling Hong in
     the laboratory of Gerald M. Rubin (University of
     California, Berkeley) using ZAP-cDNA synthesis kit
     (Stratagene) and Superscript II RT (Life Technologies)."
```

```

BASE COUNT      0 a      2 c      1 g      14 t
ORIGIN

```

```

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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```

alignment_block:
US-09-528-682-2 x AW245664/rev ..
Align seg 1/1 to reverse of: AW245664 from: 1 to: 17

```

```

1 LysLysAsn 3
13 AAAAAAAC 5

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seq_name: gb_est1:AW248747

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seq_documentation_block:
LOCUS      AW248747              19 bp  mRNA  linear  EST 07-JAN-2000
DEFINITION 2821119.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821119 3',
            mRNA sequence.
ACCESSION  AW248747
VERSION    AW248747.1 GI:6591740
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens

```

```

REFERENCE  1 (bases 1 to 19)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Other_ESTs: 2821119.5prime
          Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-r@mail.nih.gov
          Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
          Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
          Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
          project Clone distribution: MGC clone distribution information can
          be found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
          Scores: PHRED from University of Washington Genome Center. Vector
          Trimming: cross_match from University of Washington Genome Center
          PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
          Drosophila Genome Project. University of Washington Genome Center:
          http://www.genome.washington.edu Low Quality Sequence: 7 contiguous
          PHRED high quality bases following vector sequence. Very Low
          Quality Sequence: Trace file contained 19 contiguous distinct peaks
          following vector sequence. Polyadenylation: Based upon the presence
          of a XhoI site followed by a run of 14 or more T residues at the
          beginning of the sequence, this cDNA insert was polyadenylated.
          Plate: LCM5 row: P column: 16
          High quality sequence stop: 7.

```

```

FEATURES             Location/Qualifiers
     source            1..19
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821119"
                     /clone_lib="NIH_MGC_7"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"

```

```

     note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
     EcoRI; cDNA made by oligo-dT priming. Directionally
     cloned into EcoRI/XhoI sites using the following 5',
     adaptor: GGCACGAG(G). Size-selected >500bp for average
     insert size 1.8kb. Library constructed by Ling Hong in
     the laboratory of Gerald M. Rubin (University of
     California, Berkeley) using ZAP-cDNA synthesis kit
     (Stratagene) and Superscript II RT (Life Technologies)."
```

```

BASE COUNT      1 a      0 c      0 g      18 t
ORIGIN

```

```

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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alignment_block:

US-09-528-682-2 x AW248747/rev ..

Align seg 1/1 to reverse of: AW248747 from: 1 to: 19

1 LysLysAsn 3
 |||||
 19 AAAAAAAAAAT 11

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ357587 ..

Align seg 1/1 to: AZ357587 from: 1 to: 19

seq_documentation_block:
 LOCUS AZ357587 19 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0099C15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0099C15 F, DNA sequence.

ACCESSION AZ357587
 VERSION AZ357587.1 GI:10471287
 KEYWORDS GSS.

SOURCE

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0099 row: C column: 15
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

1..19
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0099C15"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi14732114|gbAF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT

10 a 0 c 0 g

ORIGIN

9 t

seq_name: gb_gss:AZ357587

seq_documentation_block:

LOCUS AZ357587 19 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0099C15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0099C15 F, DNA sequence.

ACCESSION AZ357587
 VERSION AZ357587.1 GI:10471287
 KEYWORDS GSS.

SOURCE

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0099 row: C column: 15
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

TITLE

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0099 row: C column: 15
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

1..19
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0099C15"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi14732114|gbAF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 10 a 0 c 0 g 9 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ357587/rev ..

Align seg 1/1 to reverse of: AZ357587 from: 1 to: 19

1 LysLysAsn 3
|||||||
18 AAAAAAAT 10

seq_name: gb_gss:AZ358099

seq_documentation_block:

LOCUS AZ358099 19 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0100N12F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0100N12 F, DNA sequence.

ACCESSION AZ358099
VERSION AZ358099
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0100 row: N column: 12

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES
source

1. .19 Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0100N12"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 11 a 0 c 0 g 8 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ358099 ..

Align seg 1/1 to: AZ358099 from: 1 to: 19

1 LysLysAsn 3
|||||||
4 AAAAAAAT 12

seq_name: gb_gss:AZ358099

seq_documentation_block:

LOCUS AZ358099 19 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0100N12F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0100N12 F, DNA sequence.

ACCESSION AZ358099
VERSION AZ358099
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0100 row: N column: 12

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCLM0100N12"

/clone_lib="Mouse 10kb plasmid UUGCLM library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 11 a 0 c 0 g 8 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ358099/rev ..

Align seg 1/1 to reverse of: AZ358099 from: 1 to: 19

1 LysLysAsn 3
|||||
19 AAAAAAAT 11

seq_name: gb_gss:AZ363907

seq_documentation_block:
LOCUS AZ363907 19 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0109113R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0109113 R, DNA sequence.
ACCESSION AZ363907
VERSION AZ363907.1 GI:10477607
KEYWORDS GSS
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0109 row: I column: 13
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19

FEATURES
source

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0109113"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 0 c 0 g 18 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ363907/rev ..

Align seg 1/1 to reverse of: AZ363907 from: 1 to: 19

1 LysLysAsn 3
|||||
18 AAAAAAAT 10

seq_name: gb_gss:AZ509929

seq_documentation_block:
LOCUS AZ509929 19 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0354A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0354A07 F, DNA sequence.

ACCESSION AZ509929
VERSION AZ509929.1 GI:10691245
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0354 row: A column: 07

Seq primer: CGTGTAAACAGCAGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

```
1. .19
Location/Qualifiers
/organism="Mus musculus"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
BASE COUNT      17 a      0 c      0 g      2 t
ORIGIN

alignment_scores:
  Quality:      16.00      Length:      3
  Ratio:        5.333      Gaps:      0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ509929 ..
Align seg 1/1 to: AZ509929 from: 1 to: 19

1 LysLysAsn 3
|||||
8 AAAAAAAT 16

seq_name: gb_gss:AZ514792

seq_documentation_block:
LOCUS      AZ514792      19 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION IM0361B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0361B17 R, DNA sequence.
ACCESSION  AZ514792
VERSION     AZ514792.1 GI:10696108
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
```

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: B column: 17
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

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1. .19
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361B17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

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BASE COUNT      15 a      1 c      1 g      2 t
ORIGIN

alignment_scores:
  Quality:      16.00      Length:      3
  Ratio:        5.333      Gaps:      0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ514792 ..
Align seg 1/1 to: AZ514792 from: 1 to: 19

1 LysLysAsn 3
|||||
2 AAAAAAAC 10

seq_name: gb_gss:AZ611602

seq_documentation_block:
LOCUS      AZ611602      19 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION IM0438G03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0438G03 F, DNA sequence.
ACCESSION  AZ611602
VERSION     AZ611602.1 GI:11733792
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
```


Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0438 row: G column: 03

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. 19

source

FEATURES

1. 19

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="U0GCLM0438G03"

/clone_lib="Mouse 10kb plasmid U0GCLM library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 2 g 17 t

ORIGIN

alignment_scores:

Quality: 16.00 Length: 3

Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ611602/rev

Align seg 1/1 to reverse of: AZ611602 from: 1 to: 19

1 LysLysasn 3
|||||

15 AAAAAAAC 7

seq_name: gb_gss:AZ654747

seq_documentation_block:

LOCUS AZ654747 19 bp DNA linear GSS 14-DEC-2000

DEFINITION IM0529F08F Mouse 10kb plasmid U0GCLM library Mus musculus genomic clone U0GCLM0529F08 F, DNA sequence.

ACCESSION AZ654747

VERSION AZ654747.1 GI:11791893

KEYWORDS

house mouse

Mus musculus

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: F column: 08

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. 19

source

TITLE

JOURNAL COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: F column: 08

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. 19

source

FEATURES

1. 19

source

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="U0GCLM0529F08"

/clone_lib="Mouse 10kb plasmid U0GCLM library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 0 c 0 g 18 t

ORIGIN

alignment_scores:

Quality: 16.00 Length: 3

Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ654747/rev

Align seg 1/1 to reverse of: AZ654747 from: 1 to: 19

1 LysLysasn 3
|||||

14 AAAAAAAT 6

seq_name: gb_gss:AZ764506


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seq_documentation_block:
  19 bp      DNA      linear      GSS 16-FEB-2001
LOCUS      AZ764506
DEFINITION      IM0560N04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                  clone UUGC1M0560N04 R, DNA sequence.
ACCESSION      AZ764506
VERSION        AZ764506.1 GI:12879539
KEYWORDS       GSS.
SOURCE         house mouse.
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 19)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0560 row: N column: 04
                Seq primer: CACACAGGAACACGCTATGACC
                Class: plasmid ends
                High quality sequence stop: 19.
FEATURES       location/Qualifiers
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                /organism="Mus musculus"
                /strain="C57BL/6J"
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                /clone="UUGC1M0560N04"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adapted DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adapted mouse DNA was annealed to
                adapted vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
BASE COUNT      11 a      0 c      0 g      8 t
ORIGIN
alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000
alignment_block:
  US-09-528-682-2 x AZ764506

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Align seg 1/1 to: AZ764506 from: 1 to: 19

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1 LysLysAsn 3
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4 AAAAAAAT 12

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seq_name: gb_gss:AZ764506

seq_documentation_block:

LOCUS AZ764506 19 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0560N04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560N04 R, DNA sequence.

ACCESSION AZ764506

VERSION AZ764506.1 GI:12879539

KEYWORDS GSS.
SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: N column: 04

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

location/Qualifiers

1..19

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0560N04"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 11 a 0 c 0 g 8 t

ORIGIN

alignment_scores:

Percent Similarity: 100.000

Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ764506

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ764506/rev ..

Align seg 1/1 to reverse of: AZ764506 from: 1 to: 19

1 LysLysAsn 3
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19 AAAAAAAT 11

seq_name: gb_gss:AZ764511

seq_documentation_block:

LOCUS AZ764511 19 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0560B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560B08 R, DNA sequence.

ACCESSION AZ764511

VERSION AZ764511.1 GI:12879549

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: B column: 08

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1..19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydronically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

Chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 13 a 0 c 0 g 6 t

ORIGIN

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ764511 ..

Align seg 1/1 to: AZ764511 from: 1 to: 19

1 LysLysAsn 3
|||||
6 AAAAAAAT 14

seq_name: gb_gss:AZ764517

seq_documentation_block:

LOCUS AZ764517 19 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0560L07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560L07 R, DNA sequence.

ACCESSION AZ764517

VERSION AZ764517.1 GI:12879561

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: L column: 07

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1..19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydronically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 16 a 0 c 0 g 3 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ764517 ..

Align seg 1/1 to: AZ764517 from: 1 to: 19

1 LysLysAsn 3
|||||
9 AAAAAAAT 17

seq_name: gb_gss:AZ766990

seq_documentation_block:

LOCUS AZ766990 19 bp DNA linear GSS 16-FEB-2001
DEFINITION LM0564H19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0564H19 R, DNA sequence.

ACCESSION AZ766990
VERSION AZ766990.1 GI:12884624

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mus whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0564 row: H column: 19

Seq primer: CACACAGGAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0564H19"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 16 a 0 c 2 g 1 t
ORIGIN

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ766990 ..

Align seg 1/1 to: AZ766990 from: 1 to: 19

1 LysLysAsn 3
|||||
7 AAAAAAAT 15

seq_name: gb_gss:AZ777642

seq_documentation_block:

LOCUS AZ777642 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0012M20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0012M20 F, DNA sequence.

ACCESSION AZ777642

VERSION AZ777642.1 GI:12906649

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mus whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0012 row: M column: 20

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"


```

/clone="UUGC2M0012M20"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      0 a      0 c      10 g      9 t
ORIGIN

```

```

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

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```

alignment_block:
US-09-528-682-2 x AZ777642/rev ..

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```

Align seg 1/1 to reverse of: AZ777642 from: 1 to: 19

```

```

1 LysLysAsn 3
|||||
9 AAAAAAAC 1

```

```

seq_name: gb_gss:AZ796963

```

```

seq_documentation_block:
LOCUS      AZ796963              19 bp      DNA      linear      GSS 16-FEB-2001.
DEFINITION  2M0052K24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0052K24 R, DNA sequence.

```

```

ACCESSION  AZ796963
VERSION     AZ796963.1      GI:12945556
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus

```

```

REFERENCE   1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunne@genetics.utah.edu
            Insert Length: 10000      Std Error: 0.00
            Plate: 0052 row: K column: 24
            Seq primer: CACACAGGAACAGCTATGACC

```

```

Class: plasmid ends
High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source            1..19
     organism="Mus musculus"
     strain="C57BL/6J"
     db_xref="taxon:10090"
     clone="UUGC2M0052K24"
     clone_lib="Mouse 10kb plasmid UUGC1M library"
     sex="Male"
     lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
     notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      0 a      0 c      10 g      9 t
ORIGIN

```

```

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

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alignment_block:
US-09-528-682-2 x AZ796963/rev ..

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```

Align seg 1/1 to reverse of: AZ796963 from: 1 to: 19

```

```

1 LysLysAsn 3
|||||
18 AAAAAAAC 10

```

```

seq_name: gb_gss:AZ953338

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```

seq_documentation_block:
LOCUS      AZ953338              19 bp      DNA      linear      GSS 27-APR-2001
DEFINITION  2M0218104R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0218104 R, DNA sequence.

```

```

ACCESSION  AZ953338
VERSION     AZ953338.1      GI:13824565
KEYWORDS    GSS.
SOURCE      house mouse.
ORGANISM    Mus musculus

```

```

REFERENCE   1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

```


COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCGTTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13F.
Location/Qualifiers
1. .20
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="ROS060A07"
/clone_lib="BP Chicken Brain Library"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Clon-
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCGCGTTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
Clontech (*6854-1)"
BASE COUNT 2 a 2 c 1 g 15 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AL587630/rev ..

Align seg 1/1 to reverse of: AL587630 from: 1 to: 20

seq_name: gb_est1:AL587727

seq_documentation_block:
LOCUS AL587727 20 bp mRNA linear EST 02-MAR-20
DEFINITION AL587727 BP Chicken Brain Library Gallus gallus cdna clone
ROS061D01, mRNA sequence.
ACCESSION AL587727.1 GI:13192761
VERSION AL587727
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 20)
Murray, F.
AUTHORS BP Chicken Brain Library
TITLE Unpublished (2001)
JOURNAL Contact: Frazer Murray
COMMENT Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCGTTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13F.
Location/Qualifiers
1. .20
/organism="Gallus gallus"


```

/db_xref="taxon:9031"
/clone_lib="BP Chicken Brain Library"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/notes="vector: pSPORT1; Site_1: NotI; Site_2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
CGGCCCGCTTTTTTTTTTTT 3' Poly A RNA purchased from
Clonetechn (*6854-1)"
BASE COUNT      1 a      0 c      1 g      18 t
ORIGIN

```

```

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AL587727/rev ..

```

Align seg 1/1 to reverse of: AL587727 from: 1 to: 20

```

1 LysLysAsn 3
|||||
9 AAAAAAAT 1

```

seq_name: gb_est1:AL587759

```

seq_documentation_block:
LOCUS      AL587759      20 bp      mRNA      linear      EST 02-MAR-2001
DEFINITION      BP Chicken Brain Library Gallus gallus cDNA clone
                ROS061G06, mRNA sequence.
ACCESSION      AL587759
VERSION        AL587759.1 GI:13192793
KEYWORDS       EST.
SOURCE         chicken.
ORGANISM       Gallus gallus

```

```

REFERENCE      1 (bases 1 to 20)
AUTHORS        Murray,F.
TITLE          BP Chicken Brain Library
JOURNAL        Unpublished (2001)
COMMENT        Contact: Frazer Murray
                Dept. Genomics and Bioinformatics
                Roslin Institute
                Roslin, Midlothian, EH25 9PS, UK
                Tel: +44 (0)131 527 4200
                Fax: +44 (0)131 440 0434
                Email: frazer.murray@bbsrc.ac.uk
                CGGCCCGCTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetechn
                (*6854-1)

```

```

Seq primer: M13F.
FEATURES             Location/Qualifiers
     source
     1..20
     /organism="Gallus gallus"
     /db_xref="taxon:9031"
     /clone_lib="BP Chicken Brain Library"
     /tissue_type="Brain"
     /dev_stage="Unknown"
     /lab_host="DH10B"
     /notes="vector: pSPORT1; Site_1: NotI; Site_2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
CGGCCCGCTTTTTTTTTTTT 3' Poly A RNA purchased from
Clonetechn (*6854-1)"
BASE COUNT      2 a      0 c      0 g      18 t
ORIGIN

```

```

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AL587759/rev ..

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Align seg 1/1 to reverse of: AL587759 from: 1 to: 20

```

1 LysLysAsn 3
|||||
9 AAAAAAAT 1

```

seq_name: gb_gss:AZ310481

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seq_documentation_block:
LOCUS      AZ310481
DEFINITION      LM0025023F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
                clone UUGCLM0025023 F, DNA sequence.
ACCESSION      AZ310481
VERSION        AZ310481.1 GI:10352511
KEYWORDS       GSS.
SOURCE         house mouse.
ORGANISM       Mus musculus

```

```

REFERENCE      1 (bases 1 to 20)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
                M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
                and Wright,D., Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0025 row: 0 column: 23
                Seq primer: CGTTGTAACGACGCGCCAGT
                Class: plasmid ends
                High quality sequence stop: 20.

```

```

FEATURES             Location/Qualifiers
     source
     1..20
     /organism="Mus musculus"
     /strain="C57BL/6J"
     /db_xref="taxon:10090"
     /clone_lib="Mouse 10kb plasmid UUGCLM library"
     /sex="Male"
     /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
     /note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

```


with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN

0 a 7 c 5 g 8 t

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ310481/rev ..
Align seg 1/1 to reverse of: AZ310481 from: 1 to: 20

1 LysLysAsn 3
|||||||
13 AAAAAAAC 5

seq_name: gb_gss:AZ316368

seq_documentation_block:

LOCUS AZ316368 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0034L22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0034L22 F, DNA sequence.

ACCESSION AZ316368
VERSION AZ316368.1 GI:10364124

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0034 row: L column: 22

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

FEATURES
source

1..20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0034L22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G11473211419b1AF129072.1), a copy-number inducible derivative of plasmid Ri. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 17 a 0 c 0 g 3 t
ORIGIN

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ316368 ..

Align seg 1/1 to: AZ316368 from: 1 to: 20

1 LysLysAsn 3
|||||||
8 AAAAAAAT 16

seq_name: gb_gss:AZ317019

seq_documentation_block:

LOCUS AZ317019 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0035P14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0035P14 F, DNA sequence.

ACCESSION AZ317019

VERSION AZ317019.1 GI:10365404

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0035 row: P column: 14

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

FEATURES
source

1..20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0035P14"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 0 c 7 g 1 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ317019 ..

Align seg 1/1 to: AZ317019 from: 1 to: 20

1 LysLysAsn 3
|||||
3 AAAAAAAT 11

seq_name: gb_gss:AZ341237

seq_documentation_block:

LOCUS AZ341237 20 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0073G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0073G03 R, DNA sequence.

ACCESSION AZ341237
VERSION AZ341237.1 GI:10417288
KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL plasmid inserts

COMMENT Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0073 row: G column: 03

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

FEATURES source

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC1M0073G03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 19 a 0 c 0 g 1 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ341237 ..

Align seg 1/1 to: AZ341237 from: 1 to: 20

1 LysLysAsn 3
|||||
12 AAAAAAAT 20

seq_name: gb_gss:AZ368518

seq_documentation_block:

LOCUS AZ368518 20 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0118G09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0118G09 R, DNA sequence.

ACCESSION AZ368518
VERSION AZ368518.1 GI:10482218
KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL plasmid inserts

COMMENT Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0118 row: G column: 09
 Seq primer: CACACAGGAACAGCTAGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES

source

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1..20
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0118G09"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
  
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BASE COUNT 16 a 1 c 0 g 3 t
 ORIGIN

alignment_scores:
 Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ368518 ..

Align seg 1/1 to: AZ368518 from: 1 to: 20

1 LysLysAsn 3
 |||||
 7 AAAAAAAC 15

seq_name: gb_gss:AZ375620

seq_documentation_block:

LOCUS AZ375620 20 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0129A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0129A08 F. DNA sequence.

ACCESSION AZ375620

VERSION AZ375620.1 GI:10489320

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 20)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
 and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0129 row: A column: 08
 Seq primer: CGTTGTAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES

source

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1..20
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0129A08"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
  
```

BASE COUNT 19 a 0 c 0 g 1 t
 ORIGIN

alignment_scores:

Quality: 16.00 Length: 3
 Ratio: 5.333 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ375620 ..

Align seg 1/1 to: AZ375620 from: 1 to: 20

1 LysLysAsn 3
 |||||
 1 AAAAAAAT 9

seq_name: gb_gss:AZ427740

seq_documentation_block:

LOCUS AZ427740 20 bp DNA linear GSS 03-OCT-2000
 DEFINITION 1M0209J23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0209J23 R. DNA sequence.

ACCESSION AZ427740

VERSION AZ427740.1 GI:10551753

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 20)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
 and Wright,D., Weiss,R.

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0209 row: J column: 23

Seq primer: CACACGAGAACACGTATGACC

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

Location/Qualifiers

1..20

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0209J23"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

12 a 5 c 3 t

BASE COUNT

ORIGIN

alignment_scores:

Quality: 16.00 Length: 3

Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ427740 ..

Align seg 1/1 to: AZ427740 from: 1 to: 20

1 LysLysAsn 3

|||||

6 AAAAAAAC 14

seq_name: gb_gss:AZ486787

seq_documentation_block:

LOCUS AZ486787 20 bp DNA linear GSS 05-OCT-2000

DEFINITION IM0315D23F Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC1M0315D23 F, DNA sequence.

ACCESSION AZ486787

VERSION AZ486787.1 GI:10653904

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

GSS.

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0315 row: D column: 23

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0315D23"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

0 a 0 c 1 g 19 t

BASE COUNT

ORIGIN

alignment_scores:

Quality: 16.00 Length: 3

Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ486787/rev ..

Align seg 1/1 to reverse of: AZ486787 from: 1 to: 20

1 LysLysAsn 3

|||||

12 AAAAAAAC 4

seq_name: gb_gss:AZ506216


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seq_documentation_block:
  20 bp      DNA      linear      GSS 05-OCT-2000
LOCUS      1M0347G11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION      clone UUGCIM0347G11 F, DNA sequence.
ACCESSION      AZ506216
VERSION        AZ506216.1 GI:10687532
KEYWORDS       GSS.
SOURCE         house mouse.
ORGANISM       Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D.,Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0347 row: G column: 11
              Seq primer: CGTGTAAACACGCGCCAGT
              Class: plasmid ends
              High quality sequence stop: 20.
FEATURES       Location/Qualifiers
              1..20
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGCIM0347G11"
                /clone_lib="Mouse 10kb plasmid UUGCIM library"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydronamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptored DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gil4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptored mouse DNA was annealed to
                adaptored vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
              13 a      0 c      0 g      7 t
BASE COUNT      13 a      0 c      0 g      7 t
ORIGIN
alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000
alignment_block:
  US-09-528-682-2 x AZ506216

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Align seg 1/1 to: AZ506216 from: 1 to: 20

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1 LysLysAsn 3
|||||
6 AAAAAAAT 14

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seq_name: gb_gss:AZ584232

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seq_documentation_block:
  20 bp      DNA      linear      GSS 13-DEC-2000
LOCUS      AZ584232
DEFINITION      1M0388A12R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
              clone UUGCIM0388A12 R, DNA sequence.
ACCESSION      AZ584232
VERSION        AZ584232.1 GI:11704906
KEYWORDS       GSS.
SOURCE         house mouse.
ORGANISM       Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D.,Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0388 row: A column: 12
              Seq primer: CACACAGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 20.
FEATURES       Location/Qualifiers
              1..20
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGCIM0388A12"
                /clone_lib="Mouse 10kb plasmid UUGCIM library"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydronamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptored DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gil4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptored mouse DNA was annealed to
                adaptored vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
              8 a      12 c      0 g      0 t
BASE COUNT      8 a      12 c      0 g      0 t
ORIGIN
alignment_scores:

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Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ584232 ..

Align seg 1/1 to: AZ584232 from: 1 to: 20

1 LysLysasn 3
|||||
1 AAAAAAAC 9

seq_name: gb_gss:AZ633741

seq_documentation_block:

LOCUS AZ633741 20 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0489G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0489G12 F, DNA sequence.

ACCESSION AZ633741

VERSION AZ633741.1 GI:11755931

KEYWORDS GSS

SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0489 row: G column: 12

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

source

1..20

Location/Qualifiers

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0489G12"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

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10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (g14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

BASE COUNT
ORIGIN

18 a 2 c 0 g 0 t

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

alignment_scores:

Quality: 16.00 Length: 3

Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ633741 ..

Align seg 1/1 to: AZ633741 from: 1 to: 20

1 LysLysasn 3

|||||

8 AAAAAAAC 16

seq_name: gb_gss:AZ764493

seq_documentation_block:

LOCUS AZ764493 20 bp DNA linear GSS 16-FEB-2001

DEFINITION IM0560E04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0560E04 R, DNA sequence.

ACCESSION AZ764493

VERSION AZ764493.1 GI:12879513

KEYWORDS GSS

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
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University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: E column: 04

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0560E04"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (g14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 0 c 0 g 8 t

ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ764493 ..

Align seg 1/1 to: AZ764493 from: 1 to: 20

1 LysLysAsn 3
|||||
5 AAAAAAAT 13

seq_name: gb_gss:AZ764493

seq_documentation_block:

LOCUS AZ764493 20 bp DNA linear GSS 16-FEB-2001
DEFINITION LM0560E04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560E04 R, DNA sequence.

ACCESSION AZ764493

VERSION AZ764493.1 GI:12879513

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: E column: 04

Seq primer: CACACGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0560E04"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold. T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted mouse DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 0 c 0 g 8 t

ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ764493/rev ..

Align seg 1/1 to reverse of: AZ764493 from: 1 to: 20

1 LysLysAsn 3
|||||
20 AAAAAAAT 12

seq_name: gb_gss:AZ764514

seq_documentation_block:

LOCUS AZ764514 20 bp DNA linear GSS 16-FEB-2001
DEFINITION LM0560F09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560F09 R, DNA sequence.

ACCESSION AZ764514

VERSION AZ764514.1 GI:12879555

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: F column: 09

Seq primer: CACACGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"


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/clone="UUGC1M0560F09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gii14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      13 a      0 c      0 g      7 t
ORIGIN

```

```

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

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alignment_block:
US-09-528-682-2 x AZ764514 ..

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Align seg 1/1 to: AZ764514 from: 1 to: 20

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1 LysLysAsn 3
|||||
6 AAAAAAAT 14

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```
seq_name: gb_gss:AZ773905

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seq_documentation_block:
LOCUS      AZ773905      20 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION  2M0001C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0001C15 R, DNA sequence.

```

```

ACCESSION  AZ773905
VERSION    AZ773905.1 GI:12898761
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus

```

```

REFERENCE
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,
and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

```

JOURNAL
COMMENT    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0001 row: C column: 15
Seq primer: CACACAGGAACAGCTATGACC

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```

Class: plasmid ends
High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source            1..20
     organism="Mus musculus"
     strain="C57BL/6J"
     db_xref="taxon:10090"
     clone="UUGC2M0001C15"
     clone_lib="Mouse 10kb plasmid UUGC1M library"
     sex="Male"
     lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
     notes="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gii14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      7 a      0 c      0 g      13 t
ORIGIN

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alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

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alignment_block:
US-09-528-682-2 x AZ773905/rev ..

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Align seg 1/1 to reverse of: AZ773905 from: 1 to: 20

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1 LysLysAsn 3
|||||
15 AAAAAAAT 7

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seq_name: gb_gss:AZ786781

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seq_documentation_block:
LOCUS      AZ786781      20 bp      DNA      linear      GSS-16-FEB-2001
DEFINITION  2M0032C03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0032C05 R, DNA sequence.

```

```

ACCESSION  AZ786781
VERSION    AZ786781.1 GI:12924886
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus

```

```

REFERENCE
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,
and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

```

JOURNAL
COMMENT    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

```



```

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0032 row: C column: 05
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0032C05"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
3 a 3 c 0 g 14 t
BASE COUNT
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ786781/rev ..
Align seg 1/1 to reverse of: AZ786781 from: 1 to: 20

1 LysLysAsn 3
|||||
18 AAAAAAAT 10

seq_name: gb_gss:AZ789280
seq_documentation_block:
LOCUS AZ789280 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0037A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0037A08 F, DNA sequence.
ACCESSION AZ789280
VERSION AZ789280.1 GI:12930134
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

TITLE
JOURNAL
COMMENT
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: A column: 08
Seq primer: CTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0037A08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
13 a 4 c 0 g 3 t
BASE COUNT
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ789280 ..
Align seg 1/1 to: AZ789280 from: 1 to: 20

1 LysLysAsn 3
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9 AAAAAAAT 17

seq_name: gb_gss:AZ816496
seq_documentation_block:
LOCUS AZ816496 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0085G16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0085G16 F, DNA sequence.
ACCESSION AZ816496
VERSION AZ816496.1 GI:12986404
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

```


REFERENCE
AUTHORS
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0085 row: G column: 16
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source

1. .20
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0085G16"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 0 a 3 c 3 g 14 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ816496/rev ..
Align seg 1/1 to reverse of: AZ816496 from: 1 to: 20

1 LysLysAsn 3
20 AAGAAAAAC 12

seq_name: gb_gss:AZ832043

seq_documentation_block:
LOCUS AZ832043 20 bp DNA linear GSS 20-FEB-2001

DEFINITION
2M0112111F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUC2M0112111 F, DNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0112 row: I column: 11
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source

1. .20
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0112111"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 3 a 5 c 1 g 11 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ832043/rev ..
Align seg 1/1 to reverse of: AZ832043 from: 1 to: 20

1 LysLysAsn 3


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|||||
12 AAGAAAAAT 4

seq_name: gb_gss:A2862308

seq_documentation_block:
LOCUS      A2862308                20 bp    DNA        linear        GSS 21-FEB-2001
DEFINITION 2M0169020F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0169020 F, DNA sequence.
ACCESSION  A2862308
VERSION    A2862308.1 GI:13059481
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0169 row: 0 column: 20
            Seq primer: CGTGTAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES   Location/Qualifiers
            source          1..20
                        /organism="Mus musculus"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="UUGC2M0169020"
                        /clone_lib="Mouse 10kb plasmid UUGC1M library"
                        /sex="Male"
                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                        /note="vector: PWD42nv; Purified genomic DNA from M.
                        Musculus C57BL/6J (male) was obtained from the Jackson
                        Laboratory Mouse DNA Resource
                        (http://www.jax.org/resources/documents/dnares/). The DNA
                        was hydrodynamically sheared by repeated passage through a
                        0.005 inch orifice at constant velocity. The sheared DNA
                        was blunt end-repaired with T4 DNA polymerase and T4
                        polynucleotide kinase. Adaptor oligonucleotides were
                        ligated to the blunt ends in high molar excess. The
                        adapted DNA was purified and size-selected for a 9.5 to
                        10.5 kb range using preparative agarose gel
                        electrophoresis. Vector DNA was prepared from a derivative
                        of pWD42 (gil14732114|gb|AF129072.1), a copy-number
                        inducible derivative of plasmid R1. The vector was ligated
                        with adaptors complementary to the insert adaptors and
                        purified. The sheared, adapted mouse DNA was annealed to
                        adapted vector DNA, and transformed into
                        chemically-competent E. coli XL10-Gold (Stratagene) cells
                        and selected for ampicillin resistance."
BASE COUNT      2 a      1 c      7 g      10 t
ORIGIN

alignment_scores:
Quality:      16.00      Length:      3
Ratio:        5.333      Gaps:      0
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ862308/rev
Align seg 1/1 to reverse of: AZ862308 from: 1 to: 20

1 LysLysAsn 3
|||||
11 AAAAAAGAAAT 3

seq_name: gb_gss:A2943013

seq_documentation_block:
LOCUS      AZ943013                20 bp    DNA        linear        GSS 26-APR-2001
DEFINITION 2M0203C01R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0203C01 R, DNA sequence.
ACCESSION  AZ943013
VERSION    AZ943013.1 GI:13806752
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0203 row: C column: 01
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES   Location/Qualifiers
            source          1..20
                        /organism="Mus musculus"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="UUGC2M0203C01"
                        /clone_lib="Mouse 10kb plasmid UUGC2M library"
                        /sex="Female"
                        /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                        /note="vector: PWD42nv; Purified genomic DNA from M.
                        Musculus C57BL/6J (female) was obtained from the Jackson
                        Laboratory Mouse DNA Resource
                        (http://www.jax.org/resources/documents/dnares/). The DNA
                        was hydrodynamically sheared by repeated passage through a
                        0.005 inch orifice at constant velocity. The sheared DNA
                        was blunt end-repaired with T4 DNA polymerase and T4
                        polynucleotide kinase. Adaptor oligonucleotides were
                        ligated to the blunt ends in high molar excess. The
                        adapted DNA was purified and size-selected for a 9.5 to
                        10.5 kb range using preparative agarose gel
                        electrophoresis. Vector DNA was prepared from a derivative
                        of pWD42 (gil14732114|gb|AF129072.1), a copy-number
                        inducible derivative of plasmid R1. The vector was ligated
                        with adaptors complementary to the insert adaptors and
                        purified. The sheared, adapted mouse DNA was annealed to
                        adapted vector DNA, and transformed into
                        chemically-competent E. coli XL10-Gold (Stratagene) cells
                        and selected for ampicillin resistance."
BASE COUNT      11 a      9 c      0 g      0 t
ORIGIN

```


ORIGIN

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ943013 ..

Align seg 1/1 to: AZ943013 from: 1 to: 20

1 LysLysAsn 3
|||||
4 AAAAAAAC 12

seq_name: gb_gss:AZ949997

seq_documentation_block:

LOCUS AZ949997 20 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0213D24R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0213D24 R, DNA sequence.

ACCESSION AZ949997

VERSION AZ949997.1 GI:13821224

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0213 row: D column: 24

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

source

1..20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0213D24"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi14732114|gb|AF129072.1), a copy-number

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x AZ949997 ..

Align seg 1/1 to: AZ949997 from: 1 to: 20

1 LysLysAsn 3

|||||

1 AAAAAAAT 9

seq_name: gb_gss:AZ969913

seq_documentation_block:

LOCUS AZ969913 20 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0242C22R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0242C22 R, DNA sequence.

ACCESSION AZ969913

VERSION AZ969913.1 GI:13841140

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

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Unpublished (2000)

Contact: Robert B. Weiss

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0242 row: C column: 22

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

source

1..20
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0242C22"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (gii4732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 2 c 3 g 12 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ969913/rev ..

Align seg 1/1 to reverse of: AZ969913 from: 1 to: 20

1 LysLysAsn 3
|||||
9 AAGAAAAAT 1

seq_name: gb_est1:AW248782

seq_documentation_block:
LOCUS AW248782 21 bp mRNA linear EST 07-JAN-2000
DEFINITION 2821017.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821017 3',
mRNA sequence.
ACCESSION AW248782
VERSION AW248782.1 GI:6591775
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 21)
NTH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other_ESTs: 2821017.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu/LowQuality> Sequence: 21 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 21 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LICM5 row: L column: 10
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Homo sapiens"

FEATURES
source

/db_xref="taxon:9606"
/clone="IMAGE:2821017"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 2 a 0 c 0 g 19 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AW248782/rev ..

Align seg 1/1 to reverse of: AW248782 from: 1 to: 21

1 LysLysAsn 3
|||||
20 AAAAAAAT 12

seq_name: gb_est2:TI7609

seq_documentation_block:
LOCUS TI7609 21 bp mRNA linear EST 06-JUN-1994
DEFINITION mps v321 The blue guys library Saccharomyces cerevisiae cDNA sequence upstream of LacZ fusion, mRNA sequence.

ACCESSION TI7609
VERSION TI7609.1 GI:458631
KEYWORDS EST.

SOURCE baker's yeast.
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 21)
Burns,N., Grimwade,B., Ross-Macdonald,P.B., Choi,E.-Y., Finberg,K., Roeder,G.S. and Snyder,M.
Large-scale analysis of gene expression, protein localization and gene disruption in Saccharomyces cerevisiae
Genes Dev. 8, 1087-1105 (1994)

REFERENCE 1 (bases 1 to 21)
AUTHORS Burns,N., Grimwade,B., Ross-Macdonald,P.B., Choi,E.-Y., Finberg,K., Roeder,G.S. and Snyder,M.
TITLE Large-scale analysis of gene expression, protein localization and gene disruption in Saccharomyces cerevisiae

JOURNAL Genes Dev. 8, 1087-1105 (1994)
MEDLINE 95011603
COMMENT Contact: Snyder M
Department of Biology
Yale University
New Haven CT 06520-8103
Tel: 2034326139
Fax: 2034326161
Email: snymicp@yalevm.ycc.yale.edu

LacZ fusion; Vegetative expression; Beta-gal fusion localization pattern:
50 cytoplasmic spots. Sequence below near or adjacent to lacZ.

Seq primer: LacZ sequences in transposon.

FEATURES
source
1..21
/organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
/clone_lib="The blue guys library"
/lab_host="E.coli"

/note="Vector: pRECMtn; A yeast genomic DNA library was prepared in the vector pHS56, and subjected to transposon mutagenesis with mtn3. This mini-transposon carries lacZ sequences that lack an initiation codon; expression of

lacZ is only provided by in frame fusion to yeast coding sequence. The yeast genomic DNA carrying the transposon was excised from pH8S6 and transplanted back onto the yeast chromosome. Yeast colonies expressing lacZ were screened for in a color assay. A plasmid containing the genomic DNA/lacZ fusion junction was recovered from each individual yeast colony that expressed lacZ activity. These recovered plasmids comprise 'The blue guys library'. The fusion junction was then sequenced to identify the expressed ORF upstream of the fusion."

BASE COUNT 5 a 4 c 1 g 11 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x T17609/rev ..

Align seg 1/1 to reverse of: T17609 from: 1 to: 21

1 LysLysAsn 3
|||||||
21 AAAAAAAT 13

seq_name: gb_gss:AZ308846

seq_documentation_block:

LOCUS AZ308846 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0012H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0012H15 F, DNA sequence.

ACCESSION AZ308846
VERSION AZ308846.1 GI:10349246
KEYWORDS GSS.
SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0012 row: H column: 15

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0012H15"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 2 c 1 g 18 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ308846/rev ..

Align seg 1/1 to reverse of: AZ308846 from: 1 to: 21

1 LysLysAsn 3
|||||||
17 AAAAAAAT 9

seq_name: gb_gss:AZ309774

seq_documentation_block:

LOCUS AZ309774 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0017F01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0017F01 F, DNA sequence.

ACCESSION AZ309774
VERSION AZ309774.1 GI:10351103
KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

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University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0017 row: F column: 01

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/strain="C57BL/6J"


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/db_xref="taxon:10090"
/clone="UUGCLM0017F01"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      0 c      11 g      10 t
ORIGIN

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ309774/rev ..

Align seg 1/1 to reverse of: AZ309774 from: 1 to: 21

1 LysLysAsn 3
|||||
19 AAAAAAAC 11

seq_name: gb_gss:AZ316019

seq_documentation_block:
LOCUS      AZ316019      21 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION IM0033C05R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0033C05 R, DNA sequence.
ACCESSION  AZ316019
VERSION     AZ316019.1 GI:10363426
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: gdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0033 row: C column: 05

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Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
FEATURES             location/Qualifiers
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     /strain="C57BL/6J"
     /db_xref="taxon:10090"
     /clone="UUGCLM0033C05"
     /clone_lib="Mouse 10kb plasmid UUGCLM library"
     /sex="Male"
     /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
     /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      18 a      3 c      0 g      0 t
ORIGIN

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x AZ316019 ..

Align seg 1/1 to: AZ316019 from: 1 to: 21

1 LysLysAsn 3
|||||
9 AAAAAAAC 17

```


Wed Jun 19 08:58:14 2002

us-09-528-682-2.p2n.rst

Page 35

/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-183-650-23 - 16.00 98.04 899.81 21 1 S
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-228-942-8 - 16.00 98.04 899.81 21 1 Se
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-726-278-2 + 16.00 98.04 899.81 21 1 Se
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-085-476-3 - 16.00 98.04 899.81 21 1 Se
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-474-542A-148 + 16.00 98.04 899.81 21 1 S
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-052-404-11 - 16.00 97.70 940.16 22 1 S
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-474-542A-148 + 16.00 97.70 940.16 22 1 S
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-474-542A-149 - 16.00 97.70 940.16 22 1 S
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-123-449A-1 - 16.00 97.70 940.16 22 1 S
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-123-449A-2 - 16.00 97.70 940.16 22 1 S
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-457-648-148 + 16.00 97.70 940.16 22 1 S
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-457-648-149 - 16.00 97.70 940.16 22 1 S
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-479-156-11 - 16.00 97.70 940.16 22 1 S
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-480-220A-5 - 16.00 97.70 940.16 22 1 S
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-458-050-2 - 16.00 97.70 940.16 22 1 S
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-458-050-2 - 16.00 97.70 940.16 22 1 S
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-690-300-1 - 16.00 97.70 940.16 22 1 S
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/cgn2_6/ptodata/2/ina/6B COMB. seq:US-08-819-646-18 +	16.00	94.95	1.3e+03	32	I	S	
/cgn2_6/ptodata/2/ina/6B COMB. seq:US-08-819-646-18 +	16.00	94.95	1.3e+03	32	I	S	
/cgn2_6/ptodata/2/ina/6B COMB. seq:US-08-819-646-18 +	16.00	94.95	1.3e+03	32	I	S	
/cgn2_6/ptodata/2/ina/6B COMB. seq:US-08-819-646-18 +	16.00	94.95	1.3e+03	32	I	S	
/cgn2_6/ptodata/2/ina/6B COMB. seq:US-08-819-646-18 +	16.00	94.95	1.3e+03	32	I	S	
/cgn2_6/ptodata/2/ina/6B COMB. seq:US-08-819-646-18 +	16.00	94.95	1.3e+03	32	I	S	
/cgn2_6/ptodata/2/ina/6B COMB. seq:US-08-819-646-18 +	16.00	94.95	1.3e+03	32	I	S	
/cgn2_6/ptodata/2/ina/6B COMB. seq:US-08-819-646-18 +	16.00	94.95	1.3e+03	32	I	S	
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/cgn2_6/ptodata/2/ina/6B COMB. seq:US-08-819-646-18 +	16.00	94.95	1.3e+03	32	I	S	
/cgn2_6/ptodata/2/ina/6B COMB. seq:US-08-819-646-18 +	16.00	94.95	1.3e+03	32	I	S	
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/cgn2_6/ptodata/2/ina/6B COMB. seq:US-08-819-646-18 +	16.00	94.95	1.3e+03	32	I	S	
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-908-317-33 - 16.00 92.95 1.7e+03 42 1 S
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-490-803-3 - 16.00 92.95 1.7e+03 42 1 Se
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-758-626-21 - 16.00 92.95 1.7e+03 42 1 S
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-453-956-7 - 16.00 92.95 1.7e+03 42 1 Se
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-086-631-7 - 16.00 92.95 1.7e+03 42 1 Se
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-629-600-13 + 16.00 92.95 1.7e+03 42 1 S
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seq_documentation_block:
; Sequence 2, Application US/08994824
; Patent No. 6008400
; GENERAL INFORMATION:
; APPLICANT: Scarlinge, Stephen A.
; APPLICANT: Caruthers, Marvin H.
; TITLE OF INVENTION: NOVEL PROTECTING GROUPS AND USE THEREOF
; TITLE OF INVENTION: IN AN IMPROVED PROCESS FOR OLIGONUCLEOTIDE SYNTHESIS
; NUMBER OF SEQUENCES: 9
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dan Cleveland, Jr.
; STREET: 1790 30th Street, Suite 140
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/994,824
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,878
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cleveland, Dan
; REGISTRATION NUMBER: 36,106
; REFERENCE/DOCKET NUMBER: 9028/103
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)449-9497
; TELEFAX: (303)449-0814
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; US-08-994-824-2
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Percent Similarity: 100.000 Percent Identity: 100.000
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US-09-528-682-2 x US-08-994-824-2 ..
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1 LysLysAsn 3
|||||
2 AAAAAAAT 10
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seq_documentation_block:
; Sequence 3, Application US/08994824
; Patent No. 6008400
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; GENERAL INFORMATION:
; APPLICANT: Scarlinge, Stephen A.
; APPLICANT: Caruthers, Marvin H.
; TITLE OF INVENTION: NOVEL PROTECTING GROUPS AND USE THEREOF
; TITLE OF INVENTION: IN AN IMPROVED PROCESS FOR OLIGONUCLEOTIDE SYNTHESIS
; NUMBER OF SEQUENCES: 9
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```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dan Cleveland, Jr.
; STREET: 1790 30th Street, Suite 140
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80301
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/994,824
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,878
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cleveland, Dan
; REGISTRATION NUMBER: 36,106
; REFERENCE/DOCKET NUMBER: 9028/103
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)449-9497
; TELEFAX: (303)449-0814
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (synthetic)
; US-08-994-824-3
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  Quality: 16.00 Length: 3
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Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:
US-09-528-682-2 x US-08-994-824-3 ..
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Align seg 1/1 to: US-08-994-824-3 from: 1 to: 10
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```
1 LysLysAsn 3
|||||
2 AAAAAAAT 10
```

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seq_documentation_block:
; Sequence 4, Application US/09404430
; Patent No. 6350853
; GENERAL INFORMATION:
; APPLICANT: Neilsen, Peter
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; APPLICANT: Knudsen, Helle
; TITLE OF INVENTION: Conjugated Peptide Nucleic Acids Having Enhanced
; TITLE OF INVENTION: Cellular Uptake
; FILE REFERENCE: ISIS4181
; CURRENT APPLICATION NUMBER: US/09/404,430
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; CURRENT FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US08/564,765
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6350853el Sequence
US-09-404-430-4

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-528-682-2 x US-09-404-430-4/rev ..

Align seg 1/1 to reverse of: US-09-404-430-4 from: 1 to: 10

1 LysLysasn 3
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10 AAAAAAAT 2

seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US96-09915-2

seq_documentation_block:
; Sequence 2, Application PC/TUS9609915
; GENERAL INFORMATION:
; APPLICANT: Scarlinge, Stephen A.
; APPLICANT: Caruthers, Marvin H.
; TITLE OF INVENTION: NOVEL PROTECTING GROUPS AND USE THEREOF
; TITLE OF INVENTION: IN AN IMPROVED PROCESS FOR OLIGONUCLEOTIDE SYNTHESIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven C. Petersen
; STREET: 1900 Fifteenth Street
; CITY: Boulder
; STATE: CO
; COUNTRY: USA
; ZIP: 80302
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09915
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/488,878
; FILING DATE: 09-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Petersen, Steven C.
; REGISTRATION NUMBER: 36,238
; REFERENCE/DOCKET NUMBER: file no. 16840-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-546-1300
; TELEFAX: 303-449-5426
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA (synthetic)"
PCT-US96-09915-2

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-528-682-2 x PCT-US96-09915-2 ..

Align seg 1/1 to: PCT-US96-09915-2 from: 1 to: 10

1 LysLysasn 3
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2 AAAAAAAT 10

seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US96-09915-3

seq_documentation_block:

; Sequence 3, Application PC/TUS9609915
; GENERAL INFORMATION:
; APPLICANT: Scarlinge, Stephen A.
; APPLICANT: Caruthers, Marvin H.
; TITLE OF INVENTION: NOVEL PROTECTING GROUPS AND USE THEREOF
; TITLE OF INVENTION: IN AN IMPROVED PROCESS FOR OLIGONUCLEOTIDE SYNTHESIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven C. Petersen
; STREET: 1900 Fifteenth Street
; CITY: Boulder
; STATE: CO
; COUNTRY: USA
; ZIP: 80302
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09915
; FILING DATE: 07-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/488,878
; FILING DATE: 09-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Petersen, Steven C.
; REGISTRATION NUMBER: 36,238
; REFERENCE/DOCKET NUMBER: file no. 16840-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-546-1300
; TELEFAX: 303-449-5426
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "RNA (synthetic)"
PCT-US96-09915-3

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x PCT-US96-09915-3 ..

Align seg 1/1 to: PCT-US96-09915-3 from: 1 to: 10


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1 LysLysAsn 3
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2 AAAAAAAT 10

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-244-794A-9

seq_documentation_block:
; Sequence 9, Application US/09244794A
; Patent No. 6214553
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350006
; CURRENT APPLICATION NUMBER: US/09/244,794A
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: 1997-01-27
; PRIOR APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: 09/007,005
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-244-794A-9

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-244-794A-9 ..

Align seg 1/1 to: US-09-244-794A-9 from: 1 to: 12

1 LysLysAsn 3
|||||
3 AAAAAAAT 10

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-007-005-9

seq_documentation_block:
; Sequence 9, Application US/09007005B
; Patent No. 6238558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
; PRIOR APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Translation template
US-09-007-005-9

alignment_scores:
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Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-007-005-9 ..

Align seg 1/1 to: US-09-007-005-9 from: 1 to: 12

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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-247-190-9

seq_documentation_block:
; Sequence 9, Application US/09247190
; Patent No. 6261804
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350005
; CURRENT APPLICATION NUMBER: US/09/247,190
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-21
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-247-190-9

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-247-190-9 ..

Align seg 1/1 to: US-09-247-190-9 from: 1 to: 12

1 LysLysAsn 3
|||||
3 AAAAAAAT 11

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-244-796-9

seq_documentation_block:
; Sequence 9, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
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;; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
;; FILE REFERENCE: 00786/350007
;; CURRENT APPLICATION NUMBER: US/09/244,796
;; CURRENT FILING DATE: 1999-02-05
;; EARLIER APPLICATION NUMBER: 60/035,963
;; EARLIER FILING DATE: 1997-01-27
;; EARLIER APPLICATION NUMBER: 60/064,491
;; EARLIER FILING DATE: 1997-11-06
;; EARLIER APPLICATION NUMBER: 09/007,005
;; EARLIER FILING DATE: 1998-01-14
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 9
;; LENGTH: 12
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Translation template
US-09-244-796-9

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-244-796-9 ..

Align seg 1/1 to: US-09-244-796-9 from: 1 to: 12

1 LysLysasn 3
|||||
3 AAAAAAAC 11

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-393-783A-39

seq_documentation_block:
; Sequence 39, Application US/09393783A
; Patent No. 6355428
; GENERAL INFORMATION:
; APPLICANT: Schroth, Gary P.
; APPLICANT: Bruice, Thomas Wayne
; APPLICANT: Sub. Young J.
; TITLE OF INVENTION: Nucleic Acid Ligand Interaction Assays
; FILE REFERENCE: 4600-0128.30
; CURRENT APPLICATION NUMBER: US/09/393,783A
; CURRENT FILING DATE: 1999-10-09
; PRIOR APPLICATION NUMBER: US 09/151,890
; PRIOR FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 3.0
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; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; NAME/KEY: misc_binding
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; OTHER INFORMATION: studies
US-09-393-783A-39

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-393-783A-39 ..

Align seg 1/1 to: US-09-393-783A-39 from: 1 to: 12

1 LysLysasn 3
|||||
3 AAAAAAAC 11

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-621-502A-3

seq_documentation_block:
; Sequence 3, Application US/08621502A
; Patent No. 5763591
; GENERAL INFORMATION:
; APPLICANT: Toyoda Ph.D., Hiroo
; APPLICANT: Formby Ph.D., Bent
; TITLE OF INVENTION: POLYNUCLEIC ACID SEQUENCES THAT ARE
; FUNCTIONALLY ASSOCIATED WITH THE DEVELOPMENT OF AUTOIMMUNE
; DISEASE
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,502A
; FILING DATE: 25-MAR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fujita Esq., Sharon M.
; REGISTRATION NUMBER: 38,459
; REFERENCE/DOCKET NUMBER: P07 34324
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213/622-7700
; TELEFAX: 213/489-4210
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
US-08-621-502A-3

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-08-621-502A-3/rev ..

Align seg 1/1 to reverse of: US-08-621-502A-3 from: 1 to: 13

1 LysLysasn 3
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10 AAAAAAAC 2

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-781-550-19

seq_documentation_block:
; Sequence 19, Application US/08781550
; Patent No. 5861242
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark


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; APPLICANT: Gingeras, Thomas R.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Morris, Macdonald S.
; TITLE OF INVENTION: HIV Diagnosis by Arrays of Nucleic Acid
; TITLE OF INVENTION: Probes on Biological Chips
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,550
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/082,937
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1046.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-781-550-19

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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1 LysLysAsn 3
13 AAAAAAAC 5

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-544-381B-198
seq_documentation_block:
; Sequence 198, Application US/08544381B
; Patent No. 6027880
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Miyada, Charles Garrett
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Chee, Mark
; APPLICANT: Fodor, Stephen P.A.
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; APPLICANT: Huang, Xiaohua C.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
; TITLE OF INVENTION: Detecting Cystic Fibrosis
; NUMBER OF SEQUENCES: 250
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/544,381B
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/510,521
; FILING DATE: 02-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-0041300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 198:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
; US-08-544-381B-198

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to reverse of: US-08-544-381B-198 from: 1 to: 13

1 LysLysAsn 3
13 AAAAAAAC 5

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-308-367-9
seq_documentation_block:
; Sequence 9, Application US/09308367A
; Patent No. 6043060
; GENERAL INFORMATION:
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; APPLICANT: IMANISHI, Takeshi
; TITLE OF INVENTION: NOVEL NUCLEOTIDE ANALOGUES
; FILE REFERENCE: IMANISHI-1
; CURRENT APPLICATION NUMBER: US/09/308,367A
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: PCT/JP97/04187
; EARLIER FILING DATE: 1997-11-18
; EARLIER APPLICATION NUMBER: JAPAN 306585/1996
; EARLIER FILING DATE: 1996-11-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-308-367-9

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-308-367-9/rev ..

Align seg 1/1 to reverse of: US-09-308-367-9 from: 1 to: 13

1 LysLysAsn 3
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9 AAAAAAAC 1

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-308-367-10

seq_documentation_block:
; Sequence 10, Application US/09308367A
; Patent No. 6043060
; GENERAL INFORMATION:
; APPLICANT: IMANISHI, Takeshi
; TITLE OF INVENTION: NOVEL NUCLEOTIDE ANALOGUES
; FILE REFERENCE: IMANISHI-1
; CURRENT APPLICATION NUMBER: US/09/308,367A
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: PCT/JP97/04187
; EARLIER FILING DATE: 1997-11-18
; EARLIER APPLICATION NUMBER: JAPAN 306585/1996
; EARLIER FILING DATE: 1996-11-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; OTHER INFORMATION: n is 3'-O, 4'-C-methylene uridine
US-09-308-367-10

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-308-367-10/rev ..

Align seg 1/1 to reverse of: US-09-308-367-10 from: 1 to: 13

1 LysLysAsn 3

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9 AAAAAAAC 1
seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-380-638A-10

seq_documentation_block:
; Sequence 10, Application US/09380638A
; Patent No. 6268490
; GENERAL INFORMATION:
; APPLICANT: IMANISHI, Takeshi
; APPLICANT: OBIKA, Satoshi
; TITLE OF INVENTION: NOVEL BICYCLONUCLEOSIDE AND OLIGONUCLEOTIDE ANALOGUE
; FILE REFERENCE: IMANISHI-2
; CURRENT APPLICATION NUMBER: US/09/380,638A
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: PCT/JP98/00945
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: JP 53409/1997
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 13
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-380-638A-10

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-380-638A-10/rev ..

Align seg 1/1 to reverse of: US-09-380-638A-10 from: 1 to: 13

1 LysLysAsn 3
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9 AAAAAAAC 1

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-380-638A-11

seq_documentation_block:
; Sequence 11, Application US/09380638A
; Patent No. 6268490
; GENERAL INFORMATION:
; APPLICANT: IMANISHI, Takeshi
; APPLICANT: OBIKA, Satoshi
; TITLE OF INVENTION: NOVEL BICYCLONUCLEOSIDE AND OLIGONUCLEOTIDE ANALOGUE
; FILE REFERENCE: IMANISHI-2
; CURRENT APPLICATION NUMBER: US/09/380,638A
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: PCT/JP98/00945
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: JP 53409/1997
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: DNA
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: n at positions 11 and 12 is unknown
US-09-380-638A-11

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-380-638A-11/rev ..

Align seg 1/1 to reverse of: US-09-380-638A-11 from: 1 to: 13

1 LysLysAsn 3
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9 AAAAAAAC 1

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-778-794A-7

seq_documentation_block:

; Sequence 7, Application US/08778794A

; Patent No. 6309823

; GENERAL INFORMATION:

; APPLICANT: Cronin, Maureen T.

; APPLICANT: Miyada, Charles Garrett

; APPLICANT: Hubbell, Earl A.

; APPLICANT: Chee, Mark

; APPLICANT: Fodor, Stephen P.A.

; APPLICANT: Huang, Xiaohua C.

; APPLICANT: Lipshutz, Robert J.

; APPLICANT: Lobban, Peter E.

; APPLICANT: Morris, MacDonald S.

; APPLICANT: Sheldon, Edward L.

; TITLE OF INVENTION: Arrays of Nucleic Acid Probes

; TITLE OF INVENTION: for Analyzing Biotransformation Genes

; NUMBER OF SEQUENCES: 156

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/778,794A

; FILING DATE: 03-JAN-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/143,312

; FILING DATE: 26-OCT-1993

; APPLICATION NUMBER: US 08/284,064

; FILING DATE: 02-AUG-1994

; APPLICATION NUMBER: WO PCT/US94/12305

; FILING DATE: 26-OCT-1994

; APPLICATION NUMBER: US 08/510,521

; FILING DATE: 02-AUG-1995

; APPLICATION NUMBER: US 08/544,381

; FILING DATE: 10-OCT-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Liebeschuetz, Joe

; REGISTRATION NUMBER: 37,505

; REFERENCE/DOCKET NUMBER: 018547-015700US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0200

; TELEX:

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; US-08-778-794A-7

alignment_scores:

Quality: 16.00 Length: 3

Ratio: 5.333 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-08-778-794A-7/rev ..

Align seg 1/1 to reverse of: US-08-778-794A-7 from: 1 to: 13

1 LysLysAsn 3
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13 AAAAAAAC 5

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-424-921-5

seq_documentation_block:

; Sequence 5, Application US/08424921

; Patent No. 5545552

; GENERAL INFORMATION:

; APPLICANT: Machur, Eric A

; TITLE OF INVENTION: PURIFIED THERMOSTABLE PYROCOCCLUS

; TITLE OF INVENTION: FURIOSUS DNA POLYMERASE I

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bingham & Fitting

; STREET: 12526 High Bluff Road, Suite 300

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92130

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/424,921

; FILING DATE: 19-APR-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/803,627

; FILING DATE: 02-DEC-1991

; APPLICATION NUMBER: US 07/620,568

; FILING DATE: 03-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/657,073

; FILING DATE: 19-FEB-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/776,552

; FILING DATE: 15-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitting, Thomas

; REGISTRATION NUMBER: 34,163

; REFERENCE/DOCKET NUMBER: STG0100P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-792-3680

; TELEFAX: 619-792-8477

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; US-08-424-921-5

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

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Align seg 1/1 to: US-08-424-921-5 from: 1 to: 14

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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-424-921-6

seq_documentation_block:

; Sequence 6, Application US/08424921
; Patent No. 5545552
; GENERAL INFORMATION:
; APPLICANT: Mathur, Eric A
; TITLE OF INVENTION: PURIFIED THERMOSTABLE PYROCOCCLUS
; TITLE OF INVENTION: FURIOUS DNA POLYMERASE I
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bingham & Fitting
; STREET: 12526 High Bluff Road, Suite 300
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,921
; FILING DATE: 19-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/803,627
; FILING DATE: 02-DEC-1991
; APPLICATION NUMBER: US 07/620,568
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/657,073
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/776,552
; FILING DATE: 15-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: STG0100P
; TELEPHONE: 619-792-3680
; TELEFAX: 619-792-8477
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-424-921-6

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-08-424-921-6/rev ..

Align seg 1/1 to reverse of: US-08-424-921-6 from: 1 to: 14

1 LysLysAsn 3
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11 AAGAAGAAC 3

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-455-627-8

seq_documentation_block:

; Sequence 8, Application US/08455627
; Patent No. 5571677
; GENERAL INFORMATION:
; APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; TITLE OF INVENTION: Connected Macromolecular Structures
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-455-627-8

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-08-455-627-8 ..

Align seg 1/1 to: US-08-455-627-8 from: 1 to: 14

1 LysLysAsn 3
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6 AAAAAAAC 14

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-689-856-8

seq_documentation_block:

; Sequence 8, Application US/08689856
; Patent No. 5830658
; GENERAL INFORMATION:

APPLICANT: Sergei M. Gryaznov
; TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,856
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,627
; FILING DATE: 31-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Jackie N.
; REGISTRATION NUMBER: 35,966
; REFERENCE/DOCKET NUMBER: LYNX-003/01 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-689-856-8

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-08-689-856-8 ..

Align seg 1/1 to: US-08-689-856-8 from: 1 to: 14

1 LysLysAsn 3
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6 AAAAAAAC 14

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-556-355A-5

seq_documentation_block:
; Sequence 5, Application US/08556355A
; Patent No. 5866395
; GENERAL INFORMATION:
; APPLICANT: MATHUR, Eric J.
; TITLE OF INVENTION: Purified Thermostable Pyrococcus
; TITLE OF INVENTION: Purified Thermostable Pyrococcus
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,355A
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,921
; FILING DATE: 19-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/803,627
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,846
; FILING DATE: 21-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/657,073
; FILING DATE: 19-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,568
; FILING DATE: 03-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barker, M. Paul
; REGISTRATION NUMBER: 32,013
; REFERENCE/DOCKET NUMBER: 04121.0004-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-556-355A-5

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to: US-08-556-355A-5 from: 1 to: 14

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4 AARARAA 12

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-556-355A-6

seq_documentation_block:
; Sequence 6, Application US/08556355A
; Patent No. 5866395
; GENERAL INFORMATION:
; APPLICANT: MATHUR, Eric J.
; TITLE OF INVENTION: Purified Thermostable Pyrococcus
; TITLE OF INVENTION: Purified Thermostable Pyrococcus
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:


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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556.355A
; FILING DATE: 13-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,921
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 07/803,627
; FILING DATE: 02-DEC-1991
; APPLICATION NUMBER: US 07/779,846
; FILING DATE: 21-OCT-1991
; APPLICATION NUMBER: US 07/657,073
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/620,568
; FILING DATE: 03-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barker, M. Paul
; REGISTRATION NUMBER: 32,013
; REFERENCE/DOCKET NUMBER: 04121.0004-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-556-355A-6

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-08-556-355A-6/rev ..

Align seg 1/1 to reverse of: US-08-556-355A-6 from: 1 to: 14
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seq_name: /cgn2_6/ptodata/2/1na/5B_COMB.seq:US-07-803-627A-5

seq_documentation_block:
; Sequence 5, Application US/07803627A
; Patent No. 5948663
; GENERAL INFORMATION:
; APPLICANT: MATHUR, Eric J.
; TITLE OF INVENTION: Purified Thermostable Pyrococcus
; TITLE OF INVENTION: furiosus DNA Polymerase I
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/803.627A
; FILING DATE: 02-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/776,552
; FILING DATE: 14-OCT-1991
; APPLICATION NUMBER: US 07/657,073
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: US 07/620,568
; FILING DATE: 03-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barker, M. Paul
; REGISTRATION NUMBER: 32,013
; REFERENCE/DOCKET NUMBER: 04121.0004-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-07-803-627A-5

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alignment_block:
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4 AAAAAAA 12

seq_name: /cgn2_6/ptodata/2/1na/5B_COMB.seq:US-07-803-627A-6

seq_documentation_block:
; Sequence 6, Application US/07803627A
; Patent No. 5948663
; GENERAL INFORMATION:
; APPLICANT: MATHUR, Eric J.
; TITLE OF INVENTION: Purified Thermostable Pyrococcus
; TITLE OF INVENTION: furiosus DNA Polymerase I
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/803.627A
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; FILING DATE: 02-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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; FILING DATE: 14-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/657,073
; FILING DATE: 19-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,568
; FILING DATE: 03-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barker, M. Paul
; REGISTRATION NUMBER: 32,013
; REFERENCE/DOCKET NUMBER: 04121.0004-00
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; US-07-803-627A-6

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
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11 AARARAAY 3

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-849-021-11

seq_documentation_block:
; Sequence 11, Application US/08849021
; Patent No. 5953276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; ADDRESSEE: COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELEPHONE: 302-892-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-849-021-11

alignment_scores:
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  Percent Similarity: 100.000  Percent Identity: 100.000

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12 AAAAAAAAC 4

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-765-340-164

seq_documentation_block:
; Sequence 164, Application US/08765340
; Patent No. 6150092
; GENERAL INFORMATION:
; APPLICANT: UCHIDA, K.,
; APPLICANT: UCHIDA, T.,
; APPLICANT: TANAKA, Y.,
; APPLICANT: MATSUDA, Y.,
; APPLICANT: KONDO, S.
; TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
; TITLE OF INVENTION: COMPOUND
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,340
; FILING DATE: 23-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 145146/94
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 311130/94
; FILING DATE: 21-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SERUNIAN, LESLIE
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 1452-4005
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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; US-08-765-340-164

alignment_scores:
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  Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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11 AAGAAAAAT 3

seq_name: /cgn2_6/ptodata/2/lna/6B_COMB.seq:US-08-787-321-8

seq_documentation_block:
; Sequence 8, Application US/08787321A
; Patent No. 6180777
; GENERAL INFORMATION:
; APPLICANT: Horn, Thomas
; TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
; FILE REFERENCE: (1300)-1199.002
; CURRENT APPLICATION NUMBER: US/08/787,321A
; CURRENT FILING DATE: 1997-01-03
; EARLIER APPLICATION NUMBER: US PROV 60/009,918
; EARLIER FILING DATE: 1996-01-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-08-787-321-8

alignment_scores:
  Quality: 16.00 Length: 3
  Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-08-787-321-8 ..
Align seg 1/1 to: US-08-787-321-8 from: 1 to: 14

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6 AAAAAAAC 14

seq_name: /cgn2_6/ptodata/2/lna/5B_COMB.seq:US-08-292-620A-355

seq_documentation_block:
; Sequence 355, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
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; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 355:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-355

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Percent Similarity: 100.000 Percent Identity: 100.000

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seq_name: /cgn2_6/ptodata/2/lna/5B_COMB.seq:US-08-292-620A-356

seq_documentation_block:
; Sequence 356, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
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two

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 356:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-356

two

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-08-292-620A-356/rev ..

Align seg 1/1 to reverse of: US-08-292-620A-356 from: 1 to: 15

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13 AAAAAAAT 5

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-292-620A-357

seq_documentation_block:
; Sequence 357, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 357:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-357

two

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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Align seg 1/1 to reverse of: US-08-292-620A-357 from: 1 to: 15

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12 AAAAAAAT 4

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-292-620A-358

seq_documentation_block:
; Sequence 358, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 358:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-358

two

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-08-292-620A-358/rev ..

Align seg 1/1 to reverse of: US-08-292-620A-358 from: 1 to: 15

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-292-620A-359

seq_documentation_block:
; Sequence 359, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:

APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 359:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-359

two

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-08-292-620A-359/rev ..

Align seg 1/1 to reverse of: US-08-292-620A-359 from: 1 to: 15

1 LysLysAsn 3
|||||||
10 AAAAAAAT 2

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-292-620A-360

seq_documentation_block:
; Sequence 360, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:


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; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 360:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-360

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-08-292-620A-360/rev ..
Align seg 1/1 to reverse of: US-08-292-620A-360 from: 1 to: 15

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-585-684B-29
seq_documentation_block:
; Sequence 29, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

two

; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-585-684B-29

alignment_scores:
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  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-08-585-684B-29/rev ..
Align seg 1/1 to reverse of: US-08-585-684B-29 from: 1 to: 15

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-585-684B-30
seq_documentation_block:
; Sequence 30, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
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; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-585-684B-30

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alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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alignment_block:
US-09-528-682-2 x US-08-585-684B-30/rev ..

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Align seg 1/1 to reverse of: US-08-585-684B-30 from: 1 to: 15

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1 LysLysAsn 3
|||||
13 AAGAAAAAT 5

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seq_name: /cgn2_6/ptodata/2/1na/5B_COMB.seq:US-08-585-684B-31

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seq_documentation_block:
; Sequence 31, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-585-684B-31

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alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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alignment_block:
US-09-528-682-2 x US-08-585-684B-31/rev ..

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Align seg 1/1 to reverse of: US-08-585-684B-31 from: 1 to: 15

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1 LysLysAsn 3
|||||
12 AAGAAAAAT 4

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seq_name: /cgn2_6/ptodata/2/1na/5B_COMB.seq:US-08-585-684B-32

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seq_documentation_block:
; Sequence 32, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995

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; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-585-684B-32

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-528-682-2 x US-08-585-684B-32/rev ..

Align seg 1/1 to reverse of: US-08-585-684B-32 from: 1 to: 15

1 LysLysAsn 3
|||||||
11 AAGAAAAAT 3

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-585-684B-33

seq_documentation_block:
; Sequence 33, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 33:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-585-684B-33

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-528-682-2 x US-08-585-684B-33/rev ..

Align seg 1/1 to reverse of: US-08-585-684B-33 from: 1 to: 15

1 LysLysAsn 3
|||||||
10 AAGAAAAAT 2

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-763-354-3

seq_documentation_block:
; Sequence 3, Application US/08763354
; Patent No. 5965721
; GENERAL INFORMATION:
; APPLICANT: Cook, Philip Dan
; APPLICANT: Sanghri, Yogesh H.
; APPLICANT: Vasseur, Jean J.
; APPLICANT: Debart, Francoise
; TITLE OF INVENTION: Backbone Modified Oligonucleotide Analogs
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/763,354
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 703,619
; FILING DATE: 21-MAY-1991
; APPLICATION NUMBER: US 566,836
; FILING DATE: 13-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 558,663
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lucci, Joseph
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2404
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: NO
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US-08-763-354-3

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-08-763-354-3/rev ..

Align seg 1/1 to reverse of: US-08-763-354-3 from: 1 to: 15

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11 AAAAAAAC 3

seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-08-956-182-32

seq_documentation_block:
; Sequence 32, Application US/08956182
; Patent No. 6100450
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: NOVEL SEED SPECIFIC PROMOTERS BASED ON
; TITLE OF INVENTION: ARABIDOPSIS GENES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,182
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-956-182-32

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-08-956-182-32 ..

Align seg 1/1 to: US-08-956-182-32 from: 1 to: 15

1 LysLysAsn 3

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3 AAGAAGAAC 11

seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-09-071-845-355

seq_documentation_block:
; Sequence 355, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 355:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-355

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-071-845-355/rev ..

Align seg 1/1 to reverse of: US-09-071-845-355 from: 1 to: 15

1 LysLysAsn 3

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14 AAAAAAAT 6

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-071-845-356

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seq_documentation_block:
; Sequence 356, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 356:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-356
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alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:

US-09-528-682-2 x US-09-071-845-356/rev ..

Align seg 1/1 to reverse of: US-09-071-845-356 from: 1 to: 15

1 LysLysAsn 3

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13 AAAAAAAT 5

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-071-845-357

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seq_documentation_block:
; Sequence 357, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 357:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-357
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  Ratio: 5.333        Gaps: 0
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alignment_block:

US-09-528-682-2 x US-09-071-845-357/rev ..

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12 AAAAAAAAAA 4

seq_name: /cgn2_6/ptodata/2/lna/6A_COMB.seq:US-09-071-845-358

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; Sequence 358, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
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; APPLICATION NUMBER: US/09/071.845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292.620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008.895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989.849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 358:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-358
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Percent Similarity: 100.000      Percent Identity: 100.000
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US-09-528-682-2 x US-09-071-845-358/rev ..

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11 AAAAAAAAAA 3

seq_name: /cgn2_6/ptodata/2/lna/6A_COMB.seq:US-09-071-845-359

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seq_documentation_block:
; Sequence 359, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
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; APPLICATION NUMBER: US/09/071.845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292.620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008.895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989.849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 359:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-359
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  Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000
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10 AAAAAAAT 2

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seq_documentation_block:
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; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
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; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 360:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-845-360
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Align seg 1/1 to reverse of: US-09-071-845-360 from: 1 to: 15

1 LysLysAsn 3

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9 AAAAAAAT 1

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-038-073-29

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; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-038-073-29
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Percent Similarity: 100.000 Percent Identity: 100.000
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Align seg 1/1 to reverse of: US-09-038-073-29 from: 1 to: 15

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14 AAAAAAAT 6

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-038-073-30

seq_documentation_block:

; Sequence 30, Application US/09038073

; Patent No. 6194150

; GENERAL INFORMATION:

; APPLICANT: Stinchcomb, Daniel T.

APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038.073
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-038-073-30

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

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Align seg 1/1 to reverse of: US-09-038-073-30 from: 1 to: 15

1 LysLysAsn 3
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13 AAGAAAAAT 5

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Date: Jun 18, 2002 9:42 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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Search information block:

Query: US-09-528-682-2

Query length: 3

Database: Pending_Patents_NA_Main:*

Database sequences: 21979536

Database length: -2067452561

Search time (sec): 7363.740000

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; Sequence 66, Application PC/TUS0116352
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc
; APPLICANT: Anastasio, Allison E
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y
; APPLICANT: Denton, R. Rex
; APPLICANT: Lee, Helen H.
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: Haplotypes of the PON2 Gene
; FILE REFERENCE: MWH-0563PCT PON2
; CURRENT APPLICATION NUMBER: PCT/US01/16352
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,145
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
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; Sequence 130, Application PC/TUS0123100
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Duda, Amy
; APPLICANT: Koshi, Beena
; APPLICANT: Sanchis, Angela
; TITLE OF INVENTION: Haplotypes of the CHRNA1 Gene
; FILE REFERENCE: MWH-0771PCT CHRNA1
; CURRENT APPLICATION NUMBER: PCT/US01/23100
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/219,538
; PRIOR FILING DATE: 2000-07-20
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; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Duda, Amy
; APPLICANT: Koshi, Beena
; APPLICANT: Sanchis, Angela
; TITLE OF INVENTION: Haplotypes of the CHRNA1 Gene
; FILE REFERENCE: MWH-0771PCT CHRNA1
; CURRENT APPLICATION NUMBER: PCT/US01/23100
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/219,538
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 189
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seq_documentation_block:
; Sequence 2, Application US/08488878A
; GENERAL INFORMATION:
; APPLICANT: Scaringe, Stephen A.
; APPLICANT: Caruthers, Marvin H.
; TITLE OF INVENTION: NOVEL PROTECTING GROUPS AND USE THEREOF
; TITLE OF INVENTION: IN AN IMPROVED PROCESS FOR OLIGONUCLEOTIDE SYNTHESIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dan Cleveland, Jr.
; STREET: 1790 30th Street, Suite 140
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80301
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,878A
; FILING DATE: 09-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Cleveland, Dan
; REGISTRATION NUMBER: 36,106
; REFERENCE/DOCKET NUMBER: 9028/103
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)449-9497
; TELEFAX: (303)449-0814
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; US-08-488-878A-2
```

```
alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000
```

alignment_block:

US-09-528-682-2 x US-08-488-878A-2 ..

Align seg 1/1 to: US-08-488-878A-2 from: 1 to: 10

```
1 LysLysAsn 3
|||||
2 AAAAAAAT 10
```

seq_name: /cgn2_6/ptodata/2/pna/US084_COMB.seq:us-08-488-878A-3

```
seq_documentation_block:
; Sequence 3, Application US/08488878A
; GENERAL INFORMATION:
; APPLICANT: Scarlinge, Stephen A.
; APPLICANT: Caruthers, Marvin H.
; TITLE OF INVENTION: NOVEL PROTECTING GROUPS AND USE THEREOF
; TITLE OF INVENTION: IN AN IMPROVED PROCESS FOR OLIGONUCLEOTIDE SYNTHESIS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dan Cleveland, Jr.
; STREET: 1790 30th Street, Suite 140
; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,878A
; FILING DATE: 09-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Cleveland, Dan
; REGISTRATION NUMBER: 36,106
; REFERENCE/DOCKET NUMBER: 9028/103
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)449-9497
; TELEFAX: (303)449-0814
```

```
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (synthetic)
; US-08-488-878A-3
```

alignment_scores:

```
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000
```

alignment_block:

US-09-528-682-2 x US-08-488-878A-3 ..

Align seg 1/1 to: US-08-488-878A-3 from: 1 to: 10

```
1 LysLysAsn 3
|||||
2 AAAAAAAT 10
```

seq_name: /cgn2_6/ptodata/2/pna/US088_COMB.seq:us-08-864-765A-4

seq_documentation_block:

```
; Sequence 4, Application US/08864765A
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Peter
; APPLICANT: Knudsen, Helle
; TITLE OF INVENTION: Conjugated Peptide Nucleic Acids Having
; TITLE OF INVENTION: Enhanced Cellular Uptake
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,765A
; FILING DATE: 28-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Luccl, Joseph
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: No
; FEATURE: aminoethyl glycine monomers
; US-08-864-765A-4
```

alignment_scores:

```
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000
```



```
alignment_block:
US-09-528-682-2 x US-08-864-765A-4/rev ..
Align seg 1/1 to reverse of: US-08-864-765A-4 from: 1 to: 10

1 LysLysAsn 3
|||||
10 AAAAAAAT 2

seq_name: /cgn2_6/ptodata/2/pna/US090_COMB.seq:US-09-012-031-29
seq_documentation_block:
; Sequence 29, Application US/09012031
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; FILE REFERENCE: 1107.73251
; CURRENT APPLICATION NUMBER: US/09/012,031A
; CURRENT FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: 60/035,917
; EARLIER FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 317
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-012-031-29

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-012-031-29/rev ..
Align seg 1/1 to reverse of: US-09-012-031-29 from: 1 to: 10

1 LysLysAsn 3
|||||
9 AAGAAAAAC 1

seq_name: /cgn2_6/ptodata/2/pna/US090_COMB.seq:US-09-012-031B-29
seq_documentation_block:
; Sequence 29, Application US/09012031B
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; FILE REFERENCE: 1107.73251
; CURRENT APPLICATION NUMBER: US/09/012,031B
; CURRENT FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/035,917
; PRIOR FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-012-031B-29

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-012-031B-29/rev ..
Align seg 1/1 to reverse of: US-09-012-031B-29 from: 1 to: 10

1 LysLysAsn 3
|||||
9 AAGAAAAAC 1

seq_name: /cgn2_6/ptodata/2/pna/US090_COMB.seq:US-09-012-031-29
seq_documentation_block:
; Sequence 29, Application US/09012031
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; FILE REFERENCE: 1107.73251
; CURRENT APPLICATION NUMBER: US/09/012,031
; CURRENT FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: 60/035,917
; EARLIER FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 301
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,031
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/035,917
; FILING DATE: 23-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.73251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-012-031-29

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-012-031-29/rev ..
Align seg 1/1 to reverse of: US-09-012-031-29 from: 1 to: 10

1 LysLysAsn 3
|||||
9 AAGAAAAAC 1

seq_name: /cgn2_6/ptodata/2/pna/US090_COMB.seq:US-09-012-031-29
seq_documentation_block:
```


seq_name: /cgn2_6/ptodata/2/pna/US090_COMB.seq:US-09-012-031C-29

```
seq_documentation_block:
; Sequence 29, Application US/09012031C
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/012,031C
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: 60/035,917
; PRIOR FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-012-031C-29
```

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-012-031C-29/rev ..
Align seg 1/1 to reverse of: US-09-012-031C-29 from: 1 to: 10

```
1 LysLysAsn 3
|||||
9 AAGAAAAAC 1
```

seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-29

```
seq_documentation_block:
; Sequence 29, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-29
```

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-335-032-29/rev ..
Align seg 1/1 to reverse of: US-09-335-032-29 from: 1 to: 10

```
1 LysLysAsn 3
|||||
9 AAGAAAAAC 1
```

seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-834

```
seq_documentation_block:
; Sequence 834, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 834
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-834
```

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-335-032-834/rev ..
Align seg 1/1 to reverse of: US-09-335-032-834 from: 1 to: 10

```
1 LysLysAsn 3
|||||
9 AAGAAAAAC 1
```

seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-1327

```
seq_documentation_block:
; Sequence 1327, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1327
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-1327
```

alignment_scores:
Quality: 16.00 Length: 3


```
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x US-09-335-032-1327/rev ..
Align seg 1/1 to reverse of: US-09-335-032-1327 from: 1 to: 10
1 LysLysAsn 3
|||||
10 AAGAAGAAT 2
seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-2227
seq_documentation_block:
; Sequence 2227, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; TITLE OF INVENTION: Transcriptome
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2227
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-2227
alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x US-09-335-032-2227/rev ..
Align seg 1/1 to reverse of: US-09-335-032-2227 from: 1 to: 10
1 LysLysAsn 3
|||||
10 AAGAAGAAT 2
seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-3613
seq_documentation_block:
; Sequence 3613, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; TITLE OF INVENTION: Transcriptome
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3613
; LENGTH: 10
```

```
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-3613
alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x US-09-335-032-3613 ..
Align seg 1/1 to: US-09-335-032-3613 from: 1 to: 10
1 LysLysAsn 3
|||||
2 AAAAAAAT 10
seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-4055
seq_documentation_block:
; Sequence 4055, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; TITLE OF INVENTION: Transcriptome
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4055
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-4055
alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x US-09-335-032-4055/rev ..
Align seg 1/1 to reverse of: US-09-335-032-4055 from: 1 to: 10
1 LysLysAsn 3
|||||
9 AAAAAAAT 1
seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-5135
seq_documentation_block:
; Sequence 5135, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; TITLE OF INVENTION: Transcriptome
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
```



```
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5135
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-5135
```

```
alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
```

```
alignment_block:
US-09-528-682-2 x US-09-335-032-5135 ..
```

```
Align seg 1/1 to: US-09-335-032-5135 from: 1 to: 10
```

```
1 LysLysAsn 3
|||||
2 AAAAAAAT 10
```

```
seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-5136
```

```
seq_documentation_block:
; Sequence 5136, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; PRIOR FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5136
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-5136
```

```
alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
```

```
alignment_block:
US-09-528-682-2 x US-09-335-032-5136 ..
```

```
Align seg 1/1 to: US-09-335-032-5136 from: 1 to: 10
```

```
1 LysLysAsn 3
|||||
1 AAAAAAAT 9
```

```
seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-5274
```

```
seq_documentation_block:
; Sequence 5274, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
```

```
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; PRIOR FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5274
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-5274
```

```
alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
```

```
alignment_block:
US-09-528-682-2 x US-09-335-032-5274 ..
```

```
Align seg 1/1 to: US-09-335-032-5274 from: 1 to: 10
```

```
1 LysLysAsn 3
|||||
2 AAGAAGAAC 10
```

```
seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-7067
```

```
seq_documentation_block:
; Sequence 7067, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; PRIOR FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7067
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-7067
```

```
alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
```

```
alignment_block:
US-09-528-682-2 x US-09-335-032-7067/rev ..
```

```
Align seg 1/1 to reverse of: US-09-335-032-7067 from: 1 to: 10
```

```
1 LysLysAsn 3
|||||
9 AAAAAAAT 1
```


seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-7234

```
seq_documentation_block:
; Sequence 7234, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; TITLE OF INVENTION: Transcriptome
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7234
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-7234
```

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-335-032-7234 ..
Align seg 1/1 to: US-09-335-032-7234 from: 1 to: 10

```
1 LysLysAsn 3
|||||
2 AAGAAAAAT 10
```

seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-8515

```
seq_documentation_block:
; Sequence 8515, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; TITLE OF INVENTION: Transcriptome
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8515
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-8515
```

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-335-032-8515 ..

Align seg 1/1 to: US-09-335-032-8515 from: 1 to: 10

```
1 LysLysAsn 3
|||||
2 AAGAAAAAT 10
```

seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-8981

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seq_documentation_block:
; Sequence 8981, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; TITLE OF INVENTION: Transcriptome
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8981
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-8981
```

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-335-032-8981/rev ..

Align seg 1/1 to reverse of: US-09-335-032-8981 from: 1 to: 10

```
1 LysLysAsn 3
|||||
10 AAGAAAAAT 2
```

seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-10245

```
seq_documentation_block:
; Sequence 10245, Application US/09335032
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; TITLE OF INVENTION: Transcriptome
; FILE REFERENCE: 01107.78572
; CURRENT APPLICATION NUMBER: US/09/335,032
; CURRENT FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: US 60/035,917
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/012,031
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 12219
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10245
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-10245
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alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
  US-09-528-682-2 x US-09-335-032-10245/rev ..
  Align seg 1/1 to reverse of: US-09-335-032-10245 from: 1 to: 10
    1 LysLysAsn 3
      |||||
      9 AAAAGAAC 1
  seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-10335
  seq_documentation_block:
    ; Sequence 10335, Application US/09335032
    ; GENERAL INFORMATION:
    ; APPLICANT: Velculescu, Victor
    ; APPLICANT: Vogelstein, Bert
    ; APPLICANT: Kinzler, Kenneth
    ; TITLE OF INVENTION: Characterization of the Yeast
    ; TITLE OF INVENTION: Transcriptome
    ; FILE REFERENCE: 01107.78572
    ; CURRENT APPLICATION NUMBER: US/09/335.032
    ; PRIOR FILING DATE: 1999-06-16
    ; PRIOR APPLICATION NUMBER: US 60/035,917
    ; PRIOR FILING DATE: 1997-01-23
    ; PRIOR APPLICATION NUMBER: US 09/012,031
    ; PRIOR FILING DATE: 1998-01-22
    ; NUMBER OF SEQ ID NOS: 12219
    ; SOFTWARE: FastSeq for Windows Version 4.0
    ; SEQ ID NO 10335
    ; LENGTH: 10
    ; TYPE: DNA
    ; ORGANISM: Saccharomyces cerevisiae
    ; US-09-335-032-10335

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
  US-09-528-682-2 x US-09-335-032-10335/rev ..
  Align seg 1/1 to reverse of: US-09-335-032-10335 from: 1 to: 10
    1 LysLysAsn 3
      |||||
      9 AAGAAAC 1
  seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-10339
  seq_documentation_block:
    ; Sequence 10339, Application US/09335032
    ; GENERAL INFORMATION:
    ; APPLICANT: Velculescu, Victor
    ; APPLICANT: Vogelstein, Bert
    ; APPLICANT: Kinzler, Kenneth
    ; TITLE OF INVENTION: Characterization of the Yeast
    ; TITLE OF INVENTION: Transcriptome
    ; FILE REFERENCE: 01107.78572
    ; CURRENT APPLICATION NUMBER: US/09/335.032
    ; CURRENT FILING DATE: 1999-06-16
    ; PRIOR APPLICATION NUMBER: US 60/035,917
    ; PRIOR FILING DATE: 1997-01-23
    ; PRIOR APPLICATION NUMBER: US 09/012,031
    ; PRIOR FILING DATE: 1998-01-22
    ; NUMBER OF SEQ ID NOS: 12219
    ; SOFTWARE: FastSeq for Windows Version 4.0
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```
; SEQ ID NO 10339
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-10339

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
  US-09-528-682-2 x US-09-335-032-10339 ..
  Align seg 1/1 to: US-09-335-032-10339 from: 1 to: 10
    1 LysLysAsn 3
      |||||
      2 AAAAAAAT 10
  seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-336-376-4493
  seq_documentation_block:
    ; Sequence 4493, Application US/09336376
    ; GENERAL INFORMATION:
    ; APPLICANT: Roberts, Bruce L.
    ; TITLE OF INVENTION: POLYNUCLEOTIDE POPULATION ISOLATED FROM
    ; FILE REFERENCE: 126745205600
    ; CURRENT APPLICATION NUMBER: US/09/336.376
    ; CURRENT FILING DATE: 1999-06-17
    ; EARLIER APPLICATION NUMBER: 60/090,039
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/090,040
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/090,041
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/089,853
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/089,997
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/090,079
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/090,035
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/089,993
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/089,992
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/090,072
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/089,878
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/089,991
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/090,000
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/090,048
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/089,999
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/090,043
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/090,042
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/090,036
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/090,044
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/089,844
    ; EARLIER FILING DATE: 1998-06-19
    ; EARLIER APPLICATION NUMBER: 60/090,080
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EARLIER FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/089,833
EARLIER FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/089,994
EARLIER FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,077
EARLIER FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,078
EARLIER FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,047
EARLIER FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,076
EARLIER FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,045
EARLIER FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/111,715
EARLIER FILING DATE: 1998-12-08
NUMBER OF SEQ ID NOS: 5980
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4493
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-09-336-376-4493

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-336-376-4493 ..

Align seg 1/1 to: US-09-336-376-4493 from: 1 to: 10

1 LysLysAsn 3
|||||||
2 AAGAAAAAC 10

seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-424-521-4

seq_documentation_block:

Sequence 4, Application US/09424521
GENERAL INFORMATION:
APPLICANT: Neilsen, Peter
APPLICANT: Knudsen, Helle
TITLE OF INVENTION: Conjugated Peptide Nucleic Acids Having Enhanced Cellular Uptake
FILE REFERENCE: ISIS3070
CURRENT APPLICATION NUMBER: US/09/424,521
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: US 08/864,765
PRIOR FILING DATE: 1997-05-28
PRIOR APPLICATION NUMBER: PCT/US98/10804
PRIOR FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
US-09-424-521-4

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-424-521-4/rev ..
Align seg 1/1 to reverse of: US-09-424-521-4 from: 1 to: 10
1 LysLysAsn 3
|||||||
10 AAAAAAAT 2

seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-475-947A-98

seq_documentation_block:

Sequence 98, Application US/09475947A
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 98
LENGTH: 10
TYPE: DNA
ORGANISM: human
US-09-475-947A-98

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-475-947A-98 ..

Align seg 1/1 to: US-09-475-947A-98 from: 1 to: 10

1 LysLysAsn 3
|||||||
1 AAAAAAAT 9

seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-475-947A-127

seq_documentation_block:

Sequence 127, Application US/09475947A
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 127
LENGTH: 10
TYPE: DNA
ORGANISM: human
US-09-475-947A-127

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-475-947A-127 ..

Align seg 1/1 to: US-09-475-947A-127 from: 1 to: 10


```
1 LysLysAsn 3
|||||
1 AAAAAAAC 9

seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-475-947A-132
seq_documentation_block:
; Sequence 132, Application US/09475947A
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475.947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-132

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-475-947A-132 ..
Align seg 1/1 to: US-09-475-947A-132 from: 1 to: 10

1 LysLysAsn 3
|||||
1 AAAAAAAC 9

seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-475-947A-190
seq_documentation_block:
; Sequence 190, Application US/09475947A
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475.947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 190
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-190

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-475-947A-190 ..
Align seg 1/1 to: US-09-475-947A-190 from: 1 to: 10

1 LysLysAsn 3
|||||
```

```
1 AAGAAGAAC 9

seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-475-947A-198
seq_documentation_block:
; Sequence 198, Application US/09475947A
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475.947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 198
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-198

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-475-947A-198 ..
Align seg 1/1 to: US-09-475-947A-198 from: 1 to: 10

1 LysLysAsn 3
|||||
2 AAAAAAAC 10

seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-475-947A-212
seq_documentation_block:
; Sequence 212, Application US/09475947A
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475.947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 212
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-212

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-475-947A-212 ..
Align seg 1/1 to: US-09-475-947A-212 from: 1 to: 10

1 LysLysAsn 3
|||||
1 AAAAAAAC 9

seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-475-947A-295
```



```
seq_documentation_block:
; Sequence 295, Application US/09475947A
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS00667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 295
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-295

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-475-947A-295 ..
Align seg 1/1 to: US-09-475-947A-295 from: 1 to: 10
1 LysLysAsn 3
|||||||
2 AAAAAAAC 10

seq_name: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:US-09-857-723-171

seq_documentation_block:
; Sequence 171, Application US/09857723
; GENERAL INFORMATION:
; APPLICANT: Alcivar-Warren, Acacia
; APPLICANT: Xu, Zhenkang
; APPLICANT: Dhar, Arun K.
; APPLICANT: Fan, Yongjun
; APPLICANT: Meehan, Dawn
; APPLICANT: Garcia, Denise K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES OF SHRIMP
; FILE REFERENCE: 1322.1023-003
; CURRENT APPLICATION NUMBER: US/09/857,723
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/111,670
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Litopenaeus vannamei
US-09-857-723-171

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-857-723-171 ..
Align seg 1/1 to: US-09-857-723-171 from: 1 to: 10
1 LysLysAsn 3
|||||||
2 AAAAAAAT 10

seq_name: /cgn2_6/ptodata/2/pna/US080_COMB.seq:US-08-083-639C-23

seq_documentation_block:
; Sequence 23, Application US/08083639C
; GENERAL INFORMATION:
; APPLICANT: Herr, John C.
; TITLE OF INVENTION: Novel Intra-Acrosomal Endoproteases
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon H. Parker, Esq.
; STREET: 300 Preston Avenue
; CITY: Charlottesville
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22902
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083,639C
; FILING DATE: 28-June-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/890,433
; FILING DATE: 28-May-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Sheldon H.
; REGISTRATION NUMBER: 20,738
; REFERENCE/DOCKET NUMBER: GC-193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 804-977-6606
; TELEFAX: 804-296-7605
; TELEX: Not applicable
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11bp
; TYPE: nucleotide
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: - cDNA to mRNA
; DESCRIPTION: Native SP-10 peptides isolated
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal fragment
; ORIGINAL SOURCE: A37225
; ORGANISM: Homo sapien
; STRAIN: N/A
; INDIVIDUAL ISOLATE: N/A
; DEVELOPMENTAL STAGE: Adult
; HAPLOTYPE: N/A
; TISSUE TYPE: Testis
; CELL TYPE: Protein - sperm, cDNA from
; CELL LINE: N/A
; ORGANELLE: N/A
; IMMEDIATE SOURCE:
; LIBRARY: cDNA from human testis library
; CLONE: AP-10 cDNA from human testis library
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 1
; MAP POSITION: 11 of 24
; UNITS: N/A
; FEATURE:
; NAME/KEY: SP-10 is a unique sperm protein found
; LOCATION: N/A
; IDENTIFICATION METHOD: SP-10 is unique
; OTHER INFORMATION: Product appears to be
; PUBLICATION INFORMATION:
; AUTHORS: Herr, John C.
; TITLE: Purification and Microsequencing of the
; JOURNAL: Biology of Reproduction
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; VOLUME: 47
; ISSUE:
; PAGES: 11-20
; DATE: 1992
; US-08-083-639C-23

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-528-682-2 x US-08-083-639C-23/rev ..

Align seg 1/1 to reverse of: US-08-083-639C-23 from: 1 to: 11

  1 LysLysAsn 3
  |||||
  11 AAAAAAAT 3

seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-475-947A-112

seq_documentation_block:
; Sequence 112, Application US/09475947A
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 11
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-112

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-528-682-2 x US-09-475-947A-112 ..

Align seg 1/1 to: US-09-475-947A-112 from: 1 to: 11

  1 LysLysAsn 3
  |||||
  2 AAAAAAAT 10

seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-475-947A-167

seq_documentation_block:
; Sequence 167, Application US/09475947A
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 167
; LENGTH: 11
; TYPE: DNA
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; ORGANISM: human
US-09-475-947A-167

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-528-682-2 x US-09-475-947A-167 ..

Align seg 1/1 to: US-09-475-947A-167 from: 1 to: 11

  1 LysLysAsn 3
  |||||
  1 AAAAAAAT 9

seq_name: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:US-09-628-987B-1840

seq_documentation_block:
; Sequence 1840, Application US/09628987B
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-1075P
; CURRENT APPLICATION NUMBER: US/09/628,987B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 1862
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1840
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..11
; OTHER INFORMATION: any n = a, g, c, t, unknown, or other
; NAME/KEY: misc_feature
; LOCATION: 1..11
; OTHER INFORMATION: Ceres Seq. ID 1447829
US-09-628-987B-1840

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-528-682-2 x US-09-628-987B-1840 ..

Align seg 1/1 to: US-09-628-987B-1840 from: 1 to: 11

  1 LysLysAsn 3
  |||||
  2 AAGAGAAC 10

seq_name: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:US-09-775-479-12

seq_documentation_block:
; Sequence 12, Application US/09775479
; GENERAL INFORMATION:
; APPLICANT: LECLERC, Guy
; APPLICANT: MARTEL, R.mi
; TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF
; TITLE OF INVENTION: RADIOLABELED DNA CARRIER, METHOD OF PREPARATION AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 12168-1US-2
; CURRENT APPLICATION NUMBER: US/09/775,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/318,106
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; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: 08/756,728
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-775-479-12

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-775-479-12  ..
Align seg 1/1 to: US-09-775-479-12  from: 1 to: 11

1 LysLysAsn 3
1 AAAAAAAAAAT 9

seq_name: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:US-09-775-479A-12

seq_documentation_block:
; Sequence 12, Application US/09775479A
; GENERAL INFORMATION:
; APPLICANT: LECLERC, Guy
; TITLE OF INVENTION: RADIO-LABELED DNA CARRIER, METHOD OF
; TITLE OF INVENTION: RADIO-LABELED DNA CARRIER, METHOD OF PREPARATION AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; FILE REFERENCE: 01826-50018 CIP
; CURRENT APPLICATION NUMBER: US/09/775,479A
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/775,479
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/318,106
; PRIOR FILING DATE: 1999-05-24
; PRIOR APPLICATION NUMBER: 08/756,728
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-775-479A-12

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-775-479A-12  ..
Align seg 1/1 to: US-09-775-479A-12  from: 1 to: 11

1 LysLysAsn 3
1 AAAAAAAAAAT 9

seq_name: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US00-02589-9
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seq_documentation_block:
; Sequence 9, Application PC/TUS0002589
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350W05
; CURRENT APPLICATION NUMBER: PCT/US00/02589
; CURRENT FILING DATE: 2000-02-01
; EARLIER APPLICATION NUMBER: 09/247,190
; EARLIER FILING DATE: 1999-02-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
PCT-US00-02589-9

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x PCT-US00-02589-9  ..
Align seg 1/1 to: PCT-US00-02589-9  from: 1 to: 12

1 LysLysAsn 3
1 AAAAAAAAAAC 11

seq_name: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US99-06537-4

seq_documentation_block:
; Sequence 4, Application PC/TUS9906537A
; GENERAL INFORMATION:
; APPLICANT: Feng, Feng
; TITLE OF INVENTION: Identifying Ligands of Target Proteins With Target
; TITLE OF INVENTION: Complementary Library Technology (TCLT)
; FILE REFERENCE: 019815-000200PC
; CURRENT APPLICATION NUMBER: PCT/US99/06537A
; CURRENT FILING DATE: 1999-04-19
; EARLIER APPLICATION NUMBER: US 60/083,046
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:anti-sense
PCT-US99-06537-4

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x PCT-US99-06537-4  ..
Align seg 1/1 to: PCT-US99-06537-4  from: 1 to: 12

1 LysLysAsn 3
```



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|||||
1 AAAAAAGAAC 9

seq_name: /cgn2_6/ptodata/2/pna/US091_COMB.seq:US-09-151-890-39

seq_documentation_block:
; Sequence 39, Application US/09151890
; GENERAL INFORMATION:
; APPLICANT: Gary P. Schroth
; APPLICANT: Thomas Wayne Bruce
; APPLICANT: Young J. Suh
; FILE REFERENCE: 4600-0128
; CURRENT APPLICATION NUMBER: US/09/151.890
; CURRENT FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1)...(12)
; OTHER INFORMATION: synthesized test oligonucleotide for binding
US-09-151-890-39

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-151-890-39 ..
Align seg 1/1 to: US-09-151-890-39 from: 1 to: 12

1 LysLysasn 3
|||||
3 AAAAAAAGAAC 11

seq_name: /cgn2_6/ptodata/2/pna/US091_COMB.seq:US-09-151-890B-39

seq_documentation_block:
; Sequence 39, Application US/09151890B
; GENERAL INFORMATION:
; APPLICANT: Gary P. Schroth
; APPLICANT: Thomas Wayne Bruce
; APPLICANT: Young J. Suh
; FILE REFERENCE: 4600-0128
; CURRENT APPLICATION NUMBER: US/09/151.890B
; CURRENT FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1)...(12)
; OTHER INFORMATION: synthesized test oligonucleotide for binding
US-09-151-890B-39

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

|||||
1 AAAAAAGAAC 9

seq_name: /cgn2_6/ptodata/2/pna/US092_COMB.seq:US-09-238-710-9

seq_documentation_block:
; Sequence 9, Application US/09238710A
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350004
; CURRENT APPLICATION NUMBER: US/09/238,710A
; CURRENT FILING DATE: 1999-01-28
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-238-710-9

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-238-710-9 ..
Align seg 1/1 to: US-09-238-710-9 from: 1 to: 12

1 LysLysasn 3
|||||
3 AAAAAAAGAAC 11

seq_name: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:US-09-735-363A-83

seq_documentation_block:
; Sequence 83, Application US/09735363A
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 83
; LENGTH: 12
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-83

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-735-363A-83/rev ..
Align seg 1/1 to reverse of: US-09-735-363A-83 from: 1 to: 12

1 LysLysAsn 3
|||||
11 AAAAAAAC 3

seq_name: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:US-09-876-235-9

seq_documentation_block:
; Sequence 9, Application US/09876235
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350005
; CURRENT APPLICATION NUMBER: US/09/876, 235
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,190
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/007,005
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-876-235-9

alignment_scores:
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  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-876-235-9 ..
Align seg 1/1 to: US-09-876-235-9 from: 1 to: 12

1 LysLysAsn 3
|||||
3 AAAAAAAC 11

seq_name: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US98-26935-146

seq_documentation_block:
; Sequence 146, Application PC/TUS9826935
; GENERAL INFORMATION:
; APPLICANT: Jessen, Holly
; APPLICANT: Webb, David
; APPLICANT: Corvett, Virginia H.
; APPLICANT: Schupp, James M.
; APPLICANT: Keim, Paul S.
; APPLICANT: Pioneer Hi-Bred International, Inc.
; TITLE OF INVENTION: Nucleotide Polymorphisms in Soybean
; FILE REFERENCE: 018574-000110PC
; CURRENT APPLICATION NUMBER: PCT/US98/26935
; CURRENT FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: US 60/068,185
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: PCT-US98-26935-146

alignment_scores:
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  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x PCT-US98-26935-146 ..
Align seg 1/1 to: PCT-US98-26935-146 from: 1 to: 13

1 LysLysAsn 3
|||||
1 AAAAAAAC 9
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OM of: US-09-528-682-2 to: Pending_Patents_NA_New:* out_format : pfs

Date: Jun 18, 2002 9:49 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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-DB=Pending_Patents_NA_New -QFWT=fastap -SURFIX=p2n.rnpn
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -CGAPOP=4.500 -CGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FCGAPOP=6.000 -FCGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blossum62 -TRANS=human40.cdi -LIST=1000 -DOCALLIGN=200
-THR_SCORE=epct -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09528682_cg2n1_1572 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-528-682-2

Query length: 3

Database: Pending_Patents_NA_New:*

Database sequences: 1014543

Database length: 727792371

Search time (sec): 403.930000

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/cg2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-581-970A-317 +	16.00	100.10	1.8e+03	1	
/cg2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-875-433A-103 -	16.00	99.58	2.0e+03	1	
/cg2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-889-866A-54 -	16.00	99.58	2.0e+03	1	
/cg2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-889-866A-58 -	16.00	99.58	2.0e+03	1	
/cg2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-889-866A-60 -	16.00	99.58	2.0e+03	1	
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/cg2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-581-970A-383 +	16.00	99.58	2.0e+03	1	
/cg2_6/ptodata/1/pna/US08_NEW_COMB.seq:US-08-802-331-28 -	16.00	99.09	2.1e+03	16	
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[illegible]

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/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-331D-6359 -	16.00	85.09	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-331D-6850 -	16.00	84.65	1.3e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-6311 -	16.00	85.09	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-331D-12052 -	16.00	84.65	1.3e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-7555 +	16.00	85.09	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-331D-26462 -	16.00	84.65	1.3e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-8826 +	16.00	85.09	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-954-531-93 -	16.00	84.65	1.3e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-8893 +	16.00	85.09	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-806B-2770 +	16.00	84.65	1.3e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-10606 +	16.00	85.09	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-460-592B-1665 -	16.00	84.65	1.3e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-11437 +	16.00	85.09	1.3e+04	/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-11346 +	16.00	84.65	1.3e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-11437 +	16.00	85.09	1.3e+04	/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-14342 +	16.00	84.65	1.3e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-13713 +	16.00	85.09	1.3e+04	/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-14795 +	16.00	84.65	1.3e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-13890 +	16.00	85.09	1.3e+04	/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-125-968-1405 -	16.00	84.65	1.3e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-14922 +	16.00	85.09	1.3e+04	/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-632-176690 -	16.00	84.65	1.3e+04
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/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-106-698-3039 +	16.00	85.09	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-540-210B-3993 +	16.00	84.58	1.3e+04
/cgn2_6/ptodata1/pna/PCT_NEW_COMB.seq:PCT-US02-17612-1320 -	16.00	85.01	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-540-210B-32235 +	16.00	84.58	1.3e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-975-254-7257 +	16.00	85.01	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-331D-9874 +	16.00	84.58	1.3e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-540-210B-3197 +	16.00	85.01	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-800C-5511 +	16.00	84.58	1.3e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-806B-4399 -	16.00	85.01	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-800C-14878 +	16.00	84.58	1.3e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-800C-66 -	16.00	85.01	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-460-592B-849 -	16.00	84.58	1.3e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-097-105-1205 +	16.00	85.01	1.3e+04	/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-299-13729 -	16.00	84.58	1.3e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-097-105-1205 -	16.00	85.01	1.3e+04	/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-027-632-51785 +	16.00	84.58	1.3e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-125-968-1320 -	16.00	85.01	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-975-254-19879 -	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-141-324-1323 +	16.00	85.01	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-975-254-24637 +	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-09-975-254-2170 +	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-975-254-29629 -	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-540-210B-22119 +	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-540-210B-26871 -	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-540-210B-8323 -	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-540-210B-33154 -	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-540-210B-13354 -	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-331D-5536 +	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-540-210B-13833 +	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-331D-8729 +	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-540-210B-26468 +	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-331D-9440 -	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-540-210B-28995 -	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-331D-15419 +	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-331D-1557 -	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-800C-170 +	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-331D-17184 -	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-919-002-5234 -	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-331D-30491 +	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-800C-2632 -	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-331D-32765 +	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us09_NEW_COMB.seq:US-09-539-800C-14382 +	16.00	84.52	1.4e+04
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/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-106-698-3895 -	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-106-698-4205 +	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-027-632-53330 -	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-105-613-155 +	16.00	84.52	1.4e+04
/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-027-632-177239 +	16.00	84.94	1.3e+04	/cgn2_6/ptodata1/pna/us10_NEW_COMB.seq:US-10-027-632-58881 +	16.00	84.52	1.4e+04
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/cgn2_6/ptodata/1/pna/us09_NEW_COMB.seq:US-09-539-331D-13287 - 16.00 84.45 1.4e+04
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/cgn2_6/ptodata/1/pna/us09_NEW_COMB.seq:US-09-460-592B-938 + 16.00 84.45 1.4e+04
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seq_documentation_block:
; Sequence 28, Application PC/TUS0215111
; GENERAL INFORMATION:
; APPLICANT: Replydne, Inc.
; TITLE OF INVENTION: System for Discovery of Agents that Block Yersinia Pestis and Pse
; FILE REFERENCE: RDYN.02
; CURRENT APPLICATION NUMBER: PCT/US02/15111
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/290,725
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/332,644
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 28
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutation
PCT-US02-15111-28

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x PCT-US02-15111-28 ..
Align seg 1/1 to: PCT-US02-15111-28 from: 1 to: 12

1 LysLysAsn 3
2 AAAAAGAAT 10

seq_name: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:PCT-US02-15111-27

seq_documentation_block:
; Sequence 27, Application PC/TUS0215111
; GENERAL INFORMATION:
; APPLICANT: Replydne, Inc.
; TITLE OF INVENTION: System for Discovery of Agents that Block Yersinia Pestis and Pse
; FILE REFERENCE: RDYN.02
; CURRENT APPLICATION NUMBER: PCT/US02/15111
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/290,725
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/332,644
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 27
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: mutation
PCT-US02-15111-27

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x PCT-US02-15111-27 ..
Align seg 1/1 to: PCT-US02-15111-27 from: 1 to: 13

1 LysLysAsn 3
2 AAAAAGAAT 10

seq_name: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:PCT-US02-15111-30

seq_documentation_block:
; Sequence 30, Application PC/TUS0215111
; GENERAL INFORMATION:
; APPLICANT: Replydne, Inc.
; TITLE OF INVENTION: System for Discovery of Agents that Block Yersinia Pestis and
; FILE REFERENCE: RDYN.02
; CURRENT APPLICATION NUMBER: PCT/US02/15111
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/290,725
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/332,644
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutation
PCT-US02-15111-30

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x PCT-US02-15111-30 ..
Align seg 1/1 to: PCT-US02-15111-30 from: 1 to: 13

1 LysLysAsn 3
2 AAGAAAAAAC 10

seq_name: /cgn2_6/ptodata/1/pna/us09_NEW_COMB.seq:US-09-581-970A-146

seq_documentation_block:
; Sequence 146, Application US/09581970A
; GENERAL INFORMATION:
; APPLICANT: JESSEN, HOLLY
; APPLICANT: WEBB, DAVID
; APPLICANT: CORVELL, VIRGINIA H.
; APPLICANT: SCHUPP, JAMES M.
; APPLICANT: KEIM, PAUL S.
; TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISMS IN SOYBEAN
; FILE REFERENCE: 04-000111US
; CURRENT APPLICATION NUMBER: US/09/581,970A
; CURRENT FILING DATE: 2002-04-30
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; PRIOR APPLICATION NUMBER: PCT/US98/26935
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/068,185
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 798
; SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 146
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Glycine max
US-09-581-970A-146

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-581-970A-146 ..

Align seg 1/1 to: US-09-581-970A-146 from: 1 to: 13

1 LysLysAsn 3
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1 AAAAAAAT 9

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-581-970A-89

seq_documentation_block:
; Sequence 89, Application US/09581970A
; GENERAL INFORMATION:
; APPLICANT: JESSEN, HOLLY
; APPLICANT: WEBB, DAVID
; APPLICANT: CORYELL, VIRGINIA H.
; APPLICANT: SCHUPP, JAMES M.
; APPLICANT: KEIM, PAUL S.
; TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISMS IN SOYBEAN
; FILE REFERENCE: 04-000111US
; CURRENT APPLICATION NUMBER: US/09/581,970A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/US98/26935
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/068,185
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 798
; SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 89
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Glycine max
US-09-581-970A-89

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-581-970A-89/rev ..

Align seg 1/1 to reverse of: US-09-581-970A-89 from: 1 to: 14

1 LysLysAsn 3
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13 AAAAAAAT 5

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-581-970A-317

seq_documentation_block:
; Sequence 317, Application US/09581970A
; GENERAL INFORMATION:

; APPLICANT: JESSEN, HOLLY
; APPLICANT: WEBB, DAVID
; APPLICANT: CORYELL, VIRGINIA H.
; APPLICANT: SCHUPP, JAMES M.
; APPLICANT: KEIM, PAUL S.
; TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISMS IN SOYBEAN
; FILE REFERENCE: 04-000111US
; CURRENT APPLICATION NUMBER: US/09/581,970A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/US98/26935
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/068,185
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 798
; SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 317
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Glycine max
US-09-581-970A-317

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-581-970A-317 ..

Align seg 1/1 to: US-09-581-970A-317 from: 1 to: 14

1 LysLysAsn 3
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3 AAAAAAAT 11

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-875-453A-103

seq_documentation_block:
; Sequence 103, Application US/09875453A
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135, US00
; CURRENT APPLICATION NUMBER: US/09/875,453A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutant sequence
US-09-875-453A-103

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0


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Percent Similarity: 100.000   Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x US-09-875-453A-103/rev  ..
Align seg 1/1 to reverse of: US-09-875-453A-103 from: 1 to: 14
1 LysLysAsn 3
11 AAAAAAAC 3
seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-889-866A-54
seq_documentation_block:
; Sequence 54, Application US/09889866A
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Denton, R. Rex
; APPLICANT: Kliem, Stefanie E.
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: DRUG TARGET ISOGENES: POLYMORPHISMS IN THE
; TITLE OF INVENTION: IMMUNOGLOBULIN E RECEPTOR BETA CHAIN GENE
; FILE REFERENCE: MWH-0008US IGERB
; CURRENT APPLICATION NUMBER: US/09/889,866A
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/150,423
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/22175
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 54
; SOFTWARE: PatentIn Ver. 2.1 PLUS editing text file in Notepad
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-889-866A-54
alignment_scores:
Quality: 16.00   Length: 3
Ratio: 5.333    Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x US-09-889-866A-54/rev  ..
Align seg 1/1 to reverse of: US-09-889-866A-54 from: 1 to: 15
1 LysLysAsn 3
14 AAAAAAAT 6
seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-889-866A-58
seq_documentation_block:
; Sequence 58, Application US/09889866A
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Denton, R. Rex
; APPLICANT: Kliem, Stefanie E.
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: DRUG TARGET ISOGENES: POLYMORPHISMS IN THE
; TITLE OF INVENTION: IMMUNOGLOBULIN E RECEPTOR BETA CHAIN GENE
; FILE REFERENCE: MWH-0008US IGERB
; CURRENT APPLICATION NUMBER: US/09/889,866A
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/150,423
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/22175
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 145
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; SOFTWARE: PatentIn Ver. 2.1 PLUS editing text file in Notepad
; SEQ ID NO 58
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-889-866A-58
alignment_scores:
Quality: 16.00   Length: 3
Ratio: 5.333    Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x US-09-889-866A-58/rev  ..
Align seg 1/1 to reverse of: US-09-889-866A-58 from: 1 to: 15
1 LysLysAsn 3
10 AAAAAAAT 2
seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-889-866A-60
seq_documentation_block:
; Sequence 60, Application US/09889866A
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Denton, R. Rex
; APPLICANT: Kliem, Stefanie E.
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: DRUG TARGET ISOGENES: POLYMORPHISMS IN THE
; TITLE OF INVENTION: IMMUNOGLOBULIN E RECEPTOR BETA CHAIN GENE
; FILE REFERENCE: MWH-0008US IGERB
; CURRENT APPLICATION NUMBER: US/09/889,866A
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/150,423
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/22175
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn Ver. 2.1 PLUS editing text file in Notepad
; SEQ ID NO 60
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-889-866A-60
alignment_scores:
Quality: 16.00   Length: 3
Ratio: 5.333    Gaps: 0
Percent Similarity: 100.000   Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x US-09-889-866A-60/rev  ..
Align seg 1/1 to reverse of: US-09-889-866A-60 from: 1 to: 15
1 LysLysAsn 3
10 AAAAAAAT 2
seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-581-970A-76
seq_documentation_block:
; Sequence 76, Application US/09581970A
; GENERAL INFORMATION:
; APPLICANT: JESSEN, HOLLY
; APPLICANT: WEBB, DAVID
; APPLICANT: CORYELL, VIRGINIA H.
; APPLICANT: SCHUPP, JAMES M.
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seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-581-970A-346
seq_documentation_block:
; APPLICANT: KEIM, PAUL S.
; TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISMS IN SOYBEAN
; FILE REFERENCE: 04-000111US
; CURRENT APPLICATION NUMBER: US/09/581,970A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/US98/26935
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/068,185
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 798
; SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 76
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Glycine max
US-09-581-970A-76
..
alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x US-09-581-970A-76
..
Align seg 1/1 to: US-09-581-970A-76 from: 1 to: 15
1 LysLysAsn 3
|||||
1 AAAAAAAC 9

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-581-970A-346
seq_documentation_block:
; Sequence 346, Application US/09581970A
; GENERAL INFORMATION:
; APPLICANT: JESSEN, HOLLY
; APPLICANT: WEBB, DAVID
; APPLICANT: CORVELL, VIRGINIA H.
; APPLICANT: SCHUPP, JAMES M.
; APPLICANT: KEIM, PAUL S.
; TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISMS IN SOYBEAN
; FILE REFERENCE: 04-000111US
; CURRENT APPLICATION NUMBER: US/09/581,970A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/US98/26935
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/068,185
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 798
; SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 346
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Glycine max
US-09-581-970A-346
..
alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x US-09-581-970A-346
..
Align seg 1/1 to: US-09-581-970A-346 from: 1 to: 15
1 LysLysAsn 3
|||||
1 AAAAAAAC 9
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seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-581-970A-383
seq_documentation_block:
; Sequence 383, Application US/09581970A
; GENERAL INFORMATION:
; APPLICANT: JESSEN, HOLLY
; APPLICANT: WEBB, DAVID
; APPLICANT: CORVELL, VIRGINIA H.
; APPLICANT: SCHUPP, JAMES M.
; APPLICANT: KEIM, PAUL S.
; TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISMS IN SOYBEAN
; FILE REFERENCE: 04-000111US
; CURRENT APPLICATION NUMBER: US/09/581,970A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/US98/26935
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/068,185
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 798
; SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 383
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Glycine max
US-09-581-970A-383
..
alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x US-09-581-970A-383
..
Align seg 1/1 to: US-09-581-970A-383 from: 1 to: 15
1 LysLysAsn 3
|||||
4 AAAAAAAT 12

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-112-653-833
seq_documentation_block:
; Sequence 833, Application US/10112653
; GENERAL INFORMATION:
; APPLICANT: Arleg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 833
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-833
..
alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-528-682-2 x US-10-112-653-833/rev
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Align seq 1/1 to reverse of: US-10-112-653-833 from: 1 to: 15

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1 LysLysAsn 3
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11 AAAAAAAC 3
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seq_name: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:US-08-802-331-28

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seq_documentation_block:
; Sequence 28, Application US/08802331
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D.
; APPLICANT: Monia, Brett
; APPLICANT: Martin, Pierre
; APPLICANT: Altman, Karl-Heinz
; TITLE OF INVENTION: Sugar-Modified Gapped Oligonucleotides
; FILE REFERENCE: ISN00083
; CURRENT APPLICATION NUMBER: US/08/802,331
; CURRENT FILING DATE: 1997-02-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Novel Sequence
US-08-802-331-28
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alignment_scores:
  Quality: 16.00 Length: 3
  Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:
US-09-528-682-2 x US-08-802-331-28/rev ..

Align seq 1/1 to reverse of: US-08-802-331-28 from: 1 to: 16

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1 LysLysAsn 3
|||||
11 AAAAAAAC 3
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seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-131-102-7

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seq_documentation_block:
; Sequence 7, Application US/09131102
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D.
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Bhat, Balkrishen
; TITLE OF INVENTION: Oligonucleotide Analogs Having Modified Dimers
; FILE REFERENCE: ISIS-2906
; CURRENT APPLICATION NUMBER: US/09/131,102
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Methylene (methylimino) backbone, ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: 2'-O-CH3 Ribose sugar moiety
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: Methylene (methylimino) backbone, ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: 2'-O-CH3 Ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: Methylene (methylimino) backbone, ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: 2'-O-CH3 Ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: Methylene (methylimino) backbone, ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: 2'-O-CH3 Ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: Methylene (methylimino) backbone, ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: 2'-O-CH3 Ribose sugar moiety
US-09-131-102-7
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alignment_scores:
  Quality: 16.00 Length: 3
  Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:
US-09-528-682-2 x US-09-131-102-7/rev ..

Align seq 1/1 to reverse of: US-09-131-102-7 from: 1 to: 16

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1 LysLysAsn 3
|||||
11 AAAAAAAC 3
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seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-131-102-8

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seq_documentation_block:
; Sequence 8, Application US/09131102
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D.
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Bhat, Balkrishen
; TITLE OF INVENTION: Oligonucleotide Analogs Having Modified Dimers
; FILE REFERENCE: ISIS-2906
; CURRENT APPLICATION NUMBER: US/09/131,102
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Methylene (methylimino) backbone, 2'-O-CH3 ribose sugar moiety
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: 2'-O-CH3 Ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: Methylene (methylimino) backbone, 2'-O-CH3 ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: 2'-O-CH3 Ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: Methylene (methylimino) backbone, 2'-O-CH3 ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: 2'-O-CH3 ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: Methylene (methylimino) backbone, 2'-O-CH3 ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: 2'-O-CH3 Ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: 2'-O-CH3 ribose sugar moiety
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: 2'-O-CH3 ribose sugar moiety
US-09-131-102-8
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  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:

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US-09-528-682-2 x US-09-131-102-8/rev ..
Align seg 1/1 to reverse of: US-09-131-102-8 from: 1 to: 16
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1 LysLysasn 3
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11 AAAAAAAC 3
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seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-131-102-9
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seq_documentation_block:
; Sequence 9, Application US/09131102
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip D.
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Bhat, Balkrishen
; TITLE OF INVENTION: Oligonucleotide Analogs Having Modified Dimers
; FILE REFERENCE: ISIS-2906
; CURRENT APPLICATION NUMBER: US/09/131.102
; CURRENT FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Methylene (methylimino) backbone, 2'-O-CH3 ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: Methylene (methylimino) backbone, ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: Ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: Methylene (methylimino) backbone, ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: Ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: Methylene (methylimino) backbone, ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: Ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: Methylene (methylimino) backbone, ribose sugar moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Ribose sugar moiety
US-09-131-102-9
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alignment_scores:
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  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:

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US-09-528-682-2 x US-09-131-102-9/rev ..
Align seg 1/1 to reverse of: US-09-131-102-9 from: 1 to: 16
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1 LysLysasn 3
|||||||
11 AAAAAAAC 3
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seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-861-787A-1
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seq_documentation_block:
; Sequence 1, Application US/09861787A
; GENERAL INFORMATION:
; APPLICANT: Virtanen, Jorma
; TITLE OF INVENTION: Gene Sequencer and Methods
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: MS Word
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/861,787A
; FILING DATE: 21-May-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/564,399
; FILING DATE: May 1, 2000
; APPLICATION NUMBER: 09/064,635
; FILING DATE: April 21, 1998
; APPLICATION NUMBER: PCT/US/98/03362
; FILING DATE: February 20, 1998
; APPLICATION NUMBER: 60/039,027
; FILING DATE: February 21, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: SMITH, Guy P.
; REGISTRATION NUMBER: 20,142
; REFERENCE/DOCKET NUMBER: 18950-67 (formerly 18950-62)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 788-5100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded DNA
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-861-787A-1

alignment_scores:
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  Ratio: 5.333      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-861-787A-1 ..

Align seg 1/1 to: US-09-861-787A-1 from: 1 to: 16

1 LysLysAsn 3
|||||
5 AAAAAAAC 13

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-861-787A-2

seq_documentation_block:
; Sequence 2, Application US/09861787A
; GENERAL INFORMATION:
; APPLICANT: Virtanen, Jorma
; TITLE OF INVENTION: Gene Sequencer and Methods
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/861,787A
; FILING DATE: 21-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/564,399

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;
; FILING DATE: May 1, 2000
; APPLICATION NUMBER: 09/064,635
; FILING DATE: April 21, 1998
; APPLICATION NUMBER: PCT/US/98/03362
; FILING DATE: February 20, 1998
; APPLICATION NUMBER: 60/039,027
; FILING DATE: February 21, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: SMITH, Guy P.
; REGISTRATION NUMBER: 20,142
; REFERENCE/DOCKET NUMBER: 18950-67 (formerly 18950-62)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 788-5100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded DNA
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-861-787A-2

alignment_scores:
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  Ratio: 5.333      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-861-787A-2 ..

Align seg 1/1 to: US-09-861-787A-2 from: 1 to: 16

1 LysLysAsn 3
|||||
5 AAAAAAAC 13

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-861-787A-3

seq_documentation_block:
; Sequence 3, Application US/09861787A
; GENERAL INFORMATION:
; APPLICANT: Virtanen, Jorma
; TITLE OF INVENTION: Gene Sequencer and Methods
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/861,787A
; FILING DATE: 21-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/564,399
; FILING DATE: May 1, 2000
; APPLICATION NUMBER: 09/064,635
; FILING DATE: April 21, 1998
; APPLICATION NUMBER: PCT/US/98/03362
; FILING DATE: February 20, 1998
; APPLICATION NUMBER: 60/039,027
; FILING DATE: February 21, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: SMITH, Guy P.

```



```
;
; REGISTRATION NUMBER: 20,142
; REFERENCE/DOCKET NUMBER: 18950-67 (formerly 18950-62)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 788-5100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded DNA
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-861-787A-3

alignment_scores:
  Quality: 16.00 Length: 3
  Ratio: 5.333 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-861-787A-3 ..

Align seg 1/1 to: US-09-861-787A-3 from: 1 to: 16

1 LysLysAsn 3
|||||
5 AAAAAAAT 13

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-861-787A-4

seq_documentation_block:
; Sequence 4, Application US/09861787A
; GENERAL INFORMATION:
; APPLICANT: Virtanen, Jorma
; TITLE OF INVENTION: Gene Sequencer and Methods
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppeheimer Wolff & Donnelly LLP
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/861,787A
; FILING DATE: 21-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/564,399
; FILING DATE: May 1, 2000
; APPLICATION NUMBER: 09/064,635
; FILING DATE: April 21, 1998
; APPLICATION NUMBER: PCT/US/98/03362
; FILING DATE: February 20, 1998
; APPLICATION NUMBER: 60/039,027
; FILING DATE: February 21, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: SMITH, Guy P.
; REGISTRATION NUMBER: 20,142
; REFERENCE/DOCKET NUMBER: 18950-67 (formerly 18950-62)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 788-5100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: nucleic acid
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;
; STRANDEDNESS: single-stranded DNA
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-861-787A-4

alignment_scores:
  Quality: 16.00 Length: 3
  Ratio: 5.333 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-861-787A-4 ..

Align seg 1/1 to: US-09-861-787A-4 from: 1 to: 16

1 LysLysAsn 3
|||||
5 AAAAAAAC 13

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-581-970A-69

seq_documentation_block:
; Sequence 69, Application US/09581970A
; GENERAL INFORMATION:
; APPLICANT: JESSEN, HOLLY
; APPLICANT: WEBB, DAVID
; APPLICANT: CORYELL, VIRGINIA H.
; APPLICANT: SCHUPPE, JAMES M.
; APPLICANT: KEIM, PAUL S.
; TITLE OF INVENTION: NUCLEOTIDE POLYMORPHISMS IN SOYBEAN
; FILE REFERENCE: 04-000111US
; CURRENT APPLICATION NUMBER: US/09/581,970A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/US98/26935
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/068,185
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 798
; SOFTWARE: PatentIn Ver 2.1
; SEQ ID NO 69
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Glycine max
US-09-581-970A-69

alignment_scores:
  Quality: 16.00 Length: 3
  Ratio: 5.333 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-581-970A-69/rev ..

Align seg 1/1 to reverse of: US-09-581-970A-69 from: 1 to: 16

1 LysLysAsn 3
|||||
9 AAAAAAAC 1

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-941-492-16

seq_documentation_block:
; Sequence 16, Application US/09941492
; GENERAL INFORMATION:
; APPLICANT: Mitchell, Lloyd
; APPLICANT: Garcia-Blanco, Mariano M.
; APPLICANT: Puttaraju, Madalah
; APPLICANT: Mansfield, Gary S.
; TITLE OF INVENTION: METHODS OF COMPOSITIONS FOR USE IN
; SPICEOSOME MEDIATED RNA TRANS-SPICING
```



```
FILE REFERENCE: A31304-BAE (072874.0156)
CURRENT APPLICATION NUMBER: US/09/941,492
PRIOR FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 09/838,858
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 09/756,096
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 09/158,863
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 09/133,717
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: 09/087,233
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 08/766,354
PRIOR FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapien
US-09-941-492-16
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alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:
US-09-528-682-2 x US-09-941-492-16/rev ..
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Align seg 1/1 to reverse of: US-09-941-492-16 from: 1 to: 17

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1 LysLysasn 3
|||||
14 AAAAAAAC 6
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seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-725-265-58

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seq_documentation_block:
; Sequence 58, Application US/09725265
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 17
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-58
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```
alignment_scores:
  Quality: 16.00      Length: 3
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Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:

US-09-528-682-2 x US-09-725-265-58/rev ..

Align seg 1/1 to reverse of: US-09-725-265-58 from: 1 to: 17

```
1 LysLysasn 3
|||||
17 AAAAAAAC 9
```

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-725-265-59

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seq_documentation_block:
; Sequence 59, Application US/09725265
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 17
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-59
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alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:

US-09-528-682-2 x US-09-725-265-59 ..

Align seg 1/1 to: US-09-725-265-59 from: 1 to: 17

```
1 LysLysasn 3
|||||
1 AAAAAAAC 9
```

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-725-265-60

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seq_documentation_block:
; Sequence 60, Application US/09725265
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING
```


; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 17
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-60

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-725-265-60 ..
Align seg 1/1 to: US-09-725-265-60 from: 1 to: 17

1 LysLysAsn 3
|||||
1 AAAAAAAC 9

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-725-265-63

seq_documentation_block:
; Sequence 63, Application US/09725265
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KANAGAWA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; FILE REFERENCE: 199953USOXDIV
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 17
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-63

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-725-265-63/rev ..

Align seg 1/1 to reverse of: US-09-725-265-63 from: 1 to: 17

1 LysLysAsn 3
|||||
1 AAAAAAAC 9

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-745-237A-240

seq_documentation_block:
; Sequence 240, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (WBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 240
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-240

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-745-237A-240/rev ..

Align seg 1/1 to reverse of: US-09-745-237A-240 from: 1 to: 17

1 LysLysAsn 3
|||||
1 AAGAAGAA 9

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-745-237A-241

seq_documentation_block:
; Sequence 241, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (WBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 241
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-241

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-745-237A-241/rev ..

Align seg 1/1 to reverse of: US-09-745-237A-241 from: 1 to: 17

1 LysLysAsn 3
|||||
15 AAGAAGAAAT 7

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-745-237A-242

seq_documentation_block:
; Sequence 242, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 242
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-242

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-745-237A-242/rev ..

Align seg 1/1 to reverse of: US-09-745-237A-242 from: 1 to: 17

1 LysLysAsn 3
|||||
14 AAGAAGAAAT 6

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-745-237A-243

seq_documentation_block:
; Sequence 243, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 243
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-243

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-745-237A-243/rev ..

Align seg 1/1 to reverse of: US-09-745-237A-243 from: 1 to: 17

1 LysLysAsn 3
|||||
12 AAGAAGAAAT 4

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-745-237A-244

seq_documentation_block:
; Sequence 244, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 244
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-244

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-745-237A-244/rev ..

Align seg 1/1 to reverse of: US-09-745-237A-244 from: 1 to: 17

1 LysLysAsn 3
|||||
11 AAGAAGAAAT 3

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-745-237A-245

seq_documentation_block:
; Sequence 245, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 245
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-245

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-745-237A-245/rev ..

Align seg 1/1 to reverse of: US-09-745-237A-245 from: 1 to: 17

1 LysLysAsn 3
|||||
9 AAGAAGAAAT 1

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-745-237A-917


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seq_documentation_block:
; Sequence 917, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 917
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-917

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-745-237A-917/rev ..
Align seg 1/1 to reverse of: US-09-745-237A-917 from: 1 to: 17

  1 LysLysAsn 3
  |||||
  13 AAGAGAAT 5

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-745-237A-918

seq_documentation_block:
; Sequence 918, Application US/09745237A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 918
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-918

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-745-237A-918/rev ..
Align seg 1/1 to reverse of: US-09-745-237A-918 from: 1 to: 17

  1 LysLysAsn 3
  |||||
  10 AAGAGAAT 2

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-745-237A-1448

seq_documentation_block:
; Sequence 1448, Application US/09745237A
; GENERAL INFORMATION:
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; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBH00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1448
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1448

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-745-237A-1448 ..
Align seg 1/1 to: US-09-745-237A-1448 from: 1 to: 17

  1 LysLysAsn 3
  |||||
  2 AAAAAAAC 10

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-043-875-54

seq_documentation_block:
; Sequence 54, Application US/10043875
; GENERAL INFORMATION:
; APPLICANT: De Smet, Koenraad
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Re
; FILE REFERENCE: 11362-0033-NEPS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043,875
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 01870005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Human Immunodeficiency virus
US-10-043-875-54

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-10-043-875-54 ..
Align seg 1/1 to: US-10-043-875-54 from: 1 to: 17

  1 LysLysAsn 3
  |||||
  1 AAGAAAAAT 9

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-138-674-1319
```



```
seq_documentation_block:
; Sequence 1319, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1319
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1319
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alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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```
alignment_block:
US-09-528-682-2 x US-10-138-674-1319 ..
```

Align seg 1/1 to: US-10-138-674-1319 from: 1 to: 17

```
1 LysLysAsn 3
|||||
9 AAGAAAAAC 17
```

```
seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-138-674-6287
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seq_documentation_block:
; Sequence 6287, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6287
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-6287
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alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
```

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alignment_block:
US-09-528-682-2 x US-10-138-674-6287 ..
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Align seg 1/1 to: US-10-138-674-6287 from: 1 to: 17

```
1 LysLysAsn 3
|||||
9 AAGAAAAAC 17
```

```
seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-138-674-8182
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seq_documentation_block:
; Sequence 8182, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8182
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-8182
```

```
alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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```
alignment_block:
US-09-528-682-2 x US-10-138-674-8182 ..
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Align seg 1/1 to: US-10-138-674-8182 from: 1 to: 17

```
1 LysLysAsn 3
|||||
2 AAGAAAAAU 10
```

```
seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-138-674-8315
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seq_documentation_block:
; Sequence 8315, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8315
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-8315
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alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333      Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:
US-09-528-682-2 x US-10-138-674-8315 ..
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Align seg 1/1 to: US-10-138-674-8315 from: 1 to: 17

1 LysLysAsn 3
|||||
2 AAGAAAAAC 10

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-138-674-8601

seq_documentation_block:

; Sequence 8601, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138.674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8601
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-8601

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-10-138-674-8601 ..

Align seg 1/1 to: US-10-138-674-8601 from: 1 to: 17

1 LysLysAsn 3
|||||
2 AAGAAAAAC 10

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-725-265-14

seq_documentation_block:

; Sequence 14, Application US/09725265
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOKAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; FILE REFERENCE: THE METHOD
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-14

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-725-265-14 ..

Align seg 1/1 to: US-09-725-265-14 from: 1 to: 18

1 LysLysAsn 3
|||||
4 AAAAAAAT 12

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-725-265-15

seq_documentation_block:

; Sequence 15, Application US/09725265
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOKAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-15

alignment_scores:

Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-725-265-15 ..

Align seg 1/1 to: US-09-725-265-15 from: 1 to: 18

1 LysLysAsn 3
|||||
4 AAAAAAAT 12

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-725-265-16

seq_documentation_block:

; Sequence 16, Application US/09725265
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU


```
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-16

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-725-265-16 ..
Align seg 1/1 to: US-09-725-265-16 from: 1 to: 18

1 LysLysAsn 3
|||||
4 AAAAAAAT 12

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:us-09-725-265-17

seq_documentation_block:
; Sequence 17, Application US/09725265
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-17

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-725-265-17 ..
Align seg 1/1 to: US-09-725-265-17 from: 1 to: 18

1 LysLysAsn 3
|||||
4 AAAAAAAT 12

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:us-09-725-265-18

seq_documentation_block:
; Sequence 18, Application US/09725265
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-18

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-725-265-18 ..
Align seg 1/1 to: US-09-725-265-18 from: 1 to: 18

1 LysLysAsn 3
|||||
4 AAAAAAAT 12

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:us-09-725-265-19

seq_documentation_block:
; Sequence 19, Application US/09725265
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/09/725,265
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-19

alignment_scores:
  Quality: 16.00      Length: 3
  Ratio: 5.333       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-528-682-2 x US-09-725-265-19 ..
Align seg 1/1 to: US-09-725-265-19 from: 1 to: 18

1 LysLysAsn 3
|||||
4 AAAAAAAT 12
```


FILE REFERENCE: 199953USOXDIV
CURRENT APPLICATION NUMBER: US/09/725,265
CURRENT FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: US 09/556,127
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: JP 1999-111601
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 18
TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-19

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-725-265-19 ..

Align seg 1/1 to: US-09-725-265-19 from: 1 to: 18

1 LysLysasn 3
|||||
4 AAAAAAAT 12

seq_name: /cgn2_5/ptodata/1/pna/US09_NEW_COMB.seq:US-09-725-265-20

seq_documentation_block:

Sequence 20, Application US/09725265
GENERAL INFORMATION:
APPLICANT: KURANE, RYUICHIRO
APPLICANT: KANAGAWA, TAKAHIRO
APPLICANT: KAMAGATA, YOICHI
APPLICANT: YAMADA, KAZUTAKA
APPLICANT: YOKOMAKU, TOYOKAZU
APPLICANT: KOYAMA, OSAMU
APPLICANT: FURUSHO, KENTA
TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MO
TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
TITLE OF INVENTION: THE METHOD
FILE REFERENCE: 199953USOXDIV
CURRENT APPLICATION NUMBER: US/09/725,265
CURRENT FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: US 09/556,127
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: JP 1999-111601
PRIOR FILING DATE: 1999-04-20
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 18
TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: SYNTHETIC DNA
US-09-725-265-20

alignment_scores:
Quality: 16.00 Length: 3
Ratio: 5.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-528-682-2 x US-09-725-265-20 ..

Align seg 1/1 to: US-09-725-265-20 from: 1 to: 18

1 LysLysasn 3
|||||
4 AAAAAAAT 12

OM of: US-09-528-682-3 to: GenEmbl.* out_format : pfs

Date: Jun 18, 2002 7:27 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=framet.p2n.model -DEV=xlp
-Q/cg2_1/USPTO_sptol/US09528682/runat_18062002_082443_7808/app_query.fasta_1.689
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blossum62
-TRANS=human40.cdd -LIST=0 -DOCLIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09528682.ecgNL_18225 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-528-682-3

Query length: 107

Database: GenEmbl.*

Database sequences: 1797656

Database length: 187333701

Search time (sec): 3690.420000

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gb_htg:AC097953	-	83.50	117.36	357.17	172040	AC097953 Rattus norvegicus c
gb_vi:AF305738	+	83.00	165.08	0.7842	697	AF305738 Infectious bursal dise
gb_vi:AF305739	+	83.00	165.08	0.7842	697	AF305739 Infectious bursal dise
gb_htg:AC095956	-	82.50	121.84	200.91	181724	AC095956 Rattus norvegicus cl
gb_htg:AC094115	-	82.50	116.23	412.76	154035	AC094115 Rattus norvegicus c
gb_htg:AC099275	+	82.50	116.11	419.22	154175	AC099275 Rattus norvegicus c
gb_htg:AC099302	+	82.50	113.30	601.04	214474	AC099302 Rattus norvegicus c
gb_htg:AC098504	-	82.50	112.37	677.15	238216	AC098504 Rattus norvegicus c
gb_vi:AF362771	+	81.00	147.79	7.21	3055	AF362771 Infectious bursal dis
gb_htg:AC098193	-	80.50	115.20	470.84	107518	AC098193 Rattus norvegicus c
gb_htg:AC095291	+	79.50	111.69	738.95	126055	AC095291 Rattus norvegicus c
gb_htg:AC097044	+	79.50	105.82	1.6e+03	244530	AC097044 Rattus norvegicus c
gb_ba:AP003587	+	79.50	102.81	2.3e+03	343550	AP003587 Nostoc sp. PCC 7120
gb_ov:AE008162	+	79.00	146.57	8.42	2178	AE008162 Xenopus laevis N-CAM
gb_ov:XEUNCAM	+	79.00	141.83	15.47	3720	M25696 X.laevis neural cell ad
gb_htg:AC096608	-	78.50	111.22	784.09	104705	AC096608 Rattus norvegicus c
gb_htg:AC098098	-	78.50	106.30	1.5e+03	182686	AC098098 Rattus norvegicus c
gb_htg:AC094978	-	78.00	108.82	1.1e+03	121958	AC094978 Rattus norvegicus c
gb_ba:AE000673	-	77.50	127.53	96.90	13097	AE000673 Aquifex aeolicus sec
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gb_htg:AC107529	+	77.50	106.83	1.4e+03	135671	AC107529 Rattus norvegicus c
gb_htg:AC106544	-	77.50	105.20	1.7e+03	163038	AC106544 Rattus norvegicus c
gb_htg:AC096023	+	77.50	104.93	1.8e+03	168120	AC096023 Rattus norvegicus c
gb_htg:AC105576	+	77.50	102.79	2.3e+03	214033	AC105576 Rattus norvegicus c
gb_vi:HV052889	+	77.00	146.91	8.07	1303	U52889 Human immunodeficiency
gb_vi:HV052894	+	77.00	146.91	8.07	1303	U52894 Human immunodeficiency
gb_pat:134224	+	77.00	144.97	10.34	1622	I34224 Sequence 30 from patent
gb_vi:AF443294	+	77.00	139.37	21.23	3054	AF443294 Infectious bursal dis
gb_pat:134221	+	77.00	138.87	22.62	3230	I34221 Sequence 18 from patent
gb_vi:IBDVPIV	+	77.00	138.87	22.62	3230	M97346 Infectious bursal disea
gb_htg:AC107497	+	77.00	108.90	1.1e+03	92288	AC107497 Rattus norvegicus cl
gb_pi:AF083031	-	77.00	103.56	2.1e+03	174133	AF083031 Guillardia theta nu
gb_htg:AC087131	-	77.00	102.61	2.4e+03	193907	AC087131 Mus musculus clone
gb_ba:AP001514	+	77.00	98.75	3.9e+03	299850	AP001514 Bacillus halodurans
gb_pi:AF132730	+	76.50	141.14	16.91	2220	AF132730 Homo sapiens unknown
gb_pi:AK027245	+	76.50	140.39	18.61	2415	AK027245 Homo sapiens cDNA: FL
gb_htg:AC094250	+	76.50	117.29	360.25	32812	AC094250 Rattus norvegicus cl
gb_htg:AC095730	+	76.50	113.12	615.21	52562	AC095730 Rattus norvegicus cl
gb_ov:AC095923	-	76.50	105.30	1.7e+03	127014	AC095923 Rattus norvegicus c

gb_htg:AC106306	-	76.50	104.23	1.9e+03	143318	AC106306 Rattus norvegicu
gb_htg:AC099071	-	76.50	99.83	3.4e+03	235713	AC099071 Rattus norvegicu
gb_vi:IBDSEGA	+	76.00	136.98	28.84	3154	D00867 Infectious bursal di
gb_vi:IBDVA	+	76.00	136.81	29.47	3214	X16107 Chicken infectious b
gb_htg:AC107501	+	76.00	108.83	1.1e+03	75754	AC107501 Rattus norvegicus
gb_htg:AC108886	+	76.00	102.46	2.4e+03	155423	AC108886 Rattus norvegicu
gb_pi:AL136526	+	76.00	101.17	2.8e+03	179804	AL136526 Homo sapiens chr
gb_htg:AL355680	+	76.00	100.94	2.9e+03	184654	AL355680 Homo sapiens chr
gb_htg:AC094583	+	76.00	99.96	3.3e+03	206108	AC094583 Rattus norvegicu
gb_htg:AC094585	+	76.00	99.79	3.4e+03	210285	AC094585 Rattus norvegicu
gb_sts:CN50615A	-	75.50	146.12	8.93	937	AL400688 T3 end of clone ASO
gb_in:PRATP1	+	75.50	129.07	79.50	6838	X65738 P.falciparum gene fo
gb_htg:AC095462	+	75.50	112.62	655.50	43819	AC095462 Rattus norvegicu
gb_htg:AC102241	+	75.50	108.40	1.1e+03	70550	AC102241 Mus musculus clon
gb_htg:AC095555	+	75.50	104.86	1.8e+03	105262	AC095555 Rattus norvegicu
gb_htg:AC094595	+	75.50	102.74	2.3e+03	133693	AC094595 Rattus norvegicu
gb_htg:AC097194	+	75.50	100.33	3.2e+03	175602	AC097194 Rattus norvegicu
gb_htg:AC097054	-	75.50	99.21	3.7e+03	199211	AC097054 Rattus norvegicu
gb_vi:AF281227	+	75.00	148.80	6.33	654	AF281227 Infectious bursal d
gb_vi:IBDVVP2A	+	75.00	142.44	14.30	1341	X95883 Infectious bursal di
gb_ba:SPU36389	+	75.00	136.98	28.82	2485	U36389 Synchococcus PCC700
gb_ba:AF305610	+	75.00	133.34	45.98	3749	X305610 Borrelia burgdorfe
gb_in:DMTOPI1	+	75.00	127.01	103.57	7664	X61209 D.melanogaster gene
gb_ba:AE006367	+	75.00	123.11	170.73	11901	AE006367 Lactococcus lacti
gb_htg:AC018322	-	75.00	106.07	1.5e+03	81532	AC018322 Drosophila melano
gb_in:AC005428	-	75.00	105.41	1.7e+03	87835	AC005428 Drosophila melano
gb_in:AC099017	-	75.00	100.22	3.2e+03	157766	AC099017 Drosophila melano
gb_in:AC007082	-	75.00	99.49	3.5e+03	171375	AC007082 Drosophila melano
gb_htg:AC095105	+	75.00	98.86	3.8e+03	184001	AC095105 Rattus norvegicu
gb_in:AE003663	-	75.00	94.55	6.7e+03	299449	AE003663 Drosophila melano
gb_sts:CN506KRE	-	74.50	145.12	10.15	880	AL403248 T7 end of clone AT0
gb_htg:AC094283	+	74.50	108.40	1.1e+03	55663	AC094283 Rattus norvegicus
gb_htg:AC095072	+	74.50	105.11	1.7e+03	80710	AC095072 Rattus norvegicus
gb_htg:AC098996	+	74.50	103.63	2.1e+03	93531	AC098996 Rattus norvegicus
gb_htg:AC098821	+	74.50	103.54	2.1e+03	96374	AC098821 Rattus norvegicus
gb_htg:AC095491	+	74.50	102.40	2.4e+03	109620	AC095491 Rattus norvegicu
gb_htg:AC093970	+	74.50	99.03	3.7e+03	160371	AC093970 Rattus norvegicu
gb_htg:AC098087	+	74.50	98.89	3.8e+03	162892	AC098087 Rattus norvegicu
gb_ba:A414142	+	74.50	95.47	5.2e+03	214050	A414142 Versinia pestis
gb_pat:121030	+	74.00	132.69	49.96	3180	I21030 Sequence 1 from pate
gb_htg:AC103046	-	74.00	98.63	3.9e+03	148892	AC103046 Rattus norvegicu
gb_vi:HV052896	+	73.50	139.56	20.71	1300	U52896 Human immunodeficien
gb_htg:AC098003	-	73.50	103.52	2.1e+03	76122	AC098003 Rattus norvegicus
gb_htg:AC097409	+	73.50	100.08	3.3e+03	112233	AC097409 Rattus norvegicu
gb_htg:AC094327	+	73.50	98.88	3.8e+03	124898	AC094327 Rattus norvegicu
gb_htg:AC095140	+	73.50	97.94	4.3e+03	142898	AC095140 Rattus norvegicu
gb_htg:AC098497	+	73.50	96.88	4.9e+03	161042	AC098497 Rattus norvegicu
gb_htg:AC093517	-	73.50	96.66	5.1e+03	165173	AC093517 Rattus norvegicu
gb_htg:AC099117	-	73.50	96.61	5.1e+03	166069	AC099117 Rattus norvegicu
gb_htg:AC103174	+	73.50	96.32	5.3e+03	171655	AC103174 Rattus norvegicu
gb_htg:AC095865	+	73.50	96.13	5.4e+03	175435	AC095865 Rattus norvegicu
gb_htg:AC098510	+	73.50	96.01	5.5e+03	177686	AC098510 Rattus norvegicu
gb_htg:AC094413	+	73.50	95.65	5.8e+03	185150	AC094413 Rattus norvegicu
gb_htg:AC097960	+	73.50	95.17	6.1e+03	195411	AC097960 Rattus norvegicu
gb_htg:AC091232	+	73.00	144.27	11.31	678	AF281232 Infectious bursal d
gb_vi:AF281231	+	73.00	144.10	11.56	691	AF281231 Infectious bursal d
gb_vi:AF281228	+	73.00	144.00	11.71	699	AF281228 Infectious bursal d
gb_vi:AF281228	+	73.00	142.56	14.10	823	AF281228 Infectious bursal d
gb_vi:AF091098	+	73.00	142.56	14.10	823	AF091098 Infectious bursal d
gb_vi:AF091097	+	73.00	138.23	24.57	1342	AF363389 Synthetic construc
gb_sy:AF363389	+	73.00	138.17	24.74	1350	AF464901 Infectious bursal
gb_vi:AF464901	+	73.00	138.17	24.74	1350	AF464901 Infectious bursal
gb_pat:AE69274	+	73.00	138.09	24.99	1362	AE69274 Sequence 13 from Pat
gb_pat:AE71951	+	73.00	138.09	24.99	1362	AE71951 Sequence 13 from Pat
gb_pat:AR147139	+	73.00	138.09	24.99	1362	AR147139 Sequence 13 from p
gb_pat:BD009827	+	73.00	138.09	24.99	1362	BD009827 Avian polynucleoti
em_pat:EL2060	+	73.00	138.09	24.99	1362	EL2060 cDNA encoding VP2 pr
em_pat:AF06701	+	73.00	137.24	27.88	1500	AF06701 Infectious bursal
em_pat:EL2069	+	73.00	133.11	47.34	2391	EL2069 SegA sequence of Inf
gb_vi:IBDSEGA	+	73.00	131.09	61.35	3004	D00868 Infectious bursal di
gb_vi:AF140705	+	73.00	131.00	62.10	3036	AF140705 Infectious bursal
gb_pat:AE38328	+	73.00	130.92	62.72	3063	AE38328 Sequence 1 from Pat
gb_pat:AE33255	+	73.00	130.77	63.94	3115	A33255 IBDV Edgar strain se
gb_vi:IBDSEGA	+	73.00	130.56	65.69	3190	D00869 Infectious bursal di

gb.pl:YSCGLN3	71.00	126.83	105.97	3021	M35267 S.cerevisiae nitrogen d	gb.vi:IBDVP523	70.00	124.26	147.32	3183	X92760 Infectious bursal di
gb.vi:AF092171	71.00	126.60	109.17	3101	AF092171 Infectious bursal dis	gb.vi:AF054945	70.00	124.24	147.68	3190	AF454945 Infectious bursal
gb.vi:AF022776	71.00	126.32	113.17	3201	AF362776 Infectious bursal dis	gb.pat:AX074510	70.00	124.05	151.37	3260	AX074510 Sequence 70 from p
gb.pl:SE9379	71.00	103.29	2.2e+03	43100	U18796 Saccharomyces cerevisi	gb.pat:AX138259	70.00	124.05	151.37	3260	AX138259 Sequence 42 from p
gb.pl:AC006587	71.00	97.90	4.3e+03	79262	AC006587 Arabidopsis thaliana	gb.vi:AF240686	70.00	124.05	151.37	3261	AF240686 Infectious bursal
gb.pl:AC0107533	71.00	96.39	5.3e+03	93942	AC107533 Rattus norvegicus cl	gb.vi:IBU0318896	70.00	124.05	151.42	3261	AJ318896 Infectious bursal
gb.htg:AC105709	71.00	95.83	5.7e+03	100159	AC105709 Rattus norvegicus c	gb.vi:AF092943	70.00	124.03	151.84	3269	AF092943 Infectious bursal
gb.htg:AC096392	71.00	92.27	8.9e+03	149583	AC096392 Rattus norvegicus c	gb.pl:AF092943	70.00	119.58	268.40	5398	M15458 Yeast (S.cerevisiae)
gb.htg:AL330842	71.00	91.69	9.6e+03	159598	AL330842 Homo sapiens chromo	gb.pl:SCDCD25G	70.00	119.34	276.89	5548	X03579 Yeast cell division
gb.htg:AC094987	71.00	91.66	9.6e+03	160408	AC094987 Rattus norvegicus c	gb.pl:SCDCD25G	70.00	117.80	337.24	6000	L20421 Bacillus circulans b
gb.htg:AC094131	71.00	90.40	1.1e+04	184843	AC094131 Rattus norvegicus c	gb.ba:BAE002439	70.00	113.53	583.30	10692	AE002439 Neisseria meningi
gb.htg:AL645584	71.00	89.47	1.3e+04	205402	AL645584 Mus musculus chromo	gb.ba:AE007171	70.00	111.05	802.33	14157	AE007171 Mycobacterium tub
gb.vi:AF281234	70.50	138.70	23.12	702	AF281234 Infectious bursal dise	gb.ba:AE007171	70.00	110.57	852.46	14933	AE007171 Mycobacterium tub
gb.pl:ECU310028	70.50	130.62	65.20	1749	AJ310028 Erichaillea cucullat	gb.pl:MTCY7H7B	70.00	108.35	1.1e+03	19198	U17247 Saccharomyces cerev
gb.pl:PN1310053	70.50	130.61	65.25	1750	AJ310053 Erichaillea cucullat	gb.ba:MTCY7H7B	70.00	106.28	1.5e+03	24244	U29557 Mycobacterium tuber
gb.pat:EO5227	70.50	125.59	124.31	3087	E05227 cDNA encoding split vi	gb.ph:AF145054	70.00	102.91	2.3e+03	35466	AF145054 Streptococcus the
gb.ba:AF121254	70.50	113.55	581.99	12018	AF121254 Enterococcus faeculi	gb.htg:AC094827	70.00	92.12	9.1e+03	119977	AC094827 Rattus norvegicu
gb.htg:AC097307	70.50	95.07	6.2e+03	96811	AC097307 Rattus norvegicus cl	gb.htg:AC094827	70.00	89.89	1.2e+04	154405	AC012041 Homo sapiens chr
gb.htg:AC095879	70.50	94.57	6.6e+03	102529	AC095879 Rattus norvegicus c	gb.htg:AC012136	70.00	89.34	1.3e+04	164304	AC012136 Homo sapiens clo
gb.htg:AC098989	70.50	94.44	6.8e+03	104032	AC098989 Rattus norvegicus c	gb.htg:AC095615	70.00	88.82	1.4e+04	174156	AC095615 Rattus norvegicu
gb.htg:AC097389	70.50	94.37	6.8e+03	104851	AC097389 Rattus norvegicus c	gb.pr:AC026305	70.00	88.69	1.4e+04	176669	AC026305 Homo sapiens chr
gb.htg:AC073804_2	70.50	93.94	7.2e+03	110881	Continuation (3 of 6) of AC0	gb.pr:AC026305	70.00	88.27	1.5e+04	185286	AC006508 Mus musculus yp
gb.htg:AL356581	70.50	93.48	7.6e+03	115902	AL356581 Homo sapiens chromo	gb.pr:AC026167	70.00	88.10	1.5e+04	188865	AC026167 Homo sapiens chr
gb.htg:AC094962	70.50	93.48	7.6e+03	115930	AC094962 Rattus norvegicus c	gb.htg:AC024537	70.00	87.96	1.6e+04	191963	AC024537 Homo sapiens chr
gb.htg:AC095797	70.50	93.40	7.7e+03	116938	AC095797 Rattus norvegicus c	gb.pr:AC024159	70.00	87.80	1.6e+04	195544	AC024159 Homo sapiens chr
gb.htg:AC095366	70.50	93.37	7.7e+03	117368	AC095366 Rattus norvegicus c	gb.ba:AL591979	70.00	85.98	2.0e+04	240050	AL591979 Listeria monocyt
gb.htg:AC095467	70.50	93.34	7.7e+03	117802	AC095467 Rattus norvegicus c	gb.ba:AP003134	70.00	83.96	2.6e+04	301550	AP003134 Staphylococcus a
gb.htg:AC095598	70.50	93.21	7.9e+03	119539	AC095598 Rattus norvegicus c	gb.ba:AP003362	70.00	82.72	3.0e+04	346900	AP003362 Staphylococcus a
gb.htg:AC095570	70.50	92.04	9.2e+03	136295	AC095570 Rattus norvegicus c	gb.pat:AX044030	70.00	82.64	3.1e+04	349980	AX044030 Sequence 109 fro
gb.htg:AC015618	70.50	91.52	9.8e+03	144605	AC015618 Homo sapiens clone	gb.pat:AX006101	69.50	130.55	65.75	1389	AX006101 Sequence 12 from p
gb.htg:AL590643	70.50	91.50	9.8e+03	144865	AL590643 Rattus norvegicus c	gb.pl:CM3410001	69.50	128.59	84.59	1734	AJ310001 Caecalea major chlo
gb.htg:AC098608	70.50	91.44	9.9e+03	144964	AC098608 Rattus norvegicus c	gb.ba:AF327734	69.50	127.16	101.56	2037	AF327734 Riemerella anatipe
gb.htg:AC094207	70.50	91.43	9.9e+03	146009	AC094207 Rattus norvegicus c	gb.pat:AX006092	69.50	124.88	135.99	2634	AX006092 Sequence 3 from Pa
gb.pl:AL137798	70.50	91.43	9.9e+03	146141	AL137798 Human DNA sequence	gb.ba:AE000650	69.50	112.19	692.58	11043	AE000650 Helicobacter pylor
gb.htg:AC095100	70.50	91.38	1.0e+04	146950	AC095100 Rattus norvegicus c	gb.htg:AC009621	69.50	100.26	3.2e+03	42469	AC009621 Rattus norvegicu
gb.htg:AC095885	70.50	91.32	1.0e+04	147984	AC095885 Rattus norvegicus c	gb.htg:AC010269	69.50	95.87	5.6e+03	49861	AC100269 Mus musculus clon
gb.htg:AC097364	70.50	90.90	1.1e+04	155106	AC097364 Rattus norvegicus c	gb.htg:AC094226	69.50	93.27	7.8e+03	93581	AC094226 Rattus norvegicu
gb.htg:AC095919	70.50	90.63	1.1e+04	159880	AC095919 Rattus norvegicus c	gb.htg:AC098900	69.50	93.09	8.0e+03	99527	AC098900 Rattus norvegicu
gb.htg:AL354666	70.50	90.44	1.1e+04	163290	AL354666 Homo sapiens chromo	gb.htg:AC098748	69.50	93.07	8.0e+03	99711	AC098748 Rattus norvegicu
gb.htg:AC106662	70.50	90.41	1.1e+04	163974	AC106662 Rattus norvegicus c	gb.pl:AC009894	69.50	93.07	8.1e+03	96489	AC009894 Arabidopsis thali
gb.htg:AC103227	70.50	90.41	1.1e+04	164038	AC103227 Rattus norvegicus c	gb.htg:AC009389	69.50	92.26	8.9e+03	104851	AC009389 Rattus norvegicu
gb.htg:AC103222	70.50	90.25	1.2e+04	166979	AC103222 Rattus norvegicus c	gb.pl:AC002304	69.50	92.14	9.1e+03	106320	AC002304 Genomic sequence
gb.htg:AC106247	70.50	90.17	1.2e+04	168429	AC106247 Rattus norvegicus c	gb.htg:AC095783	69.50	92.13	9.6e+03	111366	AC095783 Rattus norvegicu
gb.htg:AC097820	70.50	90.15	1.2e+04	168882	AC097820 Rattus norvegicus c	gb.htg:AC106486	69.50	91.73	9.6e+03	123043	AC106486 Rattus norvegicu
gb.htg:AC106344	70.50	90.04	1.2e+04	170889	AC106344 Rattus norvegicus c	gb.htg:AC096300	69.50	90.85	1.1e+04	132763	AC096300 Rattus norvegicu
gb.htg:AC096907	70.50	90.01	1.2e+04	171522	AC096907 Rattus norvegicus c	gb.htg:AC095859	69.50	90.79	1.2e+04	132136	AC095859 Rattus norvegicu
gb.htg:AC097826	70.50	89.91	1.2e+04	173413	AC097826 Rattus norvegicus c	gb.htg:AC095509	69.50	90.12	1.2e+04	133525	AC095509 Rattus norvegicu
gb.htg:AC095930	70.50	89.88	1.2e+04	174033	AC095930 Rattus norvegicus c	gb.htg:AC103239	69.50	89.84	1.2e+04	137897	AC103239 Rattus norvegicu
gb.htg:AC095109	70.50	89.84	1.2e+04	174887	AC095109 Rattus norvegicus c	gb.htg:AC106444	69.50	89.73	1.2e+04	139510	AC106444 Rattus norvegicu
gb.htg:AC097594	70.50	89.80	1.2e+04	175531	AC097594 Rattus norvegicus c	gb.htg:AC094798	69.50	88.92	1.3e+04	150794	AC094798 Rattus norvegicu
gb.htg:AC093961	70.50	89.65	1.2e+04	178655	AC093961 Rattus norvegicus c	gb.htg:AC094798	69.50	88.92	1.4e+04	153003	AC094798 Rattus norvegicu
gb.htg:AC096178	70.50	89.49	1.3e+04	181931	AC096178 Rattus norvegicus c	gb.htg:AC106086	69.50	88.76	1.4e+04	155623	AC106086 Rattus norvegicu
gb.htg:AC105354	70.50	89.47	1.3e+04	182365	AC105354 Rattus norvegicus c	gb.htg:AC094987	69.50	88.50	1.4e+04	160408	AC094987 Rattus norvegicu
gb.htg:AC103013	70.50	89.31	1.3e+04	185713	AC103013 Rattus norvegicus c	gb.htg:AC105481	69.50	88.42	1.5e+04	161864	AC105481 Rattus norvegicu
gb.htg:AL355800	70.50	88.51	1.4e+04	203055	AL355800 Homo sapiens chromo	gb.htg:AC094520	69.50	88.36	1.5e+04	162429	AC094520 Rattus norvegicu
gb.htg:AC097948	70.50	88.28	1.5e+04	208587	AC097948 Mus musculus clone	gb.htg:AC095088	69.50	88.33	1.5e+04	162875	AC095088 Rattus norvegicu
gb.htg:AC095514	70.50	87.88	1.6e+04	218176	AC095514 Rattus norvegicus c	gb.htg:AC096078	69.50	88.33	1.5e+04	163388	AC096078 Rattus norvegicu
gb.htg:AC098938	70.50	87.70	1.6e+04	222687	AC098938 Rattus norvegicus c	gb.htg:AC102984	69.50	88.29	1.5e+04	164191	AC102984 Rattus norvegicu
gb.htg:AC097306	70.50	86.88	1.8e+04	244215	AC073706 Mus musculus clone	gb.htg:AC095076	69.50	88.22	1.5e+04	165460	AC095076 Rattus norvegicu
gb.htg:AC094346	70.50	86.84	1.8e+04	253341	AC073436 Mus musculus clone	gb.htg:AC097210	69.50	88.16	1.5e+04	166596	AC097210 Rattus norvegicu
gb.htg:AC103341	70.50	86.63	1.8e+04	251249	AC103341 Rattus norvegicus c	gb.htg:AC094342	69.50	87.98	1.5e+04	170071	AC094342 Rattus norvegicu
gb.vi:AF281223	70.00	137.88	25.69	684	AF281223 Infectious bursal dise	gb.htg:AC103141	69.50	87.93	1.6e+04	171069	AC103141 Rattus norvegicu
gb.vi:AF281222	70.00	137.84	25.82	687	AF281222 Infectious bursal dise	gb.htg:AC106438	69.50	87.85	1.6e+04	172596	AC106438 Rattus norvegicu
gb.vi:AF281238	70.00	137.74	26.16	695	AF281238 Infectious bursal dise	gb.htg:AC106198	69.50	87.85	1.6e+04	172601	AC106198 Rattus norvegicu
gb.pat:AX343661	70.00	133.85	43.07	1078	AX343661 Sequence 1 from Paten	gb.htg:AC096094	69.50	87.65	1.6e+04	176476	AC096094 Rattus norvegicu
gb.vi:AF262030	70.00	131.85	55.66	1351	AF262030 Infectious bursal dise	gb.htg:AC099131	69.50	87.50	1.6e+04	179617	AC099131 Rattus norvegicu
gb.vi:AB024076	70.00	131.80	56.04	1359	AB024076 Infectious bursal dise	gb.htg:AC068252	69.50	86.99	1.8e+04	190256	AC068252 Mus musculus chr
gb.vi:AF281651	70.00	130.47	66.45	1579	AF281651 Infectious bursal dise	gb.htg:AC105544	69.50	86.98	1.8e+04	190405	AC105544 Rattus norvegicu
gb.vi:AF051838	70.00	128.57	84.79	1957	AF051838 Infectious bursal dise	gb.htg:AL671907	69.50	86.68	1.8e+04	196918	AL671907 Mus musculus chr
gb.vi:IBDVKS	70.00	124.67	139.77	3039	I42284 Infectious bursal disea	gb.htg:AC097050	69.50	86.56	1.9e+04	199689	AC097050 Rattus norvegicu
gb.vi:AF051837	70.00	124.49	143.12	3103	AF051837 Infectious bursal dise	gb.htg:AC098542	69.50	86.01	2.0e+04	212420	AC098542 Rattus norvegicu
gb.vi:ID49706	70.00	124.36	145.48	3148	ID49706 Infectious bursal disea	gb.htg:AC103230	69.50	85.59	2.1e+04	222679	AC103230 Rattus norvegicu
gb.vi:AF165150	70.00	124.30	146.53	3168	AF165150 Infectious bursal dise	gb.htg:AC099297	69.50	84.58	2.4e+04	249775	AC099297 Rattus norvegicu

gb_htg:AC103203	-	69.50	83.53	2.7e+04	281229	! AC103203 Rattus norvegicus d	gb_htg:AC096872	-	68.50	85.48	2.1e+04	17829	! AC096872 Rattus norvegicu
gb_vi:AF281221	+	69.00	135.66	34.16	693	! AF281221 Infectious bursa dise	gb_htg:AC106682	+	68.50	85.41	2.1e+04	179199	! AC106682 Rattus norvegicu
gb_vi:AF281236	+	69.00	135.66	34.16	693	! AF281236 Infectious bursa dise	gb_htg:AC097940	+	68.50	85.37	2.2e+04	180037	! AC097940 Rattus norvegicu
gb_vi:AF281237	+	69.00	135.55	34.61	701	! AF281237 Infectious bursa dise	gb_htg:AC097819	+	68.50	85.29	2.2e+04	181686	! AC097819 Rattus norvegicu
gb_vi:AF051839	+	69.00	128.05	90.63	1636	! AF051839 Infectious bursa dise	gb_htg:AC095466	+	68.50	85.13	2.2e+04	184505	! AC095466 Rattus norvegicu
gb_vi:IBDVP2	+	69.00	126.94	104.46	1854	! M04285 Infectious bursa dise	gb_htg:AC097160	+	68.50	84.58	2.4e+04	196788	! AC097160 Rattus norvegicu
gb_vi:AF001781	+	69.00	123.13	170.23	2850	! AF001781 Agrobacterium tumefac	gb_htg:AC095669	+	68.50	84.34	2.5e+04	202187	! AC095669 Rattus norvegicu
gb_vi:AF109154	+	69.00	122.35	188.31	3115	! AF109154 Infectious bursa dise	gb_htg:AL672013	+	68.50	84.19	2.5e+04	205708	! AL672013 Mus musculus chr
gb_pat:AL12620	+	69.00	122.31	189.28	3129	! AL12620 IBDV RNA segment, 12/19	gb_htg:AC096374	+	68.50	84.10	2.5e+04	207736	! AC096374 Rattus norvegicu
gb_vi:IBDVRNA	+	69.00	122.31	189.28	3129	! AC09993 Infectious bursa dise	gb_htg:AL611930	+	68.50	84.04	2.6e+04	209213	! AL611930 Mus musculus chr
gb_pat:143648	+	69.00	122.16	192.78	3180	! I43648 Sequence 1 from patent	gb_htg:AC096376	+	68.50	84.00	2.6e+04	210113	! AC096376 Rattus norvegicu
gb_vi:AF362773	+	69.00	122.13	193.54	3191	! AF362773 Infectious bursa dise	gb_htg:AC093930	+	68.50	83.90	2.6e+04	212480	! AC093930 Rattus norvegicu
gb_vi:IB2ORFSA	+	69.00	122.13	193.61	3192	! IB2ORFSA Infectious bursa dise	gb_htg:AC097232	+	68.50	83.73	2.7e+04	216659	! AC097232 Rattus norvegicu
gb_pat:AR035347	+	69.00	121.93	198.58	3264	! AR035347 Sequence 31 from pate	gb_htg:AC073553	+	68.50	83.64	2.7e+04	218873	! AC073553 Mus musculus chr
gb_pat:AR035348	+	69.00	121.93	198.58	3264	! AR035348 Sequence 33 from pate	gb_htg:AC106278	+	68.50	83.48	2.8e+04	222787	! AC106278 Rattus norvegicu
gb_pat:BD003320	+	69.00	121.93	198.58	3264	! BD003320 A method for generat	gb_htg:AC103332	+	68.50	82.93	3.0e+04	227148	! AC103332 Rattus norvegicu
gb_pat:BD003321	+	69.00	121.93	198.58	3264	! BD003321 A method for generat	gb_htg:AC097044	+	68.50	82.66	3.1e+04	244530	! AC097044 Rattus norvegicu
gb_pat:AF167102	+	69.00	118.07	325.76	5047	! AF167102 Acholeplasma laidlawi	gb_htg:AC106538	+	68.50	82.27	3.2e+04	255336	! AC106538 Rattus norvegicu
gb_pat:AC096517	+	69.00	93.32	7.8e+03	82569	! AC096517 Rattus norvegicus cl	gb_ba:AP003134	+	68.50	80.80	3.9e+04	301550	! AP003134 Staphylococcus a
gb_pl:TK17	+	69.00	92.61	8.5e+03	89473	! AC013427 Sequence of BAC TK17	gb_ba:AP003362	+	68.50	79.56	4.5e+04	346900	! AP003362 Staphylococcus a
gb_pi:AC079829	+	69.00	91.93	9.3e+03	96699	! AC079829 Arabidopsis thaliana	gb_vi:AF281226	+	68.00	133.59	44.54	690	! AF281226 Infectious bursa d
gb_htg:AC095887	+	69.00	90.75	1.1e+04	110409	! AC095887 Rattus norvegicus c	gb_vi:AF281233	+	68.00	133.44	45.42	702	! AF281233 Infectious bursa d
gb_htg:AC095225	+	69.00	88.10	1.5e+04	148921	! AC095225 Rattus norvegicus c	gb_vi:AF281235	+	68.00	133.44	45.42	702	! AF281235 Infectious bursa d
gb_to:AF129005	+	69.00	85.56	2.1e+04	198515	! AF129005 Mus musculus VNO ol	gb_vi:HIV052895	+	68.00	127.92	92.16	1309	! US28895 Human immunodeficien
gb_htg:AC023611	+	69.00	84.59	2.4e+04	221285	! AC023611 Mus musculus clone	gb_pat:134220	+	68.00	126.88	105.22	1471	! I34220 Sequence 15 from pat
gb_ba:AL596169	+	69.00	83.91	2.6e+04	239050	! AL596169 Listeria innocua Cl	gb_vi:AF165151	+	68.00	126.88	105.22	1471	! X54858 Avian infectious bur
gb_htg:AC079524	+	69.00	83.89	2.6e+04	239747	! AC079524 Mus musculus clone	gb_vi:AF006694	+	68.00	126.83	105.95	1480	! AF006694 Infectious bursa
gb_htg:AC025117	+	69.00	82.33	3.2e+04	285727	! AC025117 Mus musculus chrom	gb_pi:IBDVGVP2	+	68.00	126.68	108.97	1506	! I00665 Infectious bursa di
gb_vi:PEU42580	+	69.00	81.04	3.7e+04	330743	! U42580 Paramecium bursaria c	gb_pi:CGE310017	+	68.00	125.30	128.99	1760	! AJ310017 Cyanicula gemmata
gb_pat:AR151997	+	68.50	131.94	55.01	936	! AR151997 Sequence 3 from patent	gb_vi:DMO298034	+	68.00	124.89	135.84	1842	! AJ298034 Dasheen mosaic vir
gb_pat:AR151996	+	68.50	131.91	55.21	939	! AR151996 Sequence 1 from patent	gb_pat:IE03443	+	68.00	124.04	151.61	2029	! E03443 DNA sequence of IBDV
gb_pl:CAL330510	+	68.50	131.22	60.32	1015	! AJ330510 Candida albicans part	gb_pi:D16828	+	68.00	123.96	153.05	2046	! D16828 Infectious bursa di
gb_pi:HSGM2A2	+	68.50	130.95	62.48	1047	! AF124718 Homo sapiens GM2 acti	gb_vi:AF133904	+	68.00	120.09	251.47	3168	! AF133904 Infectious bursa
gb_cm:AF316445	+	68.50	128.61	84.30	1363	! AF316445 Diameum youngii recom	gb_pi:SCYKL105C	+	68.00	117.33	358.41	4328	! Z28105 S.cerevisiae chromos
gb_ba:AF316556	+	68.50	124.66	139.90	2129	! AF316556 Leptospira interrogan	gb_ba:AE000425	+	68.00	109.90	929.92	10095	! AE000425 Escherichia coli
gb_ba:AF316557	+	68.50	124.66	139.90	2129	! AF316557 Leptospira interrogan	gb_in:AF000580	+	68.00	106.35	1.5e+03	14955	! AF000580 Dictyostelium dis
gb_ba:AF316560	+	68.50	124.66	139.90	2129	! AF316560 Leptospira interrogan	gb_pi:SCHAPLAP	+	68.00	98.63	3.9e+03	35757	! X71133 S.cerevisiae HAP4,
gb_ba:AF316562	+	68.50	124.66	139.90	2129	! AF316562 Leptospira interrogan	gb_in:CEY19B2	+	68.00	97.87	4.3e+03	38950	! AL014447 Caenorhabditis el
gb_ba:AF316563	+	68.50	124.66	139.90	2129	! AF316563 Leptospira interrogan	gb_pi:AB022212	+	68.00	96.51	5.2e+03	45453	! AB022212 Arabidopsis thall
gb_ba:AF316568	+	68.50	124.63	140.57	2138	! AF316568 Leptospira interrogan	gb_htg:AC095592	+	68.00	91.49	9.9e+03	80105	! AC095592 Rattus norvegicus
gb_vi:AB009630	+	68.50	122.44	186.16	2738	! AB009630 Avian rotavirus RNA f	gb_htg:AC099171	+	68.00	91.10	1.0e+04	83711	! AC099171 Rattus norvegicus
gb_pat:AX074508	+	68.50	120.89	226.97	3260	! AX074508 Sequence 68 from Pat	gb_htg:CEY102033_1	+	68.00	88.58	1.4e+04	110000	! Continuation (2 of 4) of
gb_pat:AX074509	+	68.50	120.89	226.97	3260	! AX074509 Sequence 69 from Pat	gb_htg:AC096069	+	68.00	88.58	1.4e+04	110000	! AC096069 Rattus norvegicu
gb_pat:AX138257	+	68.50	120.89	226.97	3260	! AX138257 Sequence 40 from Pat	gb_htg:CEY17G7B	+	68.00	87.29	1.7e+04	128648	! AC023828 Caenorhabditis el
gb_pat:AX138258	+	68.50	120.89	226.97	3260	! AX138258 Sequence 41 from Pat	gb_ro:AC023789	+	68.00	86.35	1.9e+04	143092	! AC023789 Mus musculus chr
gb_ba:AE008658	+	68.50	110.83	825.18	10158	! AE008658 Rickettsia conorii M	gb_htg:AC109827	+	68.00	86.16	2.0e+04	146120	! AC109827 Homo sapiens chr
gb_htg:AC109901	+	68.50	101.29	2.8e+03	29819	! AC109901 Rattus norvegicus cl	gb_htg:AC109827	+	68.00	85.02	2.3e+04	166212	! AC109827 Homo sapiens chr
gb_pl:SPBC7123	+	68.50	100.89	3.0e+03	31198	! AL512943 S.pombe chromosome I	gb_htg:AC098527	+	68.00	82.95	2.6e+04	187069	! AC098527 Rattus norvegicu
gb_ba:LRU61226	+	68.50	99.61	3.5e+03	36040	! U61226 Leptospira interrogans	gb_htg:AC098567	+	68.00	82.95	2.9e+04	210037	! AC098567 Rattus norvegicu
gb_htg:AC102634	+	68.50	94.56	6.7e+03	63800	! AC102634 Mus musculus clone H	gb_pr:AC021146	+	68.00	82.62	3.1e+04	217991	! AC021146 Homo sapiens BAC
gb_htg:AC097764	+	68.50	93.95	7.2e+03	68323	! AC097764 Rattus norvegicus cl	gb_htg:AC023611	+	68.00	82.49	3.1e+04	221285	! AC023611 Mus musculus clo
gb_htg:AC105561	+	68.50	91.85	9.4e+03	86628	! AC105561 Rattus norvegicus cl	gb_ba:ECOW76	+	68.00	82.33	3.2e+04	225419	! AF250284 Ansaata moorei e
gb_htg:AC099213	+	68.50	90.52	1.1e+04	100610	! AC099213 Rattus norvegicus c	gb_vi:AF250284	+	68.00	82.06	3.3e+04	225392	! AF250284 Ansaata moorei e
gb_htg:AC103132	+	68.50	90.43	1.1e+04	101687	! AC103132 Rattus norvegicus c	gb_htg:AC023604	+	68.00	80.36	4.1e+04	281574	! AC023604 Mus musculus clo
gb_htg:AC096868	+	68.50	90.15	1.2e+04	104921	! AC096868 Rattus norvegicus c	gb_ba:BNM422491	+	68.00	78.90	4.9e+04	331801	! AL162755 Neisseria mening
gb_htg:AC011391	+	68.50	89.95	1.2e+04	107320	! AC011391 Homo sapiens chrom	gb_ov:ESM059795	+	67.50	128.30	87.74	1113	! U69795 Epitaxites striatus s
gb_htg:AC094870	+	68.50	89.51	1.3e+04	112730	! AC094870 Rattus norvegicus c	gb_pi:DB91167	+	67.50	125.70	122.48	1493	! DB9167 Schizosaccharomyces
gb_to:AC083887	+	68.50	89.51	1.3e+04	112755	! AC083887 Rattus norvegicus c	gb_pi:AK025841	+	67.50	125.51	125.56	1526	! AK025841 Homo sapiens cDNA:
gb_htg:AC097838	+	68.50	89.31	1.3e+04	115406	! AC097838 Rattus norvegicus c	gb_pr:BC015309	+	67.50	125.23	130.05	1574	! BC015309 Homo sapiens, gro
gb_htg:AC097016	+	68.50	89.14	1.3e+04	117550	! AC097016 Rattus norvegicus c	gb_pi:SCRN1631	+	67.50	124.46	143.55	1717	! Z46237 S.cerevisiae RML1 ge
gb_pr:AC011342	+	68.50	88.92	1.4e+04	120584	! AC011342 Homo sapiens chrom	gb_pat:AC098631	+	67.50	123.37	160.96	1899	! AX098631 Sequence 1 from Pa
gb_htg:AC097153	+	68.50	88.89	1.4e+04	120979	! AC097153 Rattus norvegicus c	gb_ba:ECB132325	+	67.50	121.37	213.37	2434	! AJ132325 Erwinia chrysanth
gb_htg:AC095226	+	68.50	88.62	1.4e+04	124712	! AC095226 Rattus norvegicus c	gb_pr:AK0237680	+	67.50	121.05	222.35	2524	! AK0237680 Homo sapiens cDNA
gb_htg:AC103524	+	68.50	87.79	1.6e+04	137028	! AC103524 Rattus norvegicus c	gb_pi:AX136191	+	67.50	120.92	226.26	2563	! AX136191 Sequence 113 from
gb_htg:AC098007	+	68.50	87.63	1.6e+04	139523	! AC098007 Rattus norvegicus c	gb_pr:AK027697	+	67.50	120.84	228.47	2585	! AK027697 Homo sapiens cDNA
gb_htg:AC103012	+	68.50	87.21	1.7e+04	146240	! AC103012 Rattus norvegicus c	gb_htg:AK027889	+	67.50	120.67	233.39	2634	! AC017889 Drosophila melanog
gb_htg:AC096417	+	68.50	86.91	1.8e+04	151263	! AC096417 Rattus norvegicus c	gb_pr:AK027648	+	67.50	119.54	269.84	2993	! AK027648 Homo sapiens cDNA
gb_to:AC008385	+	68.50	86.88	1.8e+04	151710	! AC008385 Homo sapiens chrom	gb_in:AY075532	+	67.50	119.54	269.84	2993	! AY075532 Drosophila melanog
gb_htg:AC103030	+	68.50	86.73	1.8e+04	154443	! AC103030 Rattus norvegicus c	gb_pi:AF321054	+	67.50	118.79	297.24	3259	! AF321054 Infectious bursa
gb_htg:AC095301	+	68.50	86.50	1.9e+04	158467	! AC095301 Rattus norvegicus c	gb_htg:AC107245	+	67.50	104.53	1.8e+03	16301	! AC107245 Rattus norvegicus
gb_to:AC020974	+	68.50	86.27	1.9e+04	162639	! AC020974 Mus musculus chrom	gb_htg:AC109067	+	67.50	99.36	3.6e+03	29232	! AC109067 Rattus norvegicus
gb_htg:AC098225	+	68.50	86.12	2.0e+04	165475	! AC098225 Rattus norvegicus c	gb_in:AE003260	+	67.50	98.16	4.2e+03	33484	! AE003260 Drosophila melano
gb_htg:AC106644	+	68.50	85.70	2.1e+04	173449	! AC106644 Rattus norvegicus c	gb_htg:AC098438	+	67.50	96.86	4.9e+03	38770	! AC098438 Rattus norvegicus

gb_hhg:AC109525	+	67.50	96.80	5.0e+03	39025	!	AC109525	Rattus norvegicus cl	gb_ba:AE005573	-	67.00	107.40	1.3e+03	10475	!	AE005573	Escherichia coli
gb_hhg:AC095971	+	67.50	96.43	5.2e+03	40721	!	AC095971	Rattus norvegicus cl	gb_ba:AE001513	+	67.00	105.86	1.6e+03	12456	!	XE001513	Helicobacter pylori
gb_hhg:AC096279	+	67.50	94.14	7.0e+03	52725	!	AC096279	Rattus norvegicus cl	gb_pi:SCX1207K	+	67.00	101.35	2.8e+03	20733	!	AF024501	Caenorhabditis el
gb_hhg:AC097199	-	67.50	93.39	7.7e+03	57387	!	AC097199	Rattus norvegicus cl	gb_hhg:AC012817	+	67.00	96.35	5.3e+03	38471	!	AC012817	Drosophila melanog
gb_hhg:AC107404	+	67.50	93.37	7.7e+03	57483	!	AC107404	Rattus norvegicus cl	gb_pi:ATW18012	-	67.00	92.40	8.8e+03	43449	!	AC011245	Homo sapiens BAC
gb_hhg:AC098192	+	67.50	93.27	7.8e+03	58187	!	AC098192	Rattus norvegicus cl	gb_pi:ATW18012	-	67.00	92.40	8.8e+03	43449	!	AC011245	Homo sapiens BAC
gb_hhg:AC102369	+	67.50	93.62	8.1e+03	59841	!	AC102369	Mus musculus clone F	gb_pi:ATW18012	-	67.00	87.36	1.7e+04	100678	!	AL138644	Arabidopsis thal
gb_hhg:AC098446	+	67.50	92.64	8.5e+03	62437	!	AC098446	Rattus norvegicus cl	gb_hhg:AC008198	+	67.00	85.95	2.0e+04	118036	!	AC008198	Drosophila melan
gb_hhg:AC099996	+	67.50	92.05	8.6e+03	63063	!	AC099996	Mus musculus clone F	gb_hhg:AL645982	+	67.00	84.88	2.3e+04	133235	!	AL645982	Mus musculus chr
gb_hhg:AC100935	+	67.50	92.09	9.1e+03	65445	!	AC100935	Mus musculus clone F	gb_hhg:AL671961	+	67.00	83.80	2.6e+04	133235	!	AL671961	Mus musculus chr
gb_hhg:AC101594	+	67.50	91.33	1.0e+04	72412	!	AC101594	Mus musculus clone F	gb_hhg:AC095498	+	67.00	83.44	2.8e+04	136754	!	AC095498	Rattus norvegicu
gb_hhg:AC095087	+	67.50	90.94	1.1e+04	75700	!	AC095087	Rattus norvegicus cl	gb_hhg:AC095298	+	67.00	83.40	2.8e+04	157444	!	AC095298	Rattus norvegicu
gb_pi:AB023033	+	67.50	90.77	1.1e+04	77129	!	AB023033	Arabidopsis thaliana	gb_hhg:AC106201	+	67.00	83.06	2.9e+04	163542	!	AC106201	Rattus norvegicu
gb_hhg:AC105791	+	67.50	90.38	1.1e+04	80569	!	AC105791	Rattus norvegicus cl	gb_hhg:AC106300	+	67.00	82.97	2.9e+04	165182	!	AC106300	Rattus norvegicu
gb_hhg:AC096790	+	67.50	89.44	1.3e+04	89600	!	AC096790	Rattus norvegicus cl	gb_in:AC017079	+	67.00	82.90	3.0e+04	165182	!	AC017079	Drosophila melan
gb_hhg:AC017901	+	67.50	89.44	1.3e+04	89670	!	AC017901	Drosophila melanogae	gb_hhg:AC027669	+	67.00	81.59	3.5e+04	193044	!	AC027669	Homo sapiens chr
gb_hhg:AC106630	-	67.50	89.40	1.3e+04	90005	!	AC106630	Rattus norvegicus cl	gb_hhg:AC080081	+	67.00	81.22	3.7e+04	201324	!	AC080081	Homo sapiens chr
gb_hhg:AC103193	+	67.50	89.36	1.3e+04	90412	!	AC103193	Rattus norvegicus cl	gb_hhg:AL645807	+	67.00	81.06	3.7e+04	205077	!	AL645807	Mus musculus chr
gb_hhg:AC095689	+	67.50	89.29	1.3e+04	91160	!	AC095689	Rattus norvegicus cl	gb_ba:AP002086	+	67.00	80.53	4.0e+04	217594	!	AP002086	Agrobacterium rh
gb_hhg:AC099348	+	67.50	88.35	1.5e+04	101368	!	AC099348	Rattus norvegicus cl	gb_ba:AJ414156	+	67.00	80.43	4.0e+04	220050	!	AJ414156	Yersinia pestis
gb_hhg:AC097339	+	67.50	88.02	1.5e+04	105162	!	AC097339	Rattus norvegicus cl	gb_ro:AC096776	+	67.00	80.43	4.0e+04	220119	!	AC096776	Mus musculus clo
gb_hhg:AC094311	+	67.50	87.60	1.6e+04	110357	!	AC094311	Rattus norvegicus cl	gb_hhg:AL611945	+	67.00	80.07	4.2e+04	229224	!	AL611945	Mus musculus chr
gb_hhg:AC103260	+	67.50	87.08	1.7e+04	117062	!	AC103260	Rattus norvegicus cl	gb_hhg:AC108602	+	67.00	79.91	4.3e+04	233552	!	AC108602	Rattus norvegicu
gb_hhg:AC094303	+	67.50	86.77	1.8e+04	121157	!	AC094303	Rattus norvegicus cl	gb_hhg:AL645753	+	67.00	79.68	4.5e+04	239557	!	AL645753	Mus musculus chr
gb_hhg:AC094733	+	67.50	85.84	2.0e+04	134533	!	AC094733	Rattus norvegicus cl	gb_hhg:AL627257	+	67.00	79.60	4.5e+04	241698	!	AL627257	Mus musculus chr
gb_hhg:AC094032	+	67.50	85.60	2.1e+04	138357	!	AC094032	Rattus norvegicus cl	gb_ba:AP002565	+	67.00	78.69	5.1e+04	267888	!	AP002565	Escherichia coli
gb_hhg:AC103488	+	67.50	85.57	2.1e+04	138784	!	AC103488	Rattus norvegicus cl	gb_in:AE003554	+	67.00	78.12	5.4e+04	285752	!	AE003554	Drosophila melan
gb_hhg:AC094940	+	67.50	85.39	2.2e+04	141532	!	AC094940	Rattus norvegicus cl	gb_ba:CU11188X3	+	67.00	77.19	6.1e+04	337511	!	CU11188X3	Campylobacter je
gb_hhg:AC091657	+	67.50	85.32	2.2e+04	142657	!	AC091657	Rattus norvegicus cl	gb_sus:CMS08F8B	+	66.50	127.65	95.45	945	!	AF396081	T7 end of clone AR0
gb_hhg:AC106423	+	67.50	85.28	2.2e+04	143437	!	AC106423	Rattus norvegicus cl	gb_ba:AF316564	+	66.50	120.45	240.09	2129	!	AF316564	Leptospira interro
gb_hhg:AC095668	+	67.50	84.79	2.3e+04	151097	!	AC095668	Rattus norvegicus cl	gb_ba:AF316559	+	66.50	120.42	243.72	2130	!	AF316559	Leptospira interro
gb_hhg:AC106459	+	67.50	84.72	2.3e+04	151548	!	AC106459	Rattus norvegicus cl	gb_in:AY061160	+	66.50	120.42	253.72	2235	!	AY061160	Drosophila melanog
gb_hhg:AC095213	+	67.50	84.58	2.4e+04	155212	!	AC095213	Rattus norvegicus cl	gb_vl:ROBK33	+	66.50	119.57	268.85	2352	!	ROBK33	Bovine rotavirus K33
gb_hhg:AC095565	+	67.50	84.52	2.4e+04	158078	!	AC095565	Rattus norvegicus cl	gb_vl:ROBK33	+	66.50	119.57	268.85	2352	!	ROBK33	Bovine rotavirus K33
gb_hhg:AC106684	+	67.50	84.31	2.5e+04	159877	!	AC106684	Rattus norvegicus cl	gb_pi:AY062536	+	66.50	116.50	398.63	3327	!	AY062536	Arabidopsis thalia
gb_hhg:AC095103	+	67.50	84.15	2.5e+04	162880	!	AC095103	Rattus norvegicus cl	gb_pi:AR166122	+	66.50	116.42	402.58	3356	!	AR166122	Sequence 4 from pa
gb_hhg:AC094890	+	67.50	84.08	2.6e+04	164243	!	AC094890	Rattus norvegicus cl	gb_pi:AR166122	+	66.50	115.83	434.20	3587	!	AR166122	Arabidopsis thaliana
gb_hhg:AC106300	+	67.50	84.04	2.6e+04	164988	!	AC106300	Rattus norvegicus cl	em_pi:EL11448	+	66.50	115.76	438.32	3617	!	EL11448	cDNA encoding plant
gb_hhg:AC095213	+	67.50	84.03	2.6e+04	165182	!	AC095213	Rattus norvegicus cl	gb_vl:AF289053	+	66.50	115.76	438.32	3617	!	AF289053	Perina nuda nucleo
gb_hhg:AC092223	+	67.50	83.69	2.7e+04	171598	!	AC092223	Drosophila melanogae	gb_in:SHA271051	+	66.50	115.19	471.64	3858	!	AJ271051	Schistosoma haemat
gb_hhg:AC106978	+	67.50	83.66	2.7e+04	172095	!	AC106978	Rattus norvegicus cl	gb_ba:AB026889	+	66.50	114.94	486.80	3967	!	AB026889	Clostridium histol
gb_hhg:AC096437	+	67.50	83.62	2.7e+04	172437	!	AC096437	Rattus norvegicus cl	gb_pi:AF394782	+	66.50	111.67	740.88	5742	!	AF394782	Homo sapiens rap g
gb_hhg:AC103145	+	67.50	83.63	2.7e+04	172818	!	AC103145	Rattus norvegicus cl	gb_ba:AE001283	+	66.50	111.41	765.14	5914	!	AE001283	Chlamydia trachom
gb_hhg:AC097612	+	67.50	83.63	2.7e+04	173469	!	AC097612	Rattus norvegicus cl	gb_pi:AF117947	+	66.50	110.70	838.18	6401	!	AF117947	Homo sapiens PD2 d
gb_hhg:AC098080	+	67.50	83.59	2.7e+04	173533	!	AC098080	Rattus norvegicus cl	gb_pi:AF039373	+	66.50	107.08	1.3e+03	9642	!	AF039373	Arabidopsis thalia
gb_hhg:AC099604	+	67.50	83.46	2.8e+04	176163	!	AC099604	Mus musculus clone	gb_pi:AF039371	+	66.50	107.08	1.3e+03	9643	!	AF039371	Arabidopsis thalia
gb_hhg:AC097877	+	67.50	83.38	2.8e+04	177596	!	AC097877	Rattus norvegicus cl	gb_pi:AF039371	+	66.50	107.08	1.3e+03	9643	!	AF039371	Arabidopsis thalia
gb_pi:AC087509	+	67.50	83.13	2.9e+04	182795	!	AC087509	Rattus norvegicus cl	gb_ba:AE007910	+	66.50	106.20	1.5e+03	10640	!	AE007910	Rattus norvegicus
gb_hhg:AC103508	+	67.50	83.12	2.9e+04	183046	!	AC103508	Oryza sativa chromo	gb_ba:AE007910	+	66.50	105.85	1.6e+03	11078	!	AE007910	Agrobacterium tum
gb_hhg:AC103275	+	67.50	83.03	2.9e+04	184922	!	AC103275	Rattus norvegicus cl	gb_ba:AE001283	+	66.50	104.80	1.8e+03	12471	!	AE001283	Chlamydia trachom
gb_hhg:AC084270	+	67.50	82.92	3.2e+04	186894	!	AC084270	Rattus norvegicus cl	gb_hhg:AC097864	+	66.50	99.05	2.4e+03	16351	!	AC097864	Rattus norvegicus
gb_hhg:AC093967	+	67.50	82.39	3.2e+04	200009	!	AC093967	Rattus norvegicus cl	gb_hhg:AC098379	+	66.50	98.76	3.9e+03	24551	!	AC098379	Rattus norvegicus
gb_hhg:AC099579	+	67.50	82.32	3.2e+04	200265	!	AC099579	Mus musculus clone	gb_hhg:AC094247	+	66.50	96.27	5.3e+03	32684	!	AC094247	Rattus norvegicu
gb_hhg:AL626805	+	67.50	82.31	3.2e+04	200559	!	AL626805	Mus musculus chromo	gb_ba:AF316500	+	66.50	95.73	5.7e+03	34723	!	AF316500	Leptospira interr
gb_hhg:AC103338	+	67.50	82.28	3.2e+04	201164	!	AC103338	Rattus norvegicus cl	gb_pi:SPAC9	+	66.50	95.66	5.8e+03	35000	!	AL121764	S.pombe chromosom
gb_hhg:AC096862	+	67.50	82.20	3.2e+04	203032	!	AC096862	Rattus norvegicus cl	gb_in:CEC05D12	+	66.50	94.04	7.1e+03	42021	!	Z50872	Caenorhabditis eleg
gb_hhg:AC097995	+	67.50	82.15	3.3e+04	204206	!	AC097995	Mus musculus clone	gb_hhg:AC103411	+	66.50	93.05	8.1e+03	47005	!	AC103411	Rattus norvegicus
gb_hhg:AL626806	+	67.50	81.87	3.4e+04	210827	!	AL626806	Mus musculus chromo	gb_hhg:AC109556	+	66.50	91.13	1.0e+04	58374	!	AC109556	Mus musculus clon
gb_hhg:AC099295	+	67.50	81.70	3.5e+04	211712	!	AC099295	Rattus norvegicus cl	gb_hhg:AC107477	+	66.50	90.80	1.1e+04	60383	!	AC107477	Rattus norvegicus
gb_hhg:AC095489	+	67.50	81.44	3.6e+04	221119	!	AC095489	Rattus norvegicus cl	gb_hhg:AC095393	+	66.50	90.32	1.1e+04	63550	!	AC095393	Rattus norvegicus
gb_hhg:AC073564	+	67.50	81.19	3.7e+04	227605	!	AC073564	Mus musculus chromo	gb_hhg:AC105584	+	66.50	90.28	1.2e+04	64676	!	AC105584	Rattus norvegicus
gb_hhg:AC096325	+	67.50	80.97	3.8e+04	233382	!	AC096325	Rattus norvegicus cl	gb_hhg:AC096238	+	66.50	88.62	1.4e+04	77506	!	AC096238	Rattus norvegicus
gb_hhg:AC106602	+	67.50	80.96	3.8e+04	233552	!	AC106602	Rattus norvegicus cl	gb_hhg:AC095945	+	66.50	88.34	1.5e+04	80008	!	AC095945	Rattus norvegicus
gb_hhg:AC096189	+	67.50	79.18	4.7e+04	285592	!	AC096189	Rattus norvegicus cl	gb_hhg:AC108506	+	66.50	88.05	1.5e+04	82625	!	AC108506	Rattus norvegicus
gb_in:AE003641	+	67.50	78.91	4.9e+04	294389	!	AE003641	Drosophila melanogae	gb_hhg:AC102983	+	66.50	87.74	1.6e+04	85655	!	AC102983	Rattus norvegicus
gb_in:DROSADH02	+	67.50	78.15	5.0e+04	320754	!	AE003640	Drosophila melanogae	gb_hhg:AC094686	+	66.50	87.35	1.7e+04	89515	!	AC094686	Rattus norvegicus
gb_ba:NMU81551																	

gb_hlg:AC095820	1.9e+04	86.32	66.50	+	100477	AC095820	Rattus norvegicus c	gb_hlg:AC087875	66.50	79.05	4.8e+04	228335	AC087875	Mus musculus clo
gb_hlg:AC094375	2.0e+04	85.87	66.50	-	103743	AC094375	Rattus norvegicus c	gb_pr:CNS01DWD	66.50	79.04	4.8e+04	228652	AL13128	Human chromosome
gb_hlg:AC095679	2.1e+04	85.62	66.50	-	103813	AC095679	Rattus norvegicus c	gb_hlg:AC099382	66.50	78.85	4.9e+04	235258	AC099382	Rattus norvegicus
gb_hlg:AC110466	2.1e+04	85.46	66.50	-	110745	AC110466	Rattus norvegicus c	gb_ba:AL596170	66.50	76.25	6.9e+04	313450	AL596170	Listeria innocua
gb_hlg:AC097846	2.1e+04	85.44	66.50	+	111075	AC097846	Rattus norvegicus c	gb_vf:AF091099	66.00	127.86	92.86	819	AF091099	Infectious bursal d
gb_hlg:AC098764	2.2e+04	85.38	66.50	+	111794	AC098764	Rattus norvegicus c	gb_vf:AB059304	66.00	125.07	132.77	1122	AB059304	Human immunodefici
gb_hlg:AC095684	2.2e+04	85.24	66.50	+	113540	AC095684	Rattus norvegicus c	gb_vf:AB059306	66.00	125.07	132.77	1122	AB059306	Human immunodefici
gb_hlg:AC105563	2.2e+04	85.03	66.50	+	116250	AC105563	Rattus norvegicus c	gb_pr:HSAT7014	66.00	123.77	156.93	1300	AJ007014	Homo sapiens mrna
gb_hlg:OSJN00211	2.3e+04	85.00	66.50	+	116667	AL663010	Oryza sativa chromo	gb_pl:SDMATK	66.00	122.36	187.99	1524	270186	S. divaricatus chloro
gb_hlg:AC093936	2.4e+04	84.70	66.50	+	120687	AC093936	Rattus norvegicus c	gb_ro:MMU243485	66.00	120.79	229.83	1819	AJ243485	Mus Musculus mrna
gb_hlg:AC097887	2.4e+04	84.60	66.50	+	122056	AC097887	Rattus norvegicus c	gb_ov:AB008163	66.00	119.20	282.00	2178	AB008163	Xenopus laevis N-C
gb_hlg:AC106133	2.6e+04	84.05	66.50	+	129868	AC106133	Rattus norvegicus c	gb_ov:AB001703	66.00	117.25	362.20	2715	AK001703	Homo sapiens cdna
gb_hlg:AC093975	2.6e+04	83.99	66.50	+	130747	AC093975	Rattus norvegicus c	gb_ov:XEJNCAMA	66.00	114.24	532.84	3814	M76710	Xenopus laevis cell
gb_hlg:AC099064	2.7e+04	83.74	66.50	+	134545	AC099064	Homo sapiens chromo	gb_pl:AF057708	66.00	113.21	608.17	4285	AF057708	Populus balsamifer
gb_hlg:AC097075	2.7e+04	83.57	66.50	+	137140	AC097075	Rattus norvegicus c	gb_vf:AB006531	66.00	106.84	1.4e+03	8797	AB006531	Plautia stali inte
gb_hlg:AC103087	2.8e+04	83.40	66.50	+	137993	AC103087	Rattus norvegicus c	gb_ba:AE006541	66.00	105.36	1.7e+03	10389	AE006541	Streptococcus pyo
gb_hlg:AC103009	2.8e+04	83.23	66.50	+	142434	AC103009	Rattus norvegicus c	gb_in:AF282241	66.00	104.99	1.7e+03	10833	AF282241	Plasmodium falcip
gb_hlg:AC095290	3.1e+04	82.66	66.50	+	151951	AC095290	Rattus norvegicus c	gb_in:AF282242	66.00	104.97	1.7e+03	10863	AF282242	Plasmodium falcip
gb_hlg:AC102964	3.1e+04	82.57	66.50	+	153486	AC102964	Rattus norvegicus c	gb_in:AF169404	66.00	104.92	1.8e+03	10919	AF169404	Plasmodium falcip
gb_hlg:AC103123	3.1e+04	82.56	66.50	+	153625	AC103123	Rattus norvegicus c	gb_ba:AE000600	66.00	103.73	2.0e+03	12489	AE000600	Helicobacter pylor
gb_hlg:AC097257	3.1e+04	82.54	66.50	+	153950	AC097257	Rattus norvegicus c	gb_ba:AE001778	66.00	100.82	3.0e+03	12735	AE001778	Thermotoga mariti
gb_hlg:AC094589	3.1e+04	82.53	66.50	+	154213	AC094589	Rattus norvegicus c	gb_hlg:AC110338	66.00	98.32	4.1e+03	23022	AC110338	Rattus norvegicus
gb_hlg:AC096059	3.2e+04	82.41	66.50	+	158224	AC096059	Rattus norvegicus c	gb_in:CEK07A1	66.00	93.63	7.5e+03	39086	Z81097	Caenorhabditis eleg
gb_hlg:AC094621	3.2e+04	82.36	66.50	+	157209	AC094621	Rattus norvegicus c	gb_hlg:AC107108	66.00	93.13	8.0e+03	41363	AC107108	Rattus norvegicus
gb_pr:AC074348	3.2e+04	82.34	66.50	+	157511	AC074348	Homo sapiens BAC cl	gb_pl:SC4357	66.00	87.82	1.6e+04	75317	Z38059	S.cerevisiae chromo
gb_hlg:AC098991	3.2e+04	82.33	66.50	+	158116	AC098991	Rattus norvegicus c	gb_hlg:AC096071	66.00	87.20	1.7e+04	80780	AC096071	Rattus norvegicus
em_hlg:hum:AL353627	3.2e+04	82.31	66.50	+	160837	AL353627	Human DNA sequence	gb_hlg:AC098025	66.00	86.98	1.8e+04	82865	AC098025	Rattus norvegicus
gb_pr:AC103552	3.3e+04	82.16	66.50	+	160837	AC103552	Homo sapiens chromo	gb_hlg:AC091353	66.00	86.24	1.9e+04	90047	AC091353	Rattus norvegicus
gb_pr:AP028006	3.3e+04	82.10	66.50	+	161871	AP028006	Homo sapiens chromo	gb_hlg:AC095999	66.00	86.12	2.0e+04	91295	AC095999	Rattus norvegicus
gb_hlg:AC097753	3.3e+04	82.10	66.50	+	161952	AC097753	Rattus norvegicus c	gb_hlg:AC098899	66.00	85.37	2.2e+04	93367	AC098899	Rattus norvegicus
gb_hlg:AC105499	3.3e+04	82.07	66.50	+	162405	AC105499	Rattus norvegicus c	gb_hlg:AC106362	66.00	85.23	2.2e+04	100982	AC106362	Rattus norvegicus
gb_hlg:OSJN00156	3.3e+04	82.05	66.50	+	162695	AL662958	Oryza sativa chromo	gb_hlg:AC094955	66.00	85.01	2.3e+04	103417	AC094955	Rattus norvegicus
gb_hlg:AC103293	3.3e+04	82.00	66.50	+	163612	AC103293	Rattus norvegicus c	gb_hlg:AL606482.2	66.00	84.47	2.4e+04	110000	Continuation (3 of 5) of	
gb_hlg:AC106496	3.4e+04	81.91	66.50	+	165435	AC106496	Rattus norvegicus c	gb_hlg:AL606482.3	66.00	84.47	2.4e+04	110000	Continuation (4 of 5) of	
gb_hlg:AC105834	3.4e+04	81.82	66.50	+	167109	AC105834	Rattus norvegicus c	gb_hlg:AC094536	66.00	83.53	2.7e+04	122225	AC094536	Rattus norvegicus
gb_hlg:AC094672	3.4e+04	81.77	66.50	+	168004	AC094672	Rattus norvegicus c	gb_hlg:PFMA1P1	66.00	81.58	3.5e+04	152409	AL031744	Plasmodium falcip
gb_hlg:AC094807	3.4e+04	81.72	66.50	+	168961	AC094807	Rattus norvegicus c	gb_pr:AC069509	66.00	81.56	3.5e+04	152832	AC069509	Homo sapiens 3 B
gb_hlg:AC094768	3.4e+04	81.69	66.50	+	168962	AC094768	Rattus norvegicus c	gb_hlg:AP003490	66.00	81.34	3.6e+04	156551	AP003490	Oryza sativa chr
gb_hlg:AC103002	3.5e+04	81.72	66.50	+	169494	AC103002	Rattus norvegicus c	gb_hlg:AC079958	66.00	80.83	3.8e+04	165865	AC079958	Mus musculus chr
gb_hlg:AC098169	3.5e+04	81.65	66.50	+	170378	AC098169	Rattus norvegicus c	gb_hlg:AC107423	66.00	80.73	3.9e+04	167751	AC107423	Homo sapiens chr
gb_hlg:AC094714	3.5e+04	81.61	66.50	+	171046	AC094714	Rattus norvegicus c	gb_hlg:AC099452	66.00	80.50	4.0e+04	172199	AC099452	Rattus norvegicus
gb_hlg:AC106449	3.5e+04	81.60	66.50	+	171233	AC106449	Rattus norvegicus c	gb_pr:AC021180	66.00	80.41	4.1e+04	173940	AC021180	Homo sapiens BAC
gb_hlg:AC097953	3.5e+04	81.56	66.50	+	172040	AC097953	Rattus norvegicus c	gb_hlg:AC095953	66.00	80.20	4.2e+04	178193	AC095953	Rattus norvegicus
gb_hlg:AC094540	3.6e+04	81.48	66.50	+	173669	AC094540	Rattus norvegicus c	gb_hlg:AC021569	66.00	79.46	4.6e+04	193552	AC021569	Homo sapiens chr
gb_hlg:AC0911720	3.6e+04	81.44	66.50	+	174393	AC0911720	Homo sapiens chromo	gb_hlg:AC024373	66.00	79.27	4.7e+04	197843	AC024373	Homo sapiens chr
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gb_hlg:AC016087	3.7e+04	81.19	66.50	+	179303	AC016087	Homo sapiens clone	gb_ro:AL604065	66.00	77.02	6.2e+04	254938	AL604065	Mouse DNA sequen
gb_hlg:AC103211	3.7e+04	81.18	66.50	+	179497	AC103211	Rattus norvegicus c	gb_ba:AP001510	66.00	75.52	7.6e+04	302150	AP001510	Bacillus halodur
gb_hlg:AC024488	3.7e+04	81.08	66.50	+	181655	AC024488	Homo sapiens chromo	gb_pat:AB5371	65.50	130.86	63.17	518	AB5371	Sequence 30 from Pat
gb_hlg:AC095154	3.8e+04	81.02	66.50	+	182794	AC095154	Rattus norvegicus c	gb_pat:AR154864	65.50	130.86	63.17	518	AR154864	Sequence 30 from Pat
gb_hlg:AC099182	3.8e+04	81.00	66.50	+	183271	AC099182	Rattus norvegicus c	gb_pat:E65389	65.50	130.86	63.17	518	E65389	Genome DNA sequence o
gb_hlg:AC099551	3.8e+04	81.00	66.50	+	183547	AC099551	Homo sapiens chromo	gb_pr:BCN07806	65.50	120.02	253.88	1763	BCN07806	Homo sapiens, clon
gb_hlg:AC063929	3.8e+04	80.89	66.50	+	183624	AC063929	Homo sapiens chromo	gb_sy:SNP8GSH	65.50	119.40	274.75	1893	D13798	Plasmid pGRS1518-4d,
gb_hlg:AC096166	3.8e+04	80.87	66.50	+	186046	AC096166	Rattus norvegicus c	gb_pr:AK055423	65.50	118.45	310.51	2105	AK055423	Homo sapiens cdna
gb_hlg:AC099631	3.8e+04	80.86	66.50	+	186242	AC099631	Mus musculus clone	gb_pat:AX073102	65.50	118.09	325.12	2152	AX073102	Sequence 213 from
gb_hlg:AC099711	3.8e+04	80.84	66.50	+	186634	AC099711	Mus musculus clone	gb_pr:AK056296	65.50	118.06	326.47	2203	AK056296	Homo sapiens cdna
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gb_hlg:AC095723	3.9e+04	80.76	66.50	+	188351	AC095723	Rattus norvegicus c	gb_in:AF284763	65.50	115.94	428.47	2795	AF284763	Plasmodium falcipa
gb_hlg:AC095148	3.9e+04	80.68	66.50	+	190097	AC095148	Rattus norvegicus c	gb_pl:SCXJL221C	65.50	114.27	530.25	3372	249496	S.cerevisiae chromos
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gb_hlg:AC095757	4.0e+04	80.62	66.50	+	191319	AC095757	Rattus norvegicus c	gb_pat:A91933	65.50	112.00	709.58	4358	A91933	Sequence 1 from Pat
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gb_hlg:AC098516	4.1e+04	80.42	66.50	+	193591	AC098516	Rattus norvegicus c	gb_ba:AE001872	65.50	102.91	2.3e+03	12172	AE001872	Beinococcus radio
gb_hlg:AC095576	4.2e+04	80.21	66.50	+	200480	AC095576	Rattus norvegicus c	gb_ba:AE001091	65.50	102.16	2.5e+03	13248	AE001091	Archaeoglobus ful
gb_hlg:AC023173	4.2e+04	80.18	66.50	+	200970	AC023173	Mus musculus chromo	gb_ba:AE006388	65.50	101.96	2.6e+03	13549	AE006388	Lactococcus lacti
gb_hlg:AC103317	4.2e+04	80.08	66.50	+	203256	AC103317	Rattus norvegicus c	gb_hlg:AC104177	65.50	101.50	2.7e+03	14272	AC104177	Rattus norvegicus
gb_hlg:AL671990	4.3e+04	79.98	66.50	+	205615	AL671990	Mus musculus chromo	gb_ba:AF167538	65.50	100.33	3.2e+03	16287	AF167538	Trichodesmium sp.
gb_hlg:AC094695	4.3e+04	79.88	66.50	+	208057	AC094695	Rattus norvegicus c	gb_pl:SC4987	65.50	97.94	4.3e+03	21330	Z50178	S.cerevisiae chromo
gb_hlg:AC073553	4.6e+04	79.43	66.50	+	218873	AC073553	Mus musculus chromo	gb_hlg:AC109541	65.50	97.78	4.4e+03	21708	AC109541	Rattus nor

Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hayes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovac,K., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulsegh,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Fu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Saverly,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalobos,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 172040)
Worley,K.C.

Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:16327659.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GFRX
Center clone name: CH230-126M14
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to findPhrapList
Consensus quality: 148034 bases at least Q40
Consensus quality: 156693 bases at least Q30
Consensus quality: 162510 bases at least Q20
Estimated insert size: 155957; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-1p estimation
Quality coverage: 2.6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft.data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 8738: contig of 8738 bp in length
* 8739 8838: gap of unknown length
* 8839 15429: contig of 6591 bp in length

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15530
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24077
24176: gap of unknown length
24177
28582: contig of 4406 bp in length
28583
28682: gap of unknown length
28683
34650: contig of 5868 bp in length
34651
39278: contig of 4628 bp in length
39279
39378: gap of unknown length
39379
43355: contig of 3977 bp in length
43356
48464: contig of 5009 bp in length
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50183: contig of 1619 bp in length
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54404: gap of unknown length
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59384: contig of 4980 bp in length
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62519
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85885: contig of 2900 bp in length
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101817: contig of 3799 bp in length
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101917: gap of unknown length
101918
106211: contig of 4294 bp in length
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT


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seq_name: gb_vi:AF305738

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DEFINITION Infectious bursal disease virus isolate 586 VP2 protein gene,
partial cds.
ACCESSION AF305738
VERSION AF305738.1 GI:11991622
KEYWORDS .
SOURCE Gumboro virus.
ORGANISM Infectious bursal disease virus
VIRUSES: dsRNA viruses; Birnaviridae; Avibirnavirus.
REFERENCE 1 (bases 1 to 697)
AUTHORS Jackwood,D.J. and Smiley,J.R.
TITLE Embryo Passed IBDV
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 697)
AUTHORS Jackwood,D.J. and Smiley,J.R.
TITLE Direct Submission
JOURNAL Submitted (15-SEP-2000) Food Animal Health, Ohio State Univ./OARDC,
1680 Madison Ave, Wooster, OH 44691, USA
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NFELINPELAKNLVTEYGRFDPGANNYTKLIISERDLRGIKIVWPTREYTDREIFM
EVA DLNSPLKIAQA"
BASE COUNT 193 a 183 c 175 g 146 t
ORIGIN

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Quality: 83.00 Length: 132
Ratio: 1.361 Gaps: 7
Percent Similarity: 46.212 Percent Identity: 23.485

alignment_block:
US-09-528-682-3 x AF305738 ..

Align seg 1/1 to: AF305738 from: 1 to: 697

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283 .....CCAATCACATCC.....ATCAAACTGGAGATAG 310

42 leSerAlaGluGlyMetGlnAspGlyAsp..... 52
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 Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 81724)
 Worley, K.C.
 Direct Submission
 Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Dec 20, 2001 this sequence version replaced gi:15627576.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GDZD
 Center clone name: CH230-16021
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329First call to
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 Consensus quality: 71574 bases at least Q40
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 Consensus quality: 82981 bases at least Q20
 Estimated insert size: 62068; sum-of-contigs estimation
 Quality coverage: 0x in Q20 bases; agarose-fp estimation
 Quality coverage: 0.7x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 41 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.

COMMENT

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BASE COUNT 24165 a 15430 c 15170 g 22781 t 4178 others
 ORIGIN

alignment_scores:
 Quality: 82.50 Length: 40
 Ratio: 2.845 Gaps: 2
 Percent Similarity: 72.500 Percent Identity: 50.000
 alignment_block:

US-09-528-682-3 x AC095956/rev ..

Align seg 1/1 to reverse of: AC095956 from: 1 to: 81724

```
64 MetSerThrPheGluGlnValProAsnAsnLysGluPheLysGlyVal.. 79
||||: ||| :|||||:|||||:|||||:|||||:|||||:|||||:
6943 ATGACTCCCTTCATAAAGTCCCAATATATAAATACCTCGGTGTAC 6894

80 .IleSerAlaAsnValLys.....TyrAspMetAsnPheLysLysLeuL 94
||||: ||| :|||||:|||||:|||||:|||||:|||||:
6893 TTTAAGCAACAGTGAAGATCTGTTGATAGATTTTCAAGAACTGA 6844

94 euArgPheMetGluAsp 100
||| :|||||:|||||:
6843 AGAGAGAACTTGAAGAAGAT 6824
```

seq_name: gb_htg:AC094115

seq_documentation_block:

LOCUS AC094115 154055 bp DNA linear HTG 20-DEC-2001

DEFINITION Rattus norvegicus clone CH230-2N6, *** SEQUENCING IN PROGRESS ***,

ACCESSION AC094115

VERSION AC094115.2 GI:17940825

KEYWORDS HTG: HTGS-PHASE1.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 154055)

AUTHORS

Munzy,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Beaton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,M., Bryant,N.P., Buhat,J.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,K., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loulseghe,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S.,
Ogulu,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooastari,N.,
Sisson,I., Sodergren,E., Sonaik,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Umani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williams,R., Wlaczky,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission

JOURNAL

REFERENCE 2 (bases 1 to 154055)

AUTHORS

TITLE

JOURNAL

COMMENT

Worley,K.C.

Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15633145.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GAAE

Center clone name: CH230-2N6

----- Summary Statistics

Assembly program: Phrap; version 0.990329First call to

findPhrapList

Consensus quality: 129933 bases at least Q40

Consensus quality: 138152 bases at least Q30

Consensus quality: 14943 bases at least Q20

Estimated insert size: 133160; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 2.1x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 54 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 7284: contig of 7284 bp in length

* 7285 7384: gap of unknown length

* 7385 16189: contig of 8805 bp in length

* 16190 16289: gap of unknown length

* 16290 21269: contig of 4980 bp in length

* 21270 21369: gap of unknown length

* 21370 24525: contig of 3156 bp in length

* 24526 24625: gap of unknown length

* 24626 29193: contig of 4568 bp in length

* 29194 29293: gap of unknown length

* 29294 32759: contig of 3466 bp in length

* 32760 32859: gap of unknown length

* 32860 36531: contig of 3672 bp in length

* 36532 36631: gap of unknown length

* 36632 41410: contig of 4779 bp in length

* 41411 41510: gap of unknown length

* 41511 46937: contig of 5427 bp in length

* 46938 47037: gap of unknown length

* 47038 51669: contig of 4632 bp in length

* 51670 51769: gap of unknown length

* 51770 55039: contig of 3270 bp in length

* 55040 55139: gap of unknown length

* 55140 58083: contig of 2944 bp in length

* 58084 58183: gap of unknown length

* 58184 60725: contig of 2542 bp in length

* 60726 60825: gap of unknown length

* 60826 65393: contig of 4568 bp in length

* 65394 65493: gap of unknown length

* 65494 69409: contig of 3916 bp in length

* 69410 69509: gap of unknown length

* 69510 72160: contig of 2651 bp in length

* 72161 72260: gap of unknown length

* 72261 75500: contig of 3240 bp in length

* 75501 75600: gap of unknown length

* 75601 79429: contig of 3829 bp in length

* 79430 79529: gap of unknown length

* 79530 81960: contig of 2431 bp in length

* 81961 82060: gap of unknown length

* 82061 85052: contig of 2992 bp in length

TITLE

JOURNAL

REFERENCE

*	85053	85152:	gap of unknown length
*	85153	contig of 2440 bp in length	
*	87592:	contig of unknown length	
*	87593	contig of 3522 bp in length	
*	87693	contig of unknown length	
*	91214:	contig of 2415 bp in length	
*	91215	contig of unknown length	
*	91315	contig of 2415 bp in length	
*	93730	contig of unknown length	
*	93820	contig of 2459 bp in length	
*	96288:	contig of unknown length	
*	96289	contig of 2327 bp in length	
*	96389	contig of unknown length	
*	98115:	contig of 2223 bp in length	
*	98116	contig of unknown length	
*	101038:	contig of 2112 bp in length	
*	101139	contig of unknown length	
*	101139	contig of unknown length	
*	103250:	contig of 2753 bp in length	
*	103251	contig of unknown length	
*	106103:	contig of 1775 bp in length	
*	106203:	contig of unknown length	
*	106204:	contig of unknown length	
*	107978:	contig of 1381 bp in length	
*	107979	contig of unknown length	
*	108079	contig of 2283 bp in length	
*	109459:	contig of unknown length	
*	109559:	contig of 2947 bp in length	
*	111842:	contig of 2947 bp in length	
*	111843	contig of unknown length	
*	111942:	contig of unknown length	
*	114889:	contig of 1812 bp in length	
*	114989:	contig of unknown length	
*	114990	contig of unknown length	
*	116801:	contig of 1364 bp in length	
*	116802	contig of unknown length	
*	116901:	contig of 1364 bp in length	
*	118265:	contig of unknown length	
*	118363:	contig of 1935 bp in length	
*	120300:	contig of unknown length	
*	120301:	contig of 1460 bp in length	
*	120400:	contig of unknown length	
*	120401	contig of unknown length	
*	121861	contig of 1611 bp in length	
*	121960:	contig of unknown length	
*	121961	contig of unknown length	
*	123571:	contig of 1390 bp in length	
*	123671:	contig of unknown length	
*	123672	contig of unknown length	
*	123751:	contig of 2332 bp in length	
*	125752:	contig of unknown length	
*	125753	contig of unknown length	
*	128084:	contig of 2292 bp in length	
*	128184	contig of unknown length	
*	130476	contig of 2017 bp in length	
*	130575:	contig of unknown length	
*	130576	contig of unknown length	
*	132592:	contig of 2150 bp in length	
*	132593	contig of unknown length	
*	132593	contig of unknown length	
*	134842:	contig of 1483 bp in length	
*	134942:	contig of unknown length	
*	134943	contig of 1526 bp in length	
*	136425:	contig of unknown length	
*	136426:	contig of 1742 bp in length	
*	136526:	contig of unknown length	
*	138267:	contig of 1774 bp in length	
*	138268	contig of unknown length	
*	138368	contig of 1656 bp in length	
*	140141:	contig of unknown length	
*	140241:	contig of 1526 bp in length	
*	140342	contig of unknown length	
*	141897:	contig of 1526 bp in length	
*	141997:	contig of unknown length	
*	141998	contig of 1822 bp in length	
*	143523:	contig of unknown length	
*	143524	contig of unknown length	
*	143524	contig of unknown length	
*	145445:	contig of 1210 bp in length	
*	145446	contig of unknown length	
*	145446	contig of unknown length	
*	145346	contig of 1374 bp in length	
*	146320:	contig of unknown length	
*	147020	contig of 1529 bp in length	
*	148549	contig of unknown length	
*	148549	contig of unknown length	
*	148649	contig of 1171 bp in length	
*	149819:	contig of unknown length	
*	149920	contig of 1210 bp in length	
*	151129:	contig of unknown length	
*	151229:	contig of unknown length	
*	151230	contig of 1312 bp in length	
*	152541:	contig of unknown length	
*	152641:	contig of unknown length	
*	152642	contig of 1414 bp in length	

alignment_scores:

Quality:	82.50		Length:	48
Ratio:	2.578		Gaps:	2
Percent Similarity:	66.667		Percent Identity:	43.750

alignment_block:
US-09-528-682-3 x AC094115 ..

Align seg 1/1 to: AC094115 from: 1 to: 154055

56 ThrValAsnGlnSerAsnPheProMetSerThrPheGluGlnValProAs 72
|||| :||| ||| | ||| | |||
72585 ACAACCGAAGAAGAAATAGGAATAATGCACCCTTCTTAATAGTCACAAA 72634

72 nAsnLysGluPheLysGlyVal...IleSerAlaAsnValLys.....T 86
||||| :||| | ||| | ||| | |||
72635 TAATAAAAAATACCTCGGTGTGACTTGACCCCAAGCAAGTGAAGAAGATCTGT 72684

86 yRspMetAsnPhelYsisLysLeuLeuArgPheMetGluAspasp 100
||||| ||||| ||| ||| ::| :|||::|||
72685 ATGATAAATAACCTTTAAGCCTCTGGAAGAAAGAAATCAAAGAAGAC 72728

seq_name: gb_htg:AC099275

seq_documentation_block:
LOCUS AC099275 156175 bp DNA linear HTG 21-DEC-2001
DEFINITION Rattus norvegicus clone CH230-32111, *** SEQUENCING IN PROGRESS
FEATURES
***, 54 unordered pieces.
ACCESSION AC099275
VERSION AC099275.2 GI:17974747
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 156175)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amarating,H.C., Are,J.R., Banks,T., Barbara,J., Benton,K.J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buha,Y.C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,W., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle-McDoll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Davy-Carroll,L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dunn,A.L., Fung,H.K., Earnhart,C., Edgar,D., Edwards,C.C., Dugan-Rocha,S., Durbin,K.J., Earhart,C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Davila,M.L., Davis,C., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Huylk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Joliviet,S., Jouhan,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtege,O., Lieu,C., Liu,J., Liu.W., Loulsegad,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M.S., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen.N., Nickerson,E., Nwokwenkw.O., Oguh,M., Okwuonu,G., Oraguynye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savory,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N., Stinson,I., Sodergren,E., Sonake,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tameris,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Tellrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,

Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
 Watlington, S., Williams, G., Williamson, A., Wlaczek, R., Wooden, S.,
 Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished
 2 (bases 1 to 156175)
 Direct Submission
 Worley, K.C.
 Submitted (09-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Dec 21, 2001 this sequence version replaced gi:16874775.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GJOP

Center clone name: CH230-32111

----- Summary Statistics

Assembly program: Phrap; version 0.990329first call to

findPhrapList

Consensus quality: 134639 bases at least Q40

Consensus quality: 142079 bases at least Q30

Consensus quality: 147257 bases at least Q20

Estimated insert size: 137844; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

consists of 54 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

1 10322: contig of 10322 bp in length

* 10323 10422: gap of unknown length

* 10423 19402: contig of 8980 bp in length

* 19403 19502: gap of unknown length

* 19503 25319: contig of 5817 bp in length

* 25320 25410: gap of unknown length

* 25420 30365: contig of 4946 bp in length

* 30366 30465: gap of unknown length

* 30466 35000: contig of 4535 bp in length

* 35001 35100: gap of unknown length

* 35101 40071: contig of 4971 bp in length

* 40072 40171: gap of unknown length

* 40172 45161: contig of 4990 bp in length

* 45162 45261: gap of unknown length

* 45262 49303: contig of 4042 bp in length

* 49304 49403: gap of unknown length

* 49404 53625: contig of 4222 bp in length

* 53626 53725: gap of unknown length

* 53726 58233: contig of 4508 bp in length

* 58234 58334: gap of unknown length

* 58334 61817: contig of 3484 bp in length

* 61818 61917: gap of unknown length

* 61918 65238: contig of 3321 bp in length

* 65239 65338: gap of unknown length

* 65339 67622: contig of 2284 bp in length

* 67623 67722: gap of unknown length

* 67723 70765: contig of 3043 bp in length

* 70766 70865: gap of unknown length

* 70866 74673: contig of 3808 bp in length

* 74674 74773: gap of unknown length

* 74774 77319: contig of 2546 bp in length

* 77320 77419: gap of unknown length

* 77420 77320

77420 80491: contig of 3072 bp in length

* 80492 80591: gap of unknown length

* 80592 83396: contig of 2805 bp in length

* 83397 83496: gap of unknown length

* 83497 85961: contig of 2465 bp in length

* 85962 85962: gap of unknown length

* 86062 87868: contig of 1807 bp in length

* 87869 87869: gap of unknown length

* 87969 91020: contig of 3052 bp in length

* 91021 91120: gap of unknown length

* 91121 93160: contig of 2040 bp in length

* 93161 93260: gap of unknown length

* 93261 94987: contig of 1727 bp in length

* 94988 95087: gap of unknown length

* 95088 97634: contig of 2547 bp in length

* 97635 97734: gap of unknown length

* 97735 99835: contig of 2101 bp in length

* 99836 101751: contig of 1816 bp in length

* 101752 101752: gap of unknown length

* 101752 104752: contig of 2901 bp in length

* 104753 104853: gap of unknown length

* 104853 107784: contig of 2932 bp in length

* 107785 107884: gap of unknown length

* 107885 110476: contig of 2592 bp in length

* 110477 110576: gap of unknown length

* 110577 112349: contig of 1773 bp in length

* 112350 112450: gap of unknown length

* 112450 114160: contig of 1711 bp in length

* 114161 114260: gap of unknown length

* 114261 116230: contig of 1970 bp in length

* 116231 116330: gap of unknown length

* 116331 118217: contig of 1887 bp in length

* 118218 118317: gap of unknown length

* 118318 120556: contig of 2239 bp in length

* 120557 120656: gap of unknown length

* 120657 123353: contig of 2697 bp in length

* 123354 123453: gap of unknown length

* 123454 126036: contig of 2583 bp in length

* 126037 126136: gap of unknown length

* 126137 127952: contig of 1816 bp in length

* 127953 128052: gap of unknown length

* 128053 130102: contig of 2050 bp in length

* 130103 130202: gap of unknown length

* 130203 131439: contig of 1237 bp in length

* 131440 131539: gap of unknown length

* 131540 133624: contig of 2085 bp in length

* 133625 133724: gap of unknown length

* 133725 134739: contig of 1015 bp in length

* 134740 134839: gap of unknown length

* 134840 136702: contig of 1863 bp in length

* 136703 136802: gap of unknown length

* 136803 138485: contig of 1883 bp in length

* 138486 138585: gap of unknown length

* 138586 140545: contig of 1960 bp in length

* 140546 140645: gap of unknown length

* 140646 142021: contig of 1376 bp in length

* 142022 142121: gap of unknown length

* 142122 143331: contig of 1210 bp in length

* 143332 143431: gap of unknown length

* 143432 145129: contig of 1698 bp in length

* 145130 145229: gap of unknown length

* 145230 145230: contig of 1463 bp in length

* 145230 146693: gap of unknown length

* 146693 146793: contig of 1717 bp in length

* 146793 148510: gap of unknown length

* 148510 150341: contig of 1732 bp in length

* 150342 150441: gap of unknown length

* 150442 151800: contig of 1359 bp in length

* 151801 151901: gap of unknown length

* 151901 153408: contig of 1508 bp in length

* 153409 153508: gap of unknown length

* 153509 154583: contig of 1075 bp in length


```

* 154584 154683: gap of unknown length
* 154684 156175: contig of 1492 bp in length.
FEATURES
    Location/Qualifiers
    1..156175
    /organism="Rattus norvegicus"
    /db_xref="taxon:10116"
    /clone="CH230-3211"

```

```

alignment_scores:
    Quality: 82.50      Length: 48
    Ratio: 2.578       Gaps: 2
    Percent Similarity: 66.667      Percent Identity: 43.750

```

```
alignment_block:

```

```
US-09-528-682-3 x AC099275 ..
```

```
Align seg 1/1 to: AC099275 from: 1 to: 156175
```

```

56 ThrValAsnGlnSerAsnPhoMetSerThrPheGluGlnValProAs 72
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
22046 ACAAGCCAAGAAAGAAATAGGAAATGACACCCCTTCTAATAGTCCCAA 22095

72 nAsnLysGluPheLysGlyVal....IleSerAlaAsnValLys.....T 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
22096 TAATATAAAATATACCTCGGTGTGACTCTAGCCCAAGCAAGTGAAGATCTGT 22145

86 yRAspMetAsnPhelLysLeuLeuArgPheMetGluAspAsp 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
22146 ATGATATACTTTATACCTCTGAAGAAAGAAATTTGAAGAAGAC 22189

```

```
seq_name: gb_htg:AC099302
```

```
seq_documentation_block:
```

```

LOCUS AC099302 214474 bp DNA linear HTG 21-DEC-2001
DEFINITION Rattus norvegicus chromosome Mcl1 clone CH230-132M17, WORKING DRAFT
SEQUENCE 27 unordered pieces.
AC099302

```

```
AC099302.3 GI:17974888
```

```
HTG: HTGS_PHASE1; HTGS_DRAFT.
```

```
KEYWORDS
```

```
SOURCE
```

```
ORGANISM
```

```
Rattus norvegicus
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
```

```
Rattus.
```

```
1 (bases 1 to 214474)
```

```

REFERENCE
AUTHORS
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarutunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Duggan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homsif,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louisege,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S.,
Ogih,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,

```

```

Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Roife,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

```

```
Center: Baylor College of Medicine
```

```
Center code: BCM
```

```
Web site: http://www.hgsc.bcm.tmc.edu/
```

```
Contact: hgsc-help@bcm.tmc.edu
```

```
----- Project Information
```

```
Center project name: GLFG
```

```
Center clone name: CH230-132M17
```

```
----- Summary Statistics
```

```
Assembly program: Phrap; version 0.990329First call to
```

```
findPhrapList
```

```
Consensus quality: 198567 bases at least Q40
```

```
Consensus quality: 201661 bases at least Q30
```

```
Consensus quality: 203796 bases at least Q20
```

```
Estimated insert size: 205244; sum-of-contigs estimation
```

```
Quality coverage: 0x in Q20 bases; agarose-1p estimation
```

```
Quality coverage: 4.2x in Q20 bases; sum-of-contigs estimation
```

```
-----
```

```
* NOTE: Estimated insert size may differ from sequence length
```

```
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
```

```
* NOTE: This is a 'working draft' sequence. It currently
```

```
consists of 27 contigs. The true order of the pieces
```

```
is not known and their order in this sequence record is
```

```
arbitrary. Gaps between the contigs are represented as
```

```
runs of N, but the exact sizes of the gaps are unknown.
```

```
* This record will be updated with the finished sequence
```

```
as soon as it is available and the accession number will
```

```
* be preserved.
```

```
* 1 25451: contig of 25451 bp in length
```

```
* 25452 25551: gap of unknown length
```

```
* 25552 43020: contig of 17469 bp in length
```

```
* 43021 43120: gap of unknown length
```

```
* 43121 58429: contig of 15309 bp in length
```

```
* 58430 58529: gap of unknown length
```

```
* 58530 71300: contig of 12771 bp in length
```

```
* 71301 71400: gap of unknown length
```

```
* 71401 87184: contig of 15784 bp in length
```

```
* 87185 87284: gap of unknown length
```

```
* 87285 102108: contig of 14824 bp in length
```

```
* 102109 102208: gap of unknown length
```

```
* 102209 111127: contig of 8919 bp in length
```

```
* 111128 111227: gap of unknown length
```

```
* 111228 123031: contig of 11804 bp in length
```

```
* 123032 123131: gap of unknown length
```

```
* 123132 132405: contig of 9274 bp in length
```

```
* 132406 132505: gap of unknown length
```

```
* 132506 139337: contig of 7432 bp in length
```

```
* 139338 140037: gap of unknown length
```

```
* 140038 147016: contig of 6979 bp in length
```

```
* 147017 147116: gap of unknown length
```

```
* 147117 151515: contig of 4399 bp in length
```

```
* 151516 151615: gap of unknown length
```

```
* 151616 158863: contig of 7248 bp in length
```

```
TITLE
```

```
JOURNAL
```

```
REFERENCE
```

```
AUTHORS
```

```
TITLE
```

```
JOURNAL
```

```
COMMENT
```



```

* 158864 158963: gap of unknown length
* 158964 163839: contig of 6876 bp in length
* 163840 165939: gap of unknown length
* 165940 172366: contig of 6427 bp in length
* 172367 172466: gap of unknown length
* 172467 177346: contig of 4880 bp in length
* 177347 177447: gap of unknown length
* 177448 181209: contig of 3763 bp in length
* 181210 181309: gap of unknown length
* 181310 186947: contig of 5638 bp in length
* 186948 187047: gap of unknown length
* 187048 193223: contig of 6176 bp in length
* 193224 193223: gap of unknown length
* 193224 197112: contig of 3789 bp in length
* 197113 197212: gap of unknown length
* 197213 201092: contig of 3880 bp in length
* 201093 201192: gap of unknown length
* 201193 204023: contig of 2831 bp in length
* 204024 204123: gap of unknown length
* 204124 206518: contig of 2395 bp in length
* 206519 206618: gap of unknown length
* 206619 208071: contig of 1453 bp in length
* 208072 208171: gap of unknown length
* 208172 210911: contig of 2740 bp in length
* 210912 211011: gap of unknown length
* 211012 212323: contig of 1312 bp in length
* 212324 212423: gap of unknown length
* 212424 214474: contig of 2051 bp in length.

```

FEATURES

```

source
1..214474
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/chromosome="Mcs1"
/clones="CH230-132M17"
BASE COUNT 67291 a 42498 c 41787 g 50272 t 2626 others
ORIGIN

```

```

alignment_scores:
Quality: 82.50 Length: 42
Ratio: 2.661 Gaps: 2
Percent Similarity: 73.810 Percent Identity: 47.619

```

alignment_block:

```

US-09-528-682-3 x AC099302 ..
Align seg 1/1 to: AC099302 from: 1 to: 214474
64 MetSerThrpheGluGlnValProAsnAsnLysGluPheLysGlyVal.. 79
||||:||||| ||||| ||||| ||||| |||||
91377 ATGACAACTTCATACAGTCCCAATAATATAATACCTTGGTGTGAC 91426

```

```

80 .IleSerAlaAsnValLys.....TyrAspMetAsnPhelLysLeuL 94
||||:||||| ||||| ||||| ||||| |||||
91427 TTTAACCAAGCAAGTGAAGATCTGATGATGAAGAACTTCAAGTCTGTA 91476

```

```

94 euA9PheMetGluAspPheille 102
||:||||:||||:||||
91477 AGAAAGAAATGGAAGAGATCTTATA 91502

```

```
seq_name: gb_htg:AC098504
```

```
seq_documentation_block:
```

```

LOCUS AC098504 238216 bp DNA linear HTG 20-DEC-2001
DEFINITION Rattus norvegicus chromosome Mcs1 clone CH230-40F5, *** SEQUENCING
IN PROGRESS ***, 71 unordered pieces.

```

```
ACCESSION AC098504
```

```
VERSION AC098504.2 GI:17973142
```

```
KEYWORDS HTG; HTGS_PHASE1.
```

```
SOURCE Norway rat.
```

```
ORGANISM Rattus norvegicus
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
```

Rattus.

```

1 (bases 1 to 238216)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Albrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bivaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,M., Bryant,N.P., Bunay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C.,
Hollins,B., Homsif,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louiseged,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Ogulu,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peirys,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoostari,N.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wlezyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 238216)
Worley,K.C.
Direct Submission
Submitted (24-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:16356709.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GHFH
Center clone name: CH230-40F5
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 206528 bases at least Q40
Consensus quality: 217991 bases at least Q30
Consensus quality: 227959 bases at least Q20
Estimated insert size: 210373; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation
-----

```

COMMENT

```

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 71 contigs. The true order of the pieces
* is not known and their order in this sequence record is

```


* arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence.
 * as soon as it is available and the accession number will
 * be preserved.

```

1 13234: contig of 13234 bp in length
* 13235: gap of unknown length
* 13335: contig of 10151 bp in length
* 23486: gap of unknown length
* 23586: contig of 9511 bp in length
* 33097: gap of unknown length
* 33197: contig of 7072 bp in length
* 40268: gap of unknown length
* 40369: contig of 8596 bp in length
* 40369: gap of unknown length
* 48964: gap of unknown length
* 49064: contig of 5744 bp in length
* 49065: gap of unknown length
* 54808: contig of 10386 bp in length
* 54909: gap of unknown length
* 65294: contig of 7122 bp in length
* 65295: gap of unknown length
* 72516: contig of 7122 bp in length
* 72517: gap of unknown length
* 72616: contig of 6863 bp in length
* 79479: gap of unknown length
* 79480: contig of 7221 bp in length
* 79580: gap of unknown length
* 86801: contig of 6142 bp in length
* 86901: gap of unknown length
* 93042: contig of 6142 bp in length
* 93043: gap of unknown length
* 93142: contig of 7013 bp in length
* 100155: gap of unknown length
* 100255: contig of 4686 bp in length
* 100256: gap of unknown length
* 104942: contig of 2922 bp in length
* 105041: gap of unknown length
* 105042: contig of 5612 bp in length
* 107964: gap of unknown length
* 108064: contig of 4126 bp in length
* 113675: gap of unknown length
* 113775: contig of 3899 bp in length
* 117901: gap of unknown length
* 118001: contig of 3899 bp in length
* 118002: gap of unknown length
* 121900: contig of 4077 bp in length
* 121901: gap of unknown length
* 126077: contig of 4522 bp in length
* 126078: gap of unknown length
* 126178: contig of 2732 bp in length
* 130699: gap of unknown length
* 130700: contig of 3860 bp in length
* 130799: gap of unknown length
* 133531: contig of 2382 bp in length
* 133532: gap of unknown length
* 133632: contig of 3472 bp in length
* 137491: contig of 3988 bp in length
* 137492: gap of unknown length
* 137591: contig of 4006 bp in length
* 139973: gap of unknown length
* 140073: contig of 2630 bp in length
* 140074: gap of unknown length
* 143545: contig of 4068 bp in length
* 143546: gap of unknown length
* 143645: contig of 3306 bp in length
* 143646: gap of unknown length
* 147633: contig of 2641 bp in length
* 147634: gap of unknown length
* 151739: contig of 2108 bp in length
* 151740: gap of unknown length
* 151839: contig of 1850 bp in length
* 151840: gap of unknown length
* 154469: contig of 1663 bp in length
* 154470: gap of unknown length
* 154570: contig of 1719 bp in length
* 158637: gap of unknown length
* 158638: contig of 3270 bp in length
* 162043: gap of unknown length
* 162044: contig of 3270 bp in length
* 162144: gap of unknown length
* 164784: contig of 3270 bp in length
* 164884: gap of unknown length
* 166982: contig of 3270 bp in length
* 166993: gap of unknown length
* 167092: contig of 3270 bp in length
* 168942: gap of unknown length
* 168943: contig of 3270 bp in length
* 169042: gap of unknown length
* 170705: contig of 3270 bp in length
* 170706: gap of unknown length
* 170805: contig of 3270 bp in length
* 172524: gap of unknown length
* 172525: contig of 3270 bp in length
* 172624: gap of unknown length
* 175894: contig of 3270 bp in length
* 175895: gap of unknown length

```

```

* 175995: contig of 1340 bp in length
* 177334: gap of unknown length
* 177335: contig of 1814 bp in length
* 179248: gap of unknown length
* 179249: contig of 1945 bp in length
* 181293: gap of unknown length
* 181294: contig of 1856 bp in length
* 181394: gap of unknown length
* 183250: contig of 2506 bp in length
* 183350: gap of unknown length
* 185855: contig of 1754 bp in length
* 185956: gap of unknown length
* 187710: contig of 2384 bp in length
* 187810: gap of unknown length
* 190194: contig of 1696 bp in length
* 190294: gap of unknown length
* 191989: contig of 1696 bp in length
* 191990: gap of unknown length
* 192089: contig of 1829 bp in length
* 192090: gap of unknown length
* 193919: contig of 1402 bp in length
* 194018: gap of unknown length
* 194019: contig of 1402 bp in length
* 195420: gap of unknown length
* 195421: contig of 2032 bp in length
* 195520: gap of unknown length
* 195521: contig of 1693 bp in length
* 197552: gap of unknown length
* 197553: contig of 1693 bp in length
* 197652: gap of unknown length
* 197653: contig of 1696 bp in length
* 199346: gap of unknown length
* 199445: contig of 1696 bp in length
* 201141: gap of unknown length
* 201142: contig of 1513 bp in length
* 201241: gap of unknown length
* 201242: contig of 1567 bp in length
* 202754: gap of unknown length
* 202755: contig of 1734 bp in length
* 202855: gap of unknown length
* 204421: contig of 2148 bp in length
* 204422: gap of unknown length
* 204522: contig of 2148 bp in length
* 206255: gap of unknown length
* 206256: contig of 2148 bp in length
* 206356: gap of unknown length
* 208503: contig of 1340 bp in length
* 208504: gap of unknown length
* 208603: contig of 1394 bp in length
* 209943: gap of unknown length
* 209944: contig of 1651 bp in length
* 210044: gap of unknown length
* 211438: contig of 2010 bp in length
* 211439: gap of unknown length
* 211538: contig of 1920 bp in length
* 211539: gap of unknown length
* 213189: contig of 1920 bp in length
* 213190: gap of unknown length
* 215299: contig of 1920 bp in length
* 215399: gap of unknown length
* 217319: contig of 1920 bp in length
* 217318: gap of unknown length
* 217319: contig of 1920 bp in length

```

alignment_scores: Quality: 82.50 Length: 42
 Ratio: 2.661 Gaps: 2
 Percent Similarity: 73.810 Percent Identity: 47.619

alignment_block:
 US-09-528-682-3 x AC098504/rev ..

Align seg 1/1 to reverse of: AC098504 from: 1 to: 238216

```

64 MetSerThrPheGluGlnValProAsnAsnLysGluPheLysGlyVal... 79
|||||
202040 ATGCAACCTTCATACAGTCCCAAAATATATATAAATACCTTGGTGTGAC 201991
|||||
80 .IleSerAlaAsnValLys.....TyrAspMetAsnPhelLysLysLeuL 94
|||||
201990 TTTAACCAAGCAAGTGAAGATCTGTATGATAAGAACTTCAAGTCTCTGA 201941
|||||
94 euArgPheMetGluAspPhePhe 102
|||||
201940 AGAAGAAATTCAGAGAGATCTTATA 201915
|||||
seq_name: gb_vi:AF362771

```

seq_documentation_block:
 LOCUS AF362771
 DEFINITION Infectious bursal disease virus strain Cu-1 M segment A structural polyprotein gene, partial cds.

3055 bp RNA linear VRL 02-JUL-2001


```

TITLE
JOURNAL
REFERENCE
2 (bases 1 to 107518)
Worley,K.C.
Direct Submission
Submitted (23-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:17064560.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GIHW
Center clone name: CH230-56K11
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 100954 bases at least Q40
Consensus quality: 112766 bases at least Q30
Consensus quality: 120930 bases at least Q20
Estimated insert size: 60056; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0.7x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 63 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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TITLE
JOURNAL

COMMENT

Direct Submission
Submitted (06-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:17064415.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GH2S
Center clone name: CH230-135H5
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 187790 bases at least Q40
Consensus quality: 204453 bases at least Q30
Consensus quality: 219075 bases at least Q20
Estimated insert size: 190140; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 114 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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DEFINITION Xenopus laevis N-CAM 1 mRNA for neural cell adhesion molecule,
complete cds.
ACCESSION AB008162
VERSION AB008162.1 GI:3116226
KEYWORDS neural cell adhesion molecule; N-CAM 1.
SOURCE Xenopus laevis adult heart cDNA to mRNA.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 2178)
Kudo,M. and Shiohawa,K.
Direct Submission
Submitted (16-OCT-1997) Mariko Kudo, Graduate School of Science,
University of Tokyo, Biological Sciences, Hongo 7-3-1, Bunkyo-ku,
Tokyo 113-0033, Japan (Tel:03-3812-2111(ex.4433), Fax:03-3816-1965)
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REFERENCE 2 (bases 1 to 2178)
AUTHORS Kudo,M., Takayama,E., Tadakuma,T. and Shikawa,K.
TITLE Molecular cloning of ssd-form neural cell adhesion molecules
(N-Cams) as the major form in Xenopus heart
JOURNAL Biochem. Res. Commun. 245 (1), 127-132 (1998)
MEDLINE 98204770
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ACCESSION M25696
VERSION M25696.1 GI:214609
KEYWORDS neural cell adhesion molecule; transmembrane protein.
SOURCE X.laevis neurula, cDNA to mRNA, clone N1.
ORGANISM Xenopus laevis
REFERENCE 1 (bases 1 to 3720)
AUTHORS Krieg,P.A., Sakaguchi,D.S. and Kintner,C.R.
TITLE Primary structure and developmental expression of a large cytoplasmic domain form of Xenopus laevis neural cell adhesion molecule (NCAM)
JOURNAL Nucleic Acids Res. 17, 10321-10335 (1989)
MEDLINE 90098871
COMMENT Draft entry and computer-readable sequence [1] kindly submitted by P.A.Krieg, 23-JUN-1989.
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                     MVKLSAMNGKLGSDTSPQSEFTTQPVREPSAPKLGVHLSDEGNSIKVDILKODDGGSP
                     IRHLYLVNRYALNALAEWPKEMRVPNSHHVLMKALEWNVYEVIVVAENQOQSKPALL
                     SPRTAKPTATTATASAGTGLGTGAIVGLIVFILLVYVDVTCFFLNKCKGLMCIA
                     VNFCCGAGPAGKAGKDIIEGKAAPSKDEKPEIVERTEERTPNHDGNSIPEPNTTP
                     LITEPEHPAAVEDMLPSVTVTITNTSDITITETATAQNSDTSETTITLSTTAPPTTAPD
                     SNTIOSIQAOTPSKAEAPTSPPPTSSPKVAPLVDLSPTPTNNPSKVVAQAQGLNPS
                     AATSAEPPTVIIKPVTVPPNAASPPPTPEPKOVQBSQSGTKSPEKEAOPSTVKNP
                     TEATKDESASLNTKPLQDEDFQIDGGTTFKPEIOLAKDVFAALGTATPTAVASCKAS
                     ELVSTADTSTVPLDSAKTEKTOVEEKSPEDVDVAGTFAEVKTVPEATQTWNANESKA
                     "
     mat_peptide      82..3288
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BASE COUNT      1158 a 851 c 801 g 910 t
ORIGIN 1 bp upstream of EcoRI site.
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    Quality: 79.00      Length: 108
    Ratio: 1.339       Gaps: 5
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alignment_block:
US-09-528-682-3 x XELNCAM ..
Align seg 1/1 to: XELNCAM from: 1 to: 3720
18 ThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLeuAspG1 34
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247 ACTTCCACACTCACCTACATCTACAATGCCAGCAGCCAAAGATGCT.....GG 290
34  YARGTYrSerAsnPhleAlaLeuIleSerAlaGluGlyMetGlnAspG 51
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291 CATCTATAATGTGAGCTTCCACAGCAGCAGGAGGAATCTGA..... 336
51  lYAspLeuPheGlyThrValAsnGlnSerAsnPhlePrometSerThrPhe 67
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337 .....GGCACTGTCAATCTTAAGATTATACAGAAATGACCTTT 375
68  GluGlnValProAsnAsnLysGluPheLys.....GlyValIle 80
    |||||:|||||
376 AAAAAATGCCACCCACCCCTCAGGAGTTTAAAGAGGGAGAGATGCAGTCAT 425
80  eSerAlaAsnValLys..... 85
    |||||:|||||
426 TATTGTGTGATGCTCAAGCTCAGCTTCATTCATTAATATACATTGGCGACATA 475
86  ....TyRAspMetAsnPhleLysLeuLeuArgPhe.....MetGlu 98
    |||||:|||||
476 AAGGCAAAAGATGTTATTTCAAAAAGATGTACGGTTTGTGCTGTGGCC 525
99  AspAspPheIleGlyValHisGly 106
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526 AACAAATTACCTCAATCAGGGGA 549
seq_name: gb_htg:AC096608

seq_documentation_block:
LOCUS AC096608
DEFINITION Rattus norvegicus clone CH230-191M17, *** SEQUENCING IN PROGRESS
***, 59 unordered pieces.
ACCESSION AC096608
VERSION AC096608.2 GI:17959897
KEYWORDS HTG; HTGS-PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 104705)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
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Hamilton,K., Harris,C., Harris,K., Hart,M., Haviak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M., Holloway,C.,
Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
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Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louiseged,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
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Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M.,
Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S.,
Ogulu,M., Okwuonu,G., Oragunye,N., Owiedo,R., Pace,A., Payton,B.,
Peirys,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,

```

Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Woodden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 104705)
Worley, K.C.
Direct Submission
Submitted (19-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15667967.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GGAN
Center clone name: CH230-191M17
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to findPhrapList
Consensus quality: 81020 bases at least Q40
Consensus quality: 94686 bases at least Q30
Consensus quality: 104037 bases at least Q20
Estimated insert size: 71682; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0.7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 59 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1877: contig of 1877 bp in length
* 1878 1977: gap of unknown length
* 1978 3148: contig of 1171 bp in length
* 3149 3248: gap of unknown length
* 3249 6384: contig of 3136 bp in length
* 6385 6484: gap of unknown length
* 6485 9073: contig of 2589 bp in length
* 9074 9173: gap of unknown length
* 9174 11452: contig of 2279 bp in length
* 11453 11552: gap of unknown length
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* 13989 14088: gap of unknown length
* 14089 15336: contig of 2448 bp in length
* 15337 16636: gap of unknown length
* 16637 19974: contig of 3338 bp in length
* 19975 20074: gap of unknown length
* 20075 23703: contig of 3629 bp in length
* 23704 23803: gap of unknown length
* 23804 25338: contig of 2735 bp in length
* 25339 26638: gap of unknown length
* 26639 29361: contig of 2723 bp in length
* 29362 29461: gap of unknown length
* 29462 31610: contig of 2149 bp in length
* 31611 31710: gap of unknown length
* 31711 34007: contig of 2297 bp in length
* 34008 34107: gap of unknown length
* 34108 36309: contig of 2202 bp in length
* 36310 36409: gap of unknown length
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* 38111: contig of 1702 bp in length

* 38112 38211: gap of unknown length
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* 40381 42131: contig of 1751 bp in length
* 42132 42231: gap of unknown length
* 42232 43660: contig of 1429 bp in length
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* 45138 45237: gap of unknown length
* 45238 47381: contig of 2144 bp in length
* 47382 47481: gap of unknown length
* 47482 49117: contig of 1636 bp in length
* 49118 49217: gap of unknown length
* 49218 50822: contig of 1605 bp in length
* 50823 50922: gap of unknown length
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* 57358 58390: contig of 1033 bp in length
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* 60059 60158: contig of 1568 bp in length
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* 62135 62234: gap of unknown length
* 62235 64058: contig of 1824 bp in length
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* 64159 65486: contig of 1328 bp in length
* 65487 65587: gap of unknown length
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* 67466 67565: gap of unknown length
* 67566 68961: contig of 1396 bp in length
* 68961 69061: gap of unknown length
* 69062 70096: contig of 1035 bp in length
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* 71508 71607: gap of unknown length
* 71608 72757: contig of 1149 bp in length
* 72757 72856: gap of unknown length
* 72857 73922: contig of 1066 bp in length
* 73923 74022: gap of unknown length
* 74023 75142: contig of 1120 bp in length
* 75143 75242: gap of unknown length
* 75243 76946: contig of 1704 bp in length
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* 79450 79549: gap of unknown length
* 79550 80568: contig of 1019 bp in length
* 80569 80668: gap of unknown length
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* 82342 83679: contig of 1338 bp in length
* 83680 83779: gap of unknown length
* 83780 85189: contig of 1410 bp in length
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* 85290 86599: contig of 1310 bp in length
* 86600 86699: gap of unknown length
* 86700 87932: contig of 1233 bp in length
* 87933 88032: gap of unknown length
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* 89477 89576: gap of unknown length
* 89578 90332: contig of 1256 bp in length
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* 96629 97970: contig of 1342 bp in length
* 97971 98070: gap of unknown length
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alignment_scores:
Quality: 78.50 Length: 41
Ratio: 2.707 Gaps: 2
Percent Similarity: 70.732 Percent Identity: 46.341

alignment_block:
US-09-528-682-3 x AC096608 ..
Align seg 1/1 to: AC096608 from: 1 to: 104705

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||||: ||| ||||||||| :|||: |||||
92406 ATGACACCCCTTCCACATAGTCCCAATAATATAATAATATCTTGGTGTGAC 92455
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LOCUS AC098098
DEFINITION Rattus norvegicus clone CH230-167C14, *** SEQUENCING IN PROGRESS
ACCESSION AC098098
VERSION AC098098.3 GI:17968986
KEYWORDS HTG: HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 182686)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
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Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
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 Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N.,
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 Weinstein, G. and Gibbs, R.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Direct Submission
 2 (bases 1 to 182686)
 Worley, K.C.

Submitted (23-OCT-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Dec 20, 2001 this sequence version replaced gi:17062348.

COMMENT

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GGBB
 Center clone name: CH230-167C14
 ----- Summary Statistics

Assembly program: Phrap; version 0.990329First call to
 findPhrapList

Consensus quality: 158745 bases at least Q40
 Consensus quality: 165166 bases at least Q30
 Consensus quality: 170378 bases at least Q20
 Estimated insert size: 160185; sum-of-contigs estimation
 Quality coverage: 0x in Q20 bases; agarose-fp estimation
 Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 64 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 10034: contig of 10034 bp in length
 * 10035 10134: gap of unknown length
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 * 106404 106504: gap of unknown length
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 * 110866 110966: gap of unknown length
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 * 139592 141470: gap of unknown length
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Huber, R., Feldman, R.A., Short, J.M., Olson, G.J. and Swanson, R.V.
 Direct Submission
 Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego,
 CA 92121

COMMENT Putative indicates no similarity to known proteins

Hypotheical indicates similarity to a protein of unknown function.

FEATURES Location/Qualifiers

source

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1. .13097
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* NOTE: Estimated insert size may differ from sequence length
(see http://www.hqsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently

* consists of 61 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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LOCUS AC107529 135671 bp DNA linear HTG 23-JAN-2002
 DEFINITION Rattus norvegicus clone CH230-15308, *** SEQUENCING IN PROGRESS

ACCESSION AC107529

VERSION AC107529.1 GI:18266521

KEYWORDS HTG; HTGS_PHASE1.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

1 (bases 1 to 135671)

REFERENCE

AUTHORS

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
 Benton,J., Blame,K., Blankenburg,K., Bonnin,D., Bouck,J.,
 Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
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 Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
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 Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
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 Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
 Lewis,L., Li,Z., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
 Loisedge,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
 Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
 Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,
 Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
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 Ogih,M., Okwuonu,G., Oragunye,N., Owiedo,R., Pace,A., Payton,B.,
 Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
 Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojebokan,I., Rolfe,M.,
 Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
 Sisson,I., Sodergren,E., Sonaik,T., Sparks,A., Stanley,H.,
 Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
 Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
 Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
 Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
 Wallington,S., Williams,G., Williams,A., Wleczyk,R., Wooden,S.,
 Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstein,G., and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 135671)

Worley,K.C.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GKPT
 Center clone name: CH230-15308
 ----- Summary Statistics
 Sequencing vector: Plasmid; M7789
 Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap; version 0.990329First call to
 findPhrapList

Consensus quality: 115465 bases at least Q40

Consensus quality: 123476 bases at least Q30

Consensus quality: 129938 bases at least Q20

Estimated insert size: 115985; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 1.6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 50 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.

* as soon as it is available and the accession number will

* be preserved.

* 1

* 7377: contig of 7377 bp in length

* 7378 7477: gap of unknown length

* 7478 15342: contig of 7865 bp in length

* 15343 15442: gap of unknown length

* 15443 22527: contig of 7085 bp in length

* 22528 22627: gap of unknown length

* 22628 29780: contig of 7153 bp in length

* 29781 29880: gap of unknown length

* 29881 35729: contig of 5849 bp in length

* 35730 35829: gap of unknown length

* 35830 40256: contig of 4427 bp in length

* 40257 40356: gap of unknown length

* 40357 43749: contig of 3393 bp in length

* 43750 43849: gap of unknown length

* 43850 47481: contig of 3632 bp in length

* 47482 47581: gap of unknown length

* 47582 51921: contig of 4340 bp in length

* 51922 52021: gap of unknown length

* 52022 55938: contig of 3817 bp in length

* 55939 55945: gap of unknown length

* 55946 59945: gap of unknown length

* 59946 62331: contig of 2385 bp in length

* 62331 62430: gap of unknown length

* 62431 65299: contig of 2869 bp in length

* 65300 65399: gap of unknown length

* 65400 67738: contig of 2339 bp in length

* 67739 67838: gap of unknown length

* 67839 71179: contig of 3341 bp in length

* 71180 71279: gap of unknown length

* 71280 73888: contig of 2609 bp in length

* 73889 73988: gap of unknown length

* 73989 76228: contig of 2340 bp in length

* 76229 76428: gap of unknown length

* 76429 78817: contig of 2389 bp in length

* 78818 78917: gap of unknown length

* 78918 81814: contig of 2897 bp in length

* 81815 83853: contig of 1939 bp in length

* 83854 83954: gap of unknown length

* 83955 85956: contig of 1903 bp in length

* 85957 85957: gap of unknown length

* 85958 88030: contig of 2074 bp in length

* 88031 88130: gap of unknown length

* 88131 89384: contig of 1254 bp in length

* 89385 89484: gap of unknown length

* 89485 91406: contig of 1922 bp in length

* 91407 91506: gap of unknown length

* 91507 94092: contig of 2586 bp in length

* 94093 96016: contig of 1824 bp in length

* 96017 96116: gap of unknown length

* 96117 98345: contig of 2229 bp in length

* 98346 98445: gap of unknown length

* *


```

----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 131897 bases at least Q40
Consensus quality: 140653 bases at least Q30
Consensus quality: 147742 bases at least Q20
Estimated insert size: 138591; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
  (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).
* NOTE: This is a 'working draft' sequence. It currently
  consists of 59 contigs. The true order of the pieces
  is not known and their order in this sequence record is
  arbitrary. Gaps between the contigs are represented as
  runs of N, but the exact sizes of the gaps are unknown.
  This record will be updated with the finished sequence
  as soon as it is available and the accession number will
  be preserved.
*
* 1 7684: contig of 7684 bp in length
* 7685 7784: gap of unknown length
* 7785 14781: contig of 6997 bp in length
* 14782 14881: gap of unknown length
* 14882 21818: contig of 6937 bp in length
* 21819 21918: gap of unknown length
* 21919 27258: contig of 5340 bp in length
* 27259 27358: gap of unknown length
* 27359 33216: contig of 5858 bp in length
* 33217 33316: gap of unknown length
* 33317 36744: contig of 3428 bp in length
* 36745 36844: gap of unknown length
* 36845 43420: contig of 6576 bp in length
* 43421 43520: gap of unknown length
* 43521 46850: contig of 3330 bp in length
* 46851 46950: gap of unknown length
* 46951 49995: contig of 3045 bp in length
* 49996 50095: gap of unknown length
* 50096 54776: contig of 4681 bp in length
* 54777 54876: gap of unknown length
* 54877 59373: contig of 4497 bp in length
* 59374 59473: gap of unknown length
* 59474 62719: contig of 3246 bp in length
* 62720 62819: gap of unknown length
* 62820 66162: contig of 3343 bp in length
* 66163 66262: gap of unknown length
* 66263 68845: contig of 2583 bp in length
* 68846 68945: gap of unknown length
* 68946 72606: contig of 3661 bp in length
* 72607 72706: gap of unknown length
* 72707 75578: contig of 2872 bp in length
* 75579 75678: gap of unknown length
* 75679 78163: contig of 2485 bp in length
* 78164 78263: gap of unknown length
* 78264 81861: contig of 3598 bp in length
* 81862 81961: gap of unknown length
* 81962 84738: contig of 2777 bp in length
* 84739 84838: gap of unknown length
* 84839 87259: contig of 2421 bp in length
* 87260 87359: gap of unknown length
* 87360 88671: contig of 1312 bp in length
* 88672 88771: gap of unknown length
* 88772 91511: contig of 2740 bp in length
* 91512 91611: gap of unknown length
* 91612 93997: contig of 2386 bp in length
* 93998 94097: gap of unknown length
* 94098 97208: contig of 3111 bp in length
* 97209 97308: gap of unknown length
* 97309 99287: contig of 1979 bp in length
* 99288 99387: gap of unknown length
* 99388 101242: contig of 1855 bp in length
* 101243 101343: gap of unknown length
* 101344 103955: contig of 2613 bp in length

```

```

* 103956 104055: gap of unknown length
* 104056 105716: contig of 1661 bp in length
* 105717 105816: gap of unknown length
* 105817 107247: contig of 1431 bp in length
* 107248 107347: gap of unknown length
* 107348 109665: contig of 2318 bp in length
* 109666 109765: gap of unknown length
* 109766 112602: contig of 2837 bp in length
* 112603 112702: gap of unknown length
* 112703 114809: contig of 2107 bp in length
* 114810 114909: gap of unknown length
* 114910 117201: contig of 2292 bp in length
* 117202 117301: gap of unknown length
* 117302 119479: contig of 2178 bp in length
* 119480 119579: gap of unknown length
* 119580 120781: contig of 1202 bp in length
* 120782 120881: gap of unknown length
* 120882 122921: contig of 2040 bp in length
* 122922 123021: gap of unknown length
* 123022 124039: contig of 1018 bp in length
* 124040 124139: gap of unknown length
* 124140 126304: contig of 2165 bp in length
* 126305 126404: gap of unknown length
* 126405 128986: contig of 2582 bp in length
* 128987 131429: contig of 2343 bp in length
* 131430 131529: gap of unknown length
* 131530 133834: contig of 2305 bp in length
* 133835 133934: gap of unknown length
* 133935 135695: contig of 1761 bp in length
* 135696 137408: contig of 1613 bp in length
* 137409 137508: gap of unknown length
* 137509 138895: contig of 1387 bp in length
* 138896 138995: gap of unknown length
* 138996 140666: contig of 1671 bp in length
* 140667 140766: gap of unknown length
* 140767 143419: contig of 2653 bp in length
* 143420 143519: gap of unknown length
* 143520 144655: contig of 1136 bp in length
* 144656 144755: gap of unknown length
* 144756 146793: contig of 2038 bp in length
* 146794 146893: gap of unknown length
* 146894 147964: contig of 1071 bp in length
* 147965 148064: gap of unknown length
* 148065 149748: contig of 1684 bp in length
* 149749 149848: gap of unknown length
* 149849 151701: contig of 1853 bp in length
* 151702 151801: gap of unknown length
* 151802 152870: contig of 1069 bp in length
* 152871 152970: gap of unknown length
* 152971 154909: contig of 1939 bp in length
* 154910 155009: gap of unknown length
* 155010 156334: contig of 1325 bp in length
* 156335 156434: gap of unknown length
* 156435 157578: contig of 1144 bp in length
* 157579 157678: gap of unknown length
* 157679 159130: contig of 1452 bp in length
* 159131 159230: gap of unknown length
* 159231 160825: contig of 1595 bp in length

```

```

alignment_scores:
  Quality: 77.50      Length: 40
  Ratio: 2.768      Gaps: 2
  Percent Similarity: 70.000      Percent Identity: 50.000

```

```
alignment_block:

```

```
US-09-528-682-3 x AC106544/rev ...
```

```
Align seg 1/1 to reverse of: AC106544 from: 1 to: 163038
```

```
64 MetSerThrPheGluGlnValProAsnAsnLysGluPhelysGlyVal.. 79
||||: ||| ||||||||| |||: |||||
```


129340 ATGACACCCCTTCATAAAGTAGTACCAAAATAATAGAAATATCTTGGTGTGAC 129291

80 .IleSerAlaAsnVallys.....TyrAspMetAsnPhelYsLysLeuL 94
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

129290 TTTAGCAAGAGAGTGAAGAGTTATATAGACAAGACTTCAAGTCTTTGA 129241

94 euArgPheMetGluAsp 100

::: :::::|||||

129240 AGAAAGAAATTGAGGAAGAT 129221

seq_name: gb_htg:AC096023

seq_documentation_block:

LOCUS AC096023 168120 bp DNA linear HTG 20-DEC-2001

DEFINITION *** 69 unordered pieces. Rattus norvegicus clone CH230-36K13, *** SEQUENCING IN PROGRESS

AC096023 AC096023.3 GI:17943680

KEYWORDS HTG; HTGS_PHASE1.

SOURCE Norway rat.

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE

AUTHORS

1 (bases 1 to 168120)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbarella,J.,
Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
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Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
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Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
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Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
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Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
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Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:16901704.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GEEY
Center clone name: CH230-36K13
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 131006 bases at least Q40
Consensus quality: 140986 bases at least Q30
Consensus quality: 150254 bases at least Q20
Estimated insert size: 136913; sum-of-ctnigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.8x in Q20 bases; sum-of-ctnigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbankdraft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 69 ctnigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the ctnigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 5507: ctnig of 5507 bp in length
* 5508 5607: gap of unknown length
* 5608 12266: ctnig of 6659 bp in length
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* 18452 18551: gap of unknown length
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* 24111 24210: gap of unknown length
* 24211 27862: ctnig of 3652 bp in length
* 27863 27962: gap of unknown length
* 27963 31550: ctnig of 3588 bp in length
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* 31651 34793: ctnig of 3143 bp in length
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* 39990 40089: gap of unknown length
* 40090 43571: ctnig of 3482 bp in length
* 43572 47520: ctnig of 3849 bp in length
* 47521 47620: gap of unknown length
* 47621 50821: ctnig of 3201 bp in length
* 50822 50921: gap of unknown length
* 50922 53742: ctnig of 2821 bp in length
* 53743 53842: gap of unknown length
* 53843 57731: ctnig of 3889 bp in length
* 57732 57831: gap of unknown length
* 57832 60937: ctnig of 3006 bp in length
* 60938 63464: ctnig of 2527 bp in length
* 63465 63564: gap of unknown length
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* 64552 65551: gap of unknown length
* 65552 69495: ctnig of 3944 bp in length
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* 71929 72028: gap of unknown length
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* 74607 74706: gap of unknown length
* 74707 77679: ctnig of 2973 bp in length
* 77680 77779: gap of unknown length
* 77780 80610: ctnig of 2831 bp in length
* 80611 80710: gap of unknown length
* 80711 83729: ctnig of 3019 bp in length
* 83730 83829: gap of unknown length
* 83830 86267: ctnig of 2438 bp in length

* 86268 86367: gap of unknown length
* 86368 87702: contig of 1335 bp in length
* 87703 87802: gap of unknown length
* 87803 90062: contig of 2260 bp in length
* 90063 90162: gap of unknown length
* 90163 92322: contig of 2160 bp in length
* 92323 92422: gap of unknown length
* 92423 95730: contig of 3308 bp in length
* 95731 95830: gap of unknown length
* 95831 98118: contig of 2288 bp in length
* 98119 98218: gap of unknown length
* 98219 99729: contig of 1511 bp in length
* 99730 101635: gap of unknown length
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* 101636 103913: contig of 2178 bp in length
* 103914 104013: gap of unknown length
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* 106601 106700: gap of unknown length
* 106701 109124: contig of 2424 bp in length
* 109125 109224: gap of unknown length
* 109225 111642: contig of 2418 bp in length
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* 122114 122213: gap of unknown length
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* 144148 144247: gap of unknown length
* 144248 145384: contig of 1137 bp in length
* 145385 145484: gap of unknown length
* 145485 147068: contig of 1584 bp in length
* 147069 147168: gap of unknown length
* 147169 148276: contig of 1108 bp in length
* 148277 148376: gap of unknown length
* 148377 149819: contig of 1443 bp in length
* 149820 149919: gap of unknown length

alignment_scores: Quality: 77.50 Length: 40
Ratio: 2.768 Gaps: 2
Percent Similarity: 70.000 Percent Identity: 50.000

alignment_block:
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Align seg 1/1 to reverse of: AC096023 from: 1 to: 168120

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101081 ATGACACCCCTTCATAATAGTACCAATAATATAGAAATCTTGGTGTGAC 101032

80 .IleSerAlaAsnVallys.....TyrAspMetAsnPhelLysLeuL 94
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seq_name: gb_htg:AC105576

seq_documentation_block:
LOCUS AC105576 214033 bp DNA linear HTG 09-JAN-2002
DEFINITION Rattus norvegicus clone CH230-236F15, WORKING DRAFT SEQUENCE, 50
unordered pieces.
ACCESSION AC105576
VERSION AC105576.1 GI:18092798
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 214033)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
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Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
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Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
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Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
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Foster,P., Frantz,P., Gabist,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
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Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C.,
Hollins,B., Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
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Weinstock,G. and Gibbs,R.
Direct Submission
TITLE
JOURNAL
Unpublished

REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 214033)

Worley, K.C.

Direct Submission

Submitted (09-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GNPN

Center clone name: CH230-236F15

----- Summary Statistics

Assembly program: Phrap; version 0.990329First call to

findPhrapList

Consensus quality: 185044 bases at least Q40

Consensus quality: 190296 bases at least Q30

Consensus quality: 194221 bases at least Q20

Estimated insert size: 190368; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 3.5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 50 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved

* 1 16332: contig of 16332 bp in length

* 16333 16432: gap of unknown length

* 16433 26891: contig of 10459 bp in length

* 26892 26991: gap of unknown length

* 26992 39114: contig of 12123 bp in length

* 39115 39214: gap of unknown length

* 39215 47706: contig of 8492 bp in length

* 47707 47806: gap of unknown length

* 47807 54905: contig of 7099 bp in length

* 54906 55005: gap of unknown length

* 55006 61730: contig of 6725 bp in length

* 61731 61830: gap of unknown length

* 61831 68922: contig of 7092 bp in length

* 68923 69022: gap of unknown length

* 69023 73955: contig of 4933 bp in length

* 73956 74055: gap of unknown length

* 74056 79739: contig of 5684 bp in length

* 79740 79839: gap of unknown length

* 79840 87203: contig of 7364 bp in length

* 87204 87303: gap of unknown length

* 87304 95716: contig of 8413 bp in length

* 95717 95816: gap of unknown length

* 95817 101220: contig of 5404 bp in length

* 101221 101320: gap of unknown length

* 101321 106991: contig of 5671 bp in length

* 106992 107091: gap of unknown length

* 107092 111184: contig of 4093 bp in length

* 111185 111284: gap of unknown length

* 111285 117002: contig of 5718 bp in length

* 117003 117102: gap of unknown length

* 117103 122719: contig of 5617 bp in length

* 122720 122819: gap of unknown length

* 122820 127676: contig of 4857 bp in length

* 127677 127776: gap of unknown length

* 127777 132248: contig of 4472 bp in length

* 132249 132348: gap of unknown length

* 132349 137419: contig of 5071 bp in length

* 137420 137519: gap of unknown length

* 137520 140519: contig of 3000 bp in length

* 140520 140619: gap of unknown length

* 140620 145613: contig of 4994 bp in length

* 145614 145713: gap of unknown length

* 145714 150743: contig of 5030 bp in length

* 150744 150843: gap of unknown length

* 150844 152229: contig of 2386 bp in length

* 152230 153230: gap of unknown length

* 153231 155705: contig of 2376 bp in length

* 155706 155805: gap of unknown length

* 155806 159641: contig of 3836 bp in length

* 159642 159741: gap of unknown length

* 159742 162037: contig of 2196 bp in length

* 162038 166136: contig of 4099 bp in length

* 166137 166236: gap of unknown length

* 166237 169654: contig of 3418 bp in length

* 169655 169754: gap of unknown length

* 169755 173209: contig of 3455 bp in length

* 173210 173309: gap of unknown length

* 173310 174872: contig of 1563 bp in length

* 174873 174972: gap of unknown length

* 174973 178370: contig of 3398 bp in length

* 178371 178470: gap of unknown length

* 178471 181766: contig of 3296 bp in length

* 181767 181866: gap of unknown length

* 181867 184177: contig of 2311 bp in length

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* 211753 212869: contig of 1117 bp in length

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* 212970 214033: contig of 1064 bp in length.

Location/Qualifiers

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/organism="Rattus norvegicus"

/db_xref="taxon:10116"

/clone="CH230-236F15"

BASE COUNT 63123 a 41277 c 42183 g 62289 t 5161 others

ORIGIN

alignment_scores:

Quality: 77.50 Length: 35

Ratio: 2.981 Gaps: 2

Percent Similarity: 74.286 Percent Identity: 54.286

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 Weinstein, G. and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 95288)
 Worley, K.C.
 Submitted (23-JAN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 ----- Genome Center
 COMMENT

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information -----
Center project name: GJAD
Center clone name: CH230-104G10
----- Summary Statistics -----
Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 78058 bases at least Q40
Consensus quality: 84258 bases at least Q30
Consensus quality: 90715 bases at least Q20
Estimated insert size: 77118; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0.7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 48 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 4072: contig of 4072 bp in length
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/db_xref="taxon:10116"
/clone="CH230-104G10"
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Quality: 77.00 Length: 37
Ratio: 3.080 Gaps: 0
Percent Similarity: 67.568 Percent Identity: 43.243
alignment_block:
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seq_name: gb_pl:AF083031
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LOCUS   AF083031                174133 bp    DNA    linear    PLN 31-OCT-2001
DEFINITION  Guillardia theta nucleomorph chromosome 3, complete sequence.
ACCESSION  AF083031
VERSION    AF083031.2  GI:13794268
KEYWORDS
SOURCE     Guillardia theta.
ORGANISM   Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
REFERENCE  1 (bases 152157 to 169088)
AUTHORS    Zauner,S., Fraunholz,M., Wastl,J., Penny,S., Beaton,M.,
            Cavalier-Smith,T., Maier,U.G. and Douglas,S.
TITLE      Chloroplast protein and centrosomal genes, a tRNA intron, and odd
            telomeres in an unusually compact eukaryotic genome, the
            cryptomonad nucleomorph
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (1), 200-205 (2000)
MEDLINE    20087226
PUBMED     10618395
REFERENCE  2 (bases 1 to 174133)
AUTHORS    Douglas,S., Zauner,S., Fraunholz,M., Beaton,M., Penny,S.,
            Deng,L.T., Wu, X., Reith,M., Cavalier-Smith,T. and Maier,U.G.
TITLE      The highly reduced genome of an enslaved algal nucleus
JOURNAL    Nature 410 (6832), 1091-1096 (2001)
PUBMED     11323671
REFERENCE  3 (bases 152157 to 169088)
AUTHORS    Douglas,S.E. and Penny,S.L.
TITLE      Direct Submission
JOURNAL    Submitted (07-AUG-1998) Institute for Marine Biosciences, 1411
            Oxford Street, Halifax, NS B3H 3Z1, Canada
REFERENCE  4 (bases 1 to 174133)
AUTHORS    Zauner,S. and Douglas,S.
TITLE      Direct Submission
JOURNAL    Submitted (25-JAN-2001) Cell Biology and applied Botany,
            Philipps-University Marburg, Karl von Frisch Str, Marburg 35032,
            Germany
COMMENT    On Apr 26, 2001 this sequence version replaced gi:6690138.
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12264..12707
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/codon_start=1
/product="ubiquitin conjugating enzyme"
/protein_id="AAF24004.1"
/db_xref="GI:6690139"
/translation="WATKRIQKHDKLLKDPSPNCAGSDENLFRWTASIIGPSDSP
YAGGVFFLSILFPDPYPPKPKVQFTTKIYHPNINSIGICLDILRDQSPALTYSKV
LLSSLLTDPNPDPPLVFETARVFRNRSRYEATREWTQRYAT"
13171..13920
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13171..13920
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/note="repeated at opposite end of chromosome"
/codon_start=1
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/db_xref="GI:6690140"
/translation="MICSKENSTGIGISOQSIDDIILKKTNNNTNNVFFQGNLHAF
DVIRTRGSTEAGQSVVFRVAVRANEITPNIQNVVSTVSLGIQLDLKIALKARNAEY"
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NPRFAAVIMRIRDPKTTALIFSSGKMWVTGAKSEDSARVACKKYARIQRLGYCHAK
FIDFRINIVASCVRPPIRLSLAHAHNOFCSYEPFLPGLIYRMITPKVVLIFVS
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/db_xref="GI:13794269"
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/db_xref="GI:13794270"
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NIIYNIIDLESRLSULFDREYFYNNVYSKFSFNTFNNLSFKNMHMYKNESIKD
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15365. .15437
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complement(15573. .16397)
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NFIHQNLFDLSNLYFHYVVPKIKSLKSTSNKKIDLPENKKQINKVKKKLSIDN
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SESNLMPQKTAHSINPAQNSIIFKINFNQYDSVKNAIHFDESLEYCLNKNFL
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QLQNTSSFGSNINYPKFNHYITLIEKISGFRFLKDNHVNLYLFPKSNKNKAS
NLSKRNFDIFKRGKISKSNKNEKILSKINQYLGFNFNINIVIKIINNTLFFKH
LNGFSINAFDVVMYLNKIKNFVLIHRSSNIRSNOKTIRKHWGFKNFKKNKNI
YKNVAFLLKKAFTKSLNFKNLSKKKIYILKEKSKYLAENSNPNNETSSLNMTN
KTLTLLTLILKRNLSIKATKCISSYIPNNQLKWTKKKKNIVINDKFFVKNIKLK
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17671. .18489
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  Ratio: 1.481      Gaps: 4
  Percent Similarity: 62.651      Percent Identity: 30.120

alignment_block:
  * 1471 1472: contig of 1472 bp in length
  * 1473 1572: gap of unknown length
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US-09-528-682-3 x AF083031/rev ..
Align seg 1/1 to reverse of: AF083031 from: 1 to: 174133

9 GlnAlaTyrGluProIleGluValAsnThrAsnThrValThrGlnIleAs 25
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
43300 CAATTATATGAGTTTGGAAATACAAAAAGTACTAACATTTTGGC 43251

25 nGlySerAsnGluValProLeuAspGlyArgTyrSerAsnPheAlaLeuI 42
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
43250 GTGGAGT.....TTAGATGGAAGTAT.....CTAGCACTT. 43220

42 IeSerAlaGluGlyMetGlnAspGlyAspLeuPheGlyThrValAsn 58
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
43219 .....GGACAAATGATGGAATTTATTATTGCGATAATG 43184

59 GlnSerAsnPheProMetSerThrPheGluGlnValPro...AsnAsnLy 74
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
43183 AATAAGAACTTCAAAAAATAAAATTAATAATGTAATAATATTACACGC 43134

74 sGluPheLysGlyValIleSerAlaAsnValLysTyrAspMetAsnPhe 90
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
43133 ACACCTTCTCAGATGATTCGATTTGAATGTCATTTGATTGATTGTTTC 43085

seq_name: gb_htg:AC087131

seq_documentation_block:
LOCUS AC087131 193907 bp DNA linear HTG 09-DEC-2000
DEFINITION Mus musculus clone RP23-113J6, WORKING DRAFT SEQUENCE, 15 unordered
pieces.
ACCESSION AC087131
VERSION AC087131.1 GI:11610857
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus.

REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 193907)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
```

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Project Information
Center Project Name: 1780486
Center clone name: RPCI-23_113J6
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Summary Statistics
Consensus quality: 177072 bases at least Q40
Consensus quality: 186496 bases at least Q30
Consensus quality: 187873 bases at least Q20
Estimated insert size: 205000; agarose-fp estimation
Estimated insert size: 192507; sum-of-contigs estimation
Quality coverage: 9.94 in Q20 bases; agarose-fp estimation
Quality coverage: 10.59 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1472: contig of 1472 bp in length
* 1473 1572: gap of unknown length
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```

68 uGlnValProAsnAsnLysGluPheLysGlyValIleSerAlaAsnValL 85
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
277105 ACAGAAGAAAACGAGAAAGG.....AAGCAAAAGTCG 277071

85 ysTyrAsp.....MetAsnPheLysLysLysLeuLeuArg 95
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
277070 AGTGGGATGGAGCGCATAAAGAAAAAATGCGGTAAACAAGCGGTGAG 277021

96 PheMetGluAsp 99
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277020 TGGATGGAGAT 277009

seq_name: gb_pr:AF132730
seq_documentation_block:
LOCUS AF132730 2220 bp mRNA linear PRI 01-MAY-2000
DEFINITION Homo sapiens unknown mRNA.
ACCESSION AF132730
VERSION AF132730.1 GI:7672342
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2220)
AUTHORS Luo,W.Q., Chen,J.H., Huang,X.W., Zhou,Y., Zhou,H.J., Hu,S.N. and
Yuan,J.G.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-1999) Dept. of Biochemistry, Ins. of Basic Med
Science, 5 Dong Dan 3 Tiao, Beijing 100005, People's Republic of
China
FEATURES
Location/Qualifiers
1..2220
/organism="Homo sapiens"
/db_xref="taxon:9606"
988..2088
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KDVNLKDKWERLAEQKTFPFFNFLEHRTGPSDAMAWYTFENIKIFHSNE
VMSQYAVILMGKRSENVYVTKETVAQLLKENTNADSONEGLLTWEQENTVLKSTFPL
KTEEQIQELMAGGHPSSNADLLNYSLFMEDEGSEPFVQKLWQYMDKDEYL
QQLKQELGELHEEVLPKRLGMLTIDPSLDKQVNTYMSOAFQLPSEMPPEGDEK
EEAVVILQTLERLQVIDIRRVGREPEPAS"
BASE COUNT 626 a 550 c 640 g 404 t
ORIGIN

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alignment_scores:
Quality: 76.50 Length: 129
Ratio: 1.177 Gaps: 5
Percent Similarity: 50.388 Percent Identity: 26.357

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alignment_block:
US-09-528-682-3 x AF132730 ..

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Align seg 1/1 to: AF132730 from: 1 to: 2220

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```

1 AspPheThrArgAlaLeuGlnGlnAlaTyrGluProIleGluValas 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1366 GATTTCCTTCATATTCCTCGAGCATCGCTTTGGGCCCTAGTGCCAT 1415

17 nThrAsnThrValThr.....GlnIleAsnGlySerAsnG 29
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1416 GGCCTGGCGCTTATCTATTTTGAATAATCATCAAGATCTTCCACTCCAACG 1465

29 LuVal.....ProLeuaspGlyArgTyrSerAsnPhe 39
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

1466 AGTTTATGAGTCAGTTCTTATGCAGTCTTGTATGGGAAAGCGGAGTGAGAT 1515
40 AlaLeuIle..... 42
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1516 GTGTATGTCACCCAGAGGAGACAGTACGCCAGCTGCTGAAGGAGATGAC 1565
43 .....SerAlaGluGlyMetGlnAspGlyAspLeuPheGlyT 56
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1566 AAATGCTGACAGTCAGAACGAGGGGCTACTACCATGTCAGCTTCAACA 1615
56 hrValAsnGlnSerAsnPheProMetSerThrPheGluGlnValProAsn 72
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1616 CTGCTCTCAAGATACCTCCCTCTCAAGACAGAGCAATCCAGGAG 1665
73 AsnLysGluPheLysGlyValIleSerAlaAsnValLysTyrAsp....Me 88
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1666 CTGATGGAGCGAGGGGCTGGCATCCAGCAGCAGCAATGCAGACTTGCT 1715
88 tAsnPheLysLysLeuLeuArgPheMetGluAspAsp 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1716 CAACTACCGCTCACTG.....TTTATGGAGGATGAG 1746

seq_name: gb_pr:AK027245
seq_documentation_block:
LOCUS AK027245 2415 bp mRNA linear PRI 29-SEP-2000
DEFINITION Homo sapiens cDNA: FLJ23592 fis, clone LNG14731, highly similar to
AF132730 Homo sapiens unknown mRNA.
ACCESSION AK027245
VERSION AK027245.1 GI:10440332
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens human lung cDNA to mRNA, clone_lib:LNG clone:LNG14731.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (sites)
AUTHORS Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T.,
Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Tanigami,A.,
Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M.,
Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T.,
Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished (2000)
REFERENCE 2 (bases 1 to 2415)
AUTHORS Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
Sugano, Institute of Medical Science, University of Tokyo,
Laboratory of Genome Structure Analysis, Human Genome Center;
Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdna1@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing; Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
FEATURES
Location/Qualifiers
1..2415
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="LNG14731"
/clone_lib="LNG"
/tissue_type="human lung"
/note="Cloning vector pME18SFL3"
misc_feature
1..2415
/note="highly similar to AF132730 Homo sapiens unknown
mRNA"
BASE COUNT 672 a 595 c 685 g 463 t
ORIGIN

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2768: contig of 2768 bp in length
* 2769 2868: gap of unknown length
* 2869 6288: contig of 3420 bp in length
* 6289 6388: gap of unknown length
* 6389 9043: contig of 2655 bp in length
* 9044 9143: gap of unknown length
* 9144 11850: contig of 2707 bp in length
* 11851 11950: gap of unknown length
* 11951 13666: contig of 1716 bp in length
* 13667 17666: gap of unknown length
* 17667 15665: contig of 1899 bp in length
* 15666 15765: gap of unknown length
* 15766 16996: contig of 1231 bp in length
* 16997 17096: gap of unknown length
* 17097 18239: contig of 1143 bp in length
* 18240 18339: gap of unknown length
* 18340 19535: contig of 1196 bp in length
* 19536 19635: gap of unknown length
* 19636 21636: contig of 2001 bp in length
* 21637 21736: gap of unknown length
* 21737 22141: contig of 1405 bp in length
* 22142 2241: gap of unknown length
* 2242 24833: contig of 1592 bp in length
* 24834 24933: gap of unknown length
* 24934 26030: contig of 1097 bp in length
* 26031 26130: gap of unknown length
* 26131 27396: contig of 1266 bp in length
* 27397 27496: gap of unknown length
* 27497 28788: contig of 1292 bp in length
* 28789 28888: gap of unknown length
* 28889 30356: contig of 1468 bp in length
* 30357 30456: gap of unknown length
* 30457 31873: contig of 1417 bp in length
* 31874 31973: gap of unknown length
* 31974 33436: contig of 1463 bp in length
* 33437 33536: gap of unknown length
* 33537 35082: contig of 1546 bp in length
* 35083 35182: gap of unknown length
* 35183 36667: contig of 1485 bp in length
* 36668 36767: gap of unknown length
* 36768 38021: contig of 1254 bp in length
* 38022 38121: gap of unknown length
* 38122 39494: contig of 1373 bp in length
* 39495 39594: gap of unknown length
* 39595 40757: contig of 1163 bp in length
* 40758 40857: gap of unknown length
* 40858 41860: contig of 1003 bp in length
* 41861 41960: gap of unknown length
* 41961 43199: contig of 1239 bp in length
* 43200 43299: gap of unknown length
* 43300 44553: contig of 1354 bp in length
* 44554 44758: gap of unknown length
* 44754 45768: contig of 1015 bp in length
* 45769 45868: gap of unknown length
* 45869 46892: contig of 1024 bp in length
* 46893 46992: gap of unknown length
* 46993 48558: contig of 1666 bp in length
* 48559 48758: gap of unknown length
* 48759 49797: contig of 1039 bp in length
* 49798 49897: gap of unknown length
* 49898 51051: contig of 1154 bp in length
* 51052 51151: gap of unknown length
* 51152 52562: contig of 1411 bp in length.
* Location/Qualifiers
* 1. 52562

FEATURES
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/db_xref="taxon:10116"
/clone="CH230-9A12"
BASE COUNT 14699 a 11464 c 10207 g 12933 t 3259 others
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Quality: 76.50 Length: 41
Ratio: 2.550 Gaps: 2
Percent Similarity: 73.171 Percent Identity: 43.902
alignment_block:
US-09-528-682-3 x AC095730 ..
Align seg 1/1 to: AC095730 from: 1 to: 52562
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||||: |||: ||||| ||||| ||||| ||||| ||||| ||||| |||||
5402 ATGACTCCCTTCAAAATAGTCCCAATAATATAATAATACCTCGTGTGAC 5451
80 .lleSerAlaAsnValLys.....TyrAspMetAsnPheLysLysLeuL 94
||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5452 TTTAACCAACGAAGTGAAGATCTGTATGACAAGAACTTCAAGTCATGA 5501
94 euArgPheMetGluAspAspPhe 101
||: |||||: |||||
5502 AGAATGAATTTGAGGAAGATTTC 5524
seq_name: gb_htg:AC095923
seq_documentation_block:
LOCUS AC095923 127014 bp DNA linear HTG 20-DEC-2001
DEFINITION Rattus norvegicus clone CH230-10115, *** SEQUENCING IN PROGRESS
AC095923 *** 64 unordered pieces.
AC095923.2 GI:17943560
VERSION HTG; HTGS_PHASE1.
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 127014)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhaq,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flaeg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Correll,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homsí,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kuresh,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loulseghe,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S.,
Oguchi,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,

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 Ratio: 2.550 Gaps: 2
 Percent Similarity: 71.429 Percent Identity: 47.619

alignment_block:
 US-09-528-682-3 x AC095923/rev ..

Align seg 1/1 to reverse of: AC095923 from: 1 to: 127014

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 24063 ATGTCAACCTTCAAAATAGTGTCAATATATAAAATACCTTGGTGTGAC 24014

80 .IleSerAlaAsnValLys.....TyrAspMetAsnPheLysLysLeuL 94
 :|||: ||||| ||||| |||||: |||||
 24013 TCTAACCAAGCAAGTGAAGATCTGTATGACAAAGAACTTCAAGTCTCTGA 23964

94 euArgPheMetGluAspAspPheIle 102
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 23963 AGAAAGAAATTCAGTAGATCTCAT 23938

seq_name: gb_htg:AC106306

seq_documentation_block:
 LOCUS AC106306 143318 bp DNA linear HTG 12-JAN-2002
 DEFINITION Rattus norvegicus clone CH230-101122, *** SEQUENCING IN PROGRESS

***, 67 unordered pieces.
 AC106306
 AC106306.1 GI:18138827
 HTG: HTGS-PHASE1.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE
 AUTHORS
 1 (bases 1 to 143318)
 Muzny D.M., Adams C., Adio-Oduola B., Ali-Osman, F.R., Allen C.,
 Albrooks S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbara, J.,
 Benton, J., Blum, K., Blankenburg, K., Bonnin, D., Bouck, J.,
 Bowie, S., Brieve, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
 Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carion, T.F.,
 Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
 Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
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 Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, T., Rolfe, M.,
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 Weinstein, G., and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 143318)
 Worley, K.C.
 Direct Submission
 Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

 Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

 Project Information
 Center project name: GKP8
 Center clone name: CH230-101122

 Summary Statistics
 Assembly program: Phrap; version 0.990329 First call to
 findPhrapList
 Consensus quality: 114900 bases at least Q40
 Consensus quality: 123396 bases at least Q30
 Consensus quality: 129515 bases at least Q20
 Estimated insert size: 107169; sum-of-contigs estimation
 Quality coverage: 0x in Q20 bases; agarose-fp estimation
 Quality coverage: 1.4x in Q20 bases; sum-of-contigs estimation

 NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 NOTE: This is a 'working draft' sequence. It currently
 consists of 67 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1
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 15928 16027: gap of unknown length
 16028 20427: contig of 4400 bp in length
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 20528 23839: contig of 3312 bp in length
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TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 JOURNAL

COMMENT


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* 77369 77469: gap of unknown length
* 77469 79290: contig of 1821 bp in length
* 79290 79390: gap of unknown length
* 79390 81563: contig of 2173 bp in length
* 81563 81663: gap of unknown length
* 81663 83185: contig of 1522 bp in length
* 83185 83285: gap of unknown length
* 83285 85338: contig of 2053 bp in length
* 85338 85438: gap of unknown length
* 85438 86906: contig of 1468 bp in length
* 86906 87006: gap of unknown length
* 87006 89351: contig of 2345 bp in length
* 89351 91130: contig of 1679 bp in length
* 91130 91230: gap of unknown length
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* 94885 94985: gap of unknown length
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* 99081 99181: gap of unknown length
* 99181 100697: contig of 1516 bp in length
* 100697 100797: gap of unknown length
* 100797 102215: contig of 1418 bp in length
* 102215 102315: gap of unknown length
* 102315 103784: contig of 1469 bp in length
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* 103884 104985: contig of 1101 bp in length
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* 105086 106614: contig of 1529 bp in length
* 106614 106714: gap of unknown length
* 106714 108997: contig of 2283 bp in length
* 108997 110453: gap of unknown length
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* 115059 115159: gap of unknown length
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* 116359 116459: gap of unknown length
* 116459 118315: contig of 1856 bp in length
* 118315 118415: gap of unknown length
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* 119813 119913: gap of unknown length
* 119913 121334: contig of 1421 bp in length
* 121334 121434: gap of unknown length
* 121434 122983: contig of 1549 bp in length
* 122983 123083: gap of unknown length
* 123083 124931: contig of 1848 bp in length
* 124931 125031: gap of unknown length
* 125031 126077: contig of 1046 bp in length
* 126077 126177: gap of unknown length
* 126177 127400: contig of 1223 bp in length
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* 127500 129156: contig of 1656 bp in length
* 129156 129501: contig of 1656 bp in length

alignment_scores:
  Quality: 76.50      Length: 40
  Ratio: 2.732       Gaps: 2
  Percent similarity: 70.000  Percent Identity: 50.000

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US-09-528-682-3 x AC106306/rev ...

Align seg 1/1 to reverse of: AC106306 from: 1 to: 143318

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80 eSerAlaAsn...Vallys.....TyrAspMetAsnPheLysLysLeuL 94
| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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89551 AGAAATAAATTTGAAGAGGAT 89532

seq_name: gb_htg:AC099071

seq_documentation_block:
LOCUS AC099071 235713 bp DNA linear HTG 20-DEC-2001
DEFINITION Rattus norvegicus chromosome Rf1 clone CH230-89J23, WORKING DRAFT
ACCESSION AC099071
VERSION AC099071.2 GI:17943950
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 235713)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
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 Weinstein,G. and Gibbs,R.

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GWTZ
 Center clone name: CH230-89J23
 ----- Summary Statistics
 Assembly program: Phrap: version 0.990329First call to
 findPhrapList
 Consensus quality: 207134 bases at least Q40
 Consensus quality: 213086 bases at least Q30
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 Estimated insert size: 212187; sum-of-contigs estimation
 Quality coverage: 0x in Q20 bases; agarose-fp estimation
 Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 49 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
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 218601 221461: contig of 2861 bp in length
 221462 221561: gap of unknown length
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FEATURES

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alignment_scores:

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Quality: 76.50 Length: 40
Ratio: 2.638 Gaps: 2
Percent Similarity: 72.500 Percent Identity: 47.500

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alignment_block:

US-09-528-682-3 x AC099071/rev ..

Align seg 1/1 to reverse of: AC099071 from: 1 to: 235713

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80 e...SerAlaAsnValLys.....TyrAspMetAsnPhelLysLysLeuL 94
| : : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
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seq_name: gb_v1:IBDSEGAC

seq_documentation_block:

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LOCUS IBDSEGAC 3154 bp RNA linear VRL 17-JUN-1998
DEFINITION Infectious bursal disease virus gene for polyprotein
(VP2a-VP4-VP3), complete cds, strain:Cu1.
D00867

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ACCESSION D00867.1 GI:221894

VERSION 110kd polyprotein; VP2a; VP3; VP4; genome segment A.

KEYWORDS Infectious bursal disease virus (strain:Cu1) cDNA to genomic RNA.

SOURCE Infectious bursal disease virus

ORGANISM Viruses; dsRNA viruses; Birnaviridae; Avibirnavirus.

REFERENCE 1 (bases 1 to 3154)

AUTHORS Bayliss,C.D., Spies,U., Shaw,K., Peters,R.W., Papageorgiou,A.,

Muller,H. and Boursnell,M.E.

TITLE A comparison of the sequences of segment A of four infectious

bursal disease virus strains and identification of a variable

region in VP2

J. Gen. Virol. 71 (Pt 6), 1303-1312 (1990)

90278420 Location/Qualifiers

source

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1452..2261
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ORIGIN

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mat_peptide

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Ratio: 1.288 Gaps: 6
Percent Similarity: 47.200 Percent Identity: 21.600

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alignment_block:

US-09-528-682-3 x IBDSEGAC ..

Align seg 1/1 to: IBDSEGAC from: 1 to: 3154

16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32

981 ATTTCAACAACAGAGATAACCCAG.....CCAAAT 1009

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49

1010 CACATCC.....ATCAAACTGGAGATAGTGACCTCCAAAAGTGTGGTC 1053

49 InAspGlyAsp.....LeuPheGlyThr 56

1054 AGGCAGGGGATCAGATGTCATGTCGGCAAAAGGAGCGCTAGCAGTGACG 1103

57 ValAsnGlnSerAsnPhePro..... 63

1104 ATCCATGTGGCAACTATCCAGGGGCGCTCCGTCCTCAGCTAGTAGGC 1153

64MetSerT 66

1154 CTACGAAGAGTGCACACAGATCCGTGTTACGGTCTCGGGGTGACCA 1203

66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82

1204 ACTTCGAGCTGATCCCAATCTCTGAACCTAGCAAGAACCTGTTACAGAA 1253

83 AsnValLysTyrAsp.....MetAsnPhelLysLysLeuLeuArgPh 96

1254 TACGGCCGATTTGACCCAGGAGCCATGAACCTACACAAATGATA...CT 1300

96 eMetGluAspAspPheIleGlyVal 104

1301 GAGTGAGAGGACCGCTCTTGCCATC 1325


```

Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Ogulu,M., Okwundu,G., Oragunye,N., Owiedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojokoban,I., Rolfe,M.,
Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczkyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 75754)
Worley,K.C.
Direct Submission
Submitted (23-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GJAS
Center clone name: CH230-126B18
----- Summary Statistics
Sequencing vector: Plasmid; M77789
Chemistry: Dye-terminator Big Dye; 99% of reads
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 55246 bases at least Q40
Consensus quality: 59652 bases at least Q30
Consensus quality: 64248 bases at least Q20
Estimated insert size: 51495; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0.5x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 40 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence.
as soon as it is available and the accession number will
be preserved.
1 2933: contig of 2933 bp in length
2934 3033: gap of unknown length
3034 3034: contig of 3381 bp in length
6415 6415: gap of unknown length
6515 6515: gap of unknown length
10834: contig of 4320 bp in length
10934: gap of unknown length
10935 13800: contig of 2866 bp in length
13801 13900: gap of unknown length
13901 17728: contig of 3828 bp in length
17729 17829: gap of unknown length
17829 20405: contig of 2577 bp in length
20406 20505: gap of unknown length
20506 22957: contig of 2452 bp in length
22958 23058: gap of unknown length
23058 25209: contig of 2152 bp in length
25210 25309: gap of unknown length
25310 27261: contig of 1952 bp in length
27262 27361: gap of unknown length

27362 30057: contig of 2695 bp in length
30057 30156: gap of unknown length
30156 32059: contig of 1903 bp in length
32059 32159: gap of unknown length
32159 32160: contig of 2073 bp in length
32160 34232: gap of unknown length
34232 34332: gap of unknown length
34332 36000: contig of 1668 bp in length
36000 36100: gap of unknown length
36100 38066: contig of 1966 bp in length
38066 38166: gap of unknown length
38166 40154: contig of 1988 bp in length
40154 40254: gap of unknown length
40254 41630: contig of 1376 bp in length
41630 41730: gap of unknown length
41730 42881: contig of 1151 bp in length
42881 42981: gap of unknown length
42981 44123: contig of 1142 bp in length
44123 44223: gap of unknown length
44223 46149: contig of 1926 bp in length
46149 46249: gap of unknown length
46249 48397: contig of 2147 bp in length
48397 48496: gap of unknown length
48496 50042: contig of 1546 bp in length
50042 50142: gap of unknown length
50142 51736: contig of 1584 bp in length
51736 51826: gap of unknown length
51826 52921: contig of 1095 bp in length
52921 53021: gap of unknown length
53021 54044: contig of 1023 bp in length
54044 54144: gap of unknown length
54144 55548: contig of 1404 bp in length
55548 55648: gap of unknown length
55648 56821: contig of 1173 bp in length
56821 56921: gap of unknown length
56921 58069: contig of 1148 bp in length
58069 58169: gap of unknown length
58169 59394: contig of 1225 bp in length
59394 59494: gap of unknown length
59494 61112: contig of 1618 bp in length
61112 61212: gap of unknown length
61212 62213: contig of 1001 bp in length
62213 62313: gap of unknown length
62313 63872: contig of 1559 bp in length
63872 65176: contig of 1204 bp in length
65176 65276: gap of unknown length
65276 66330: contig of 1054 bp in length
66330 66430: gap of unknown length
66430 67891: contig of 1461 bp in length
67891 69444: contig of 1453 bp in length
69444 69544: gap of unknown length
69544 70757: contig of 1213 bp in length
70757 70857: gap of unknown length
70857 71922: contig of 1065 bp in length
71922 72022: gap of unknown length
72022 73192: contig of 1170 bp in length
73192 73292: gap of unknown length
73292 74603: contig of 1311 bp in length
74603 74703: gap of unknown length
74703 75754: contig of 1051 bp in length.

Location/Qualifiers
1..75754
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-126B18"
BASE COUNT 20531 a 14655 c 14015 g 22583 t 3970 others
ORIGIN

alignment_scores: 76.00 Length: 92
Quality: Ratio: 1.382 Gaps: 5
FEATURES
SOURCE
1..75754
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-126B18"

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sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads

ACCESSION	AL136526	27	GT-10944529
VERSION	AL136526	27	GT-10944529

KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL 1 (bases 1 to 179804)

COMMENT
Dunn,M.
Direct Submission
Submitted (02-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Oct 21, 2000 this sequence version replaced gi:10799512.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TrEMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C.elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
RP11-151A6 is from the library RPCT-11.1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
VECTOR: pBACE3.6

FEATURES
source
1..179804
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/map="g32.21-33.3"
/clone="RP11-151A6"
/clone-lib="RPCT-11.1"
1..646
/note="LIM2 repeat: matches 595. .1243 of consensus"
648..782
/note="LIM4 repeat: matches 4418. .4555 of consensus"
783..1144
/note="THS1B repeat: matches 3. .364 of consensus"
1145..1330
/note="LIM4 repeat: matches 4555. .4744 of consensus"
1331..1615
/note="AluJo repeat: matches 2. .286 of consensus"
1616..2352
/note="LIM4 repeat: matches 4744. .5494 of consensus"
2353..2656
/note="AluY repeat: matches 1. .299 of consensus"
2657..2767
/note="LIM4 repeat: matches 5494. .5606 of consensus"
2887..3706
/note="LTR28 repeat: matches 232. .1020 of consensus"
3582..3819
/note="LTR1 repeat: matches 1. .230 of consensus"
4354..4541
/note="AluJo repeat: matches 1. .187 of consensus"
4596..4880
/note="AluJb repeat: matches 1. .298 of consensus"
5278..5575

repeat_region
/note="AluSx repeat: matches 1. .299 of consensus"
6532..6858
/note="LIM4 repeat: matches 5152. .5507 of consensus"
6959..7161
/note="AluJb repeat: matches 1. .312 of consensus"
7162..7248
/note="LIM4 repeat: matches 5507. .5585 of consensus"
7629..7930
/note="AluY repeat: matches 1. .294 of consensus"
9437..9732
/note="AluJb repeat: matches 1. .301 of consensus"
9764..10067
/note="AluSg repeat: matches 1. .303 of consensus"
10228..10340
/note="L2 repeat: matches 2616. .2742 of consensus"
10555..10882
/note="L1PA13 repeat: matches 5804. .6155 of consensus"
10912..12259
/note="L2 repeat: matches 1039. .2403 of consensus"
12274..12523
/note="AluSc repeat: matches 43. .291 of consensus"
13269..13394
/note="L2 repeat: matches 2555. .2677 of consensus"
14156..14229
/note="MIR repeat: matches 59. .129 of consensus"
14668..14966
/note="AluSg repeat: matches 1. .299 of consensus"
17363..17417
/note="MIR repeat: matches 65. .119 of consensus"
17446..17673
/note="MIR repeat: matches 7. .250 of consensus"
17845..17919
/note="AluJo repeat: matches 67. .136 of consensus"
18498..18656
/note="MIR repeat: matches 46. .212 of consensus"
21868..22166
/note="AluSg repeat: matches 10. .313 of consensus"
22493..22791
/note="AluSg repeat: matches 1. .299 of consensus"
22795..22824
/note="15 copies 2 mer tt 86% conserved"
23490..23519
/note="15 copies 2 mer tt 90% conserved"
24563..24854
/note="MSTA repeat: matches 90. .426 of consensus"
24855..25184
/note="MER61A repeat: matches 5. .354 of consensus"
25189..27016
/note="MER61-internal repeat: matches 2727. .4550 of
consensus"
27017..27310
/note="AluSc repeat: matches 5. .302 of consensus"
27311..27672
/note="MER61-internal repeat: matches 2367. .2727 of
consensus"
27673..27978
/note="AluSp repeat: matches 1. .298 of consensus"
27979..29118
/note="MER61-internal repeat: matches 1231. .2367 of
consensus"
29119..29416
/note="AluSx repeat: matches 1. .297 of consensus"
29417..30569
/note="MER61-internal repeat: matches 1. .1231 of
consensus"
30572..30885
/note="MER61A repeat: matches 4. .353 of consensus"
30886..30979
/note="MSTA repeat: matches 1. .93 of consensus"
31021..31309
/note="AluSx repeat: matches 1. .297 of consensus"
31484..31790
/note="AluSc repeat: matches 1. .307 of consensus"


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* 107562 107661: gap of 100 bp
* 107662 120654: contig of 12993 bp in length
* 120655 120754: gap of 100 bp
* 120755 144638: contig of 23884 bp in length
* 144639 144738: gap of 100 bp
* 144739 152101: contig of 7363 bp in length
* 152102 152201: gap of 100 bp
* 152202 158206: contig of 6005 bp in length
* 158207 158306: gap of 100 bp
* 158307 166363: contig of 8057 bp in length
* 166364 166463: gap of 100 bp
* 166464 175450: contig of 8987 bp in length
* 175451 175550: gap of 100 bp
* 175551 184654: contig of 9104 bp in length.

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FEATURES

Location/Qualifiers

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Source
1..184654
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/clone="RP11-466B4"
/clone_lib="RPC1-11.2"
1..10730
/note="assembly_fragment:00210
fragment_chain:1"
10831..18069
/note="assembly_fragment:01221
fragment_chain:1"
18170..45344
/note="assembly_fragment:00372
fragment_chain:1"
45445..49824
/note="assembly_fragment:01517
fragment_chain:1"
49925..60273
/note="assembly_fragment:00257
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60374..69503
/note="assembly_fragment:00447
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69604..77550
/note="assembly_fragment:00194
fragment_chain:2"
77651..90093
/note="assembly_fragment:00498
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90194..99623
/note="assembly_fragment:00320
fragment_chain:2"
99724..107561
/note="assembly_fragment:00193
fragment_chain:3"
107662..120654
/note="assembly_fragment:01081
fragment_chain:3"
120755..144638
/note="assembly_fragment:00304
fragment_chain:4"
144739..152101
/note="assembly_fragment:01234
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152202..158206
/note="assembly_fragment:00648"
fragment_chain:4"
158307..166363
/note="assembly_fragment:00797.0"
166464..175450
/note="assembly_fragment:01188"
175551..184654
/note="assembly_fragment:00675
vector_side:right"
BASE COUNT 55388 a 35202 c 36952 g 55499 t 1613 others
ORIGIN

```

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alignment_scores:
  Quality: 76.00      Length: 82
  Ratio: 1.583       Gaps: 4
  Percent Similarity: 58.537   Percent Identity: 35.366

alignment_block:
US-09-528-682-3 x AL3555680 ..
Align seg 1/1 to: AL3555680 from: 1 to: 184654

16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
154619 ATTACACAAATTTGGTTTTCAAATAAAGGACAAATATTTCCCTCT 154668

32 uasPGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
|||||
154669 GGAT.....TTTCTGTAGCCCAAGCACCACCAATTTGAAGAC 154703

49 InAspGlyAsp.LeuPheGlyThrValAsnGlnSerAsnPheProMetSe 65
|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
154704 TCGGTGGAGACTATC.....ACTTCAGATGATAGCATGCTCCAAGCAA 154747

65 rThrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSera 82
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
154748 GACAAATGAAGG.....GAAATGAAGCAAGGAGAGTGGGGAG 154788

82 laAsnValLysTyrAspMetAsnPheLysLysLeuLeuArgPhe 96
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|
154789 CTACAATAAAACCGAGCTATCTTTGCCAAGTGCCTGCTATTT 154832

seq_name: gb_htg:AC097583

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seq_documentation_block:
LOCUS AC097583 206108 bp DNA linear HTG 19-OCT-2001
DEFINITION Rattus norvegicus clone RF31-40986 strain Brown Norway, WORKING
DRAFT SEQUENCE, 10 unordered pieces.
ACCESSION AC097583
VERSION AC097583.1 GI:16271921
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 206108)
REFERENCE
AUTHORS

```

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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,K., Haghighi,P.,
Ho,S.-L., Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-Q.,
Legaspi,R., Maduro,O.L., Maduro,V.B., Masello,C., Mastrian,S.D.,
McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A., Shevchenko,Y.,
Stantipop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Zhang,L.-H. and Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 206108)
Green,E.D.
Direct Submission
Submitted (19-OCT-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.mouse@hgrl.nih.gov
----- Project Information
Center project name: cgh
Center clone name: 409E06
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```


Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R.,
 Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
 Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S.,
 Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 210285)
 Worley, K.C.
 Direct Submission
 Submitted (15-SEP-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Dec 20, 2001 this sequence version replaced gi:15624420.

COMMENT

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GAYO
 Center clone name: CH230-4B10
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329First call to
 findPhrapList
 Consensus quality: 180050 bases at least Q40
 Consensus quality: 187476 bases at least Q30
 Consensus quality: 193628 bases at least Q20
 Estimated insert size: 190299; sum-of-contigs estimation
 Quality coverage: 0x in Q20 bases; agarose-fp estimation
 Quality coverage: 2.7x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 49 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 8759: contig of 8759 bp in length
 * 8760 8859: gap of unknown length
 * 8860 17154: contig of 8295 bp in length
 * 17155 17254: gap of unknown length
 * 17255 26197: contig of 8943 bp in length
 * 26198 26297: gap of unknown length
 * 26298 36077: contig of 9780 bp in length
 * 36078 36177: gap of unknown length
 * 36178 45344: contig of 9167 bp in length
 * 45345 45444: gap of unknown length
 * 45445 51221: contig of 5777 bp in length
 * 51222 51321: gap of unknown length
 * 51322 59804: contig of 8483 bp in length
 * 59805 59904: gap of unknown length
 * 59905 67441: contig of 7537 bp in length
 * 67442 67541: gap of unknown length
 * 67542 75531: contig of 7990 bp in length
 * 75532 75631: gap of unknown length
 * 75632 82565: contig of 6934 bp in length
 * 82566 82665: gap of unknown length
 * 82666 89252: contig of 6587 bp in length
 * 89253 89352: gap of unknown length
 * 89353 96834: contig of 7502 bp in length
 * 96835 96954: gap of unknown length
 * 96955 103544: contig of 6590 bp in length
 * 103545 103644: gap of unknown length
 * 103645 108763: contig of 5119 bp in length
 * 108764 108863: gap of unknown length
 * 108864 113497: contig of 4634 bp in length
 * 113498 113597: gap of unknown length
 * 113598 119450: contig of 5853 bp in length

* 119451 119550: gap of unknown length
 * 119551 124302: contig of 4752 bp in length
 * 124303 124402: gap of unknown length
 * 124403 129683: contig of 5281 bp in length
 * 129684 129783: gap of unknown length
 * 129784 133492: contig of 3709 bp in length
 * 133493 133592: gap of unknown length
 * 133593 137612: contig of 4020 bp in length
 * 137613 137712: gap of unknown length
 * 137713 142261: contig of 4549 bp in length
 * 142262 142361: gap of unknown length
 * 142362 146179: contig of 3818 bp in length
 * 146180 146279: gap of unknown length
 * 146280 150559: contig of 4280 bp in length
 * 150560 150659: gap of unknown length
 * 150660 154983: contig of 4324 bp in length
 * 154984 155083: gap of unknown length
 * 155084 158865: contig of 3782 bp in length
 * 158866 158965: gap of unknown length
 * 158966 162292: contig of 3327 bp in length
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 * 162393 165446: contig of 3254 bp in length
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 * 167600 167699: gap of unknown length
 * 167700 170062: contig of 2363 bp in length
 * 170063 170162: gap of unknown length
 * 170163 172452: contig of 2290 bp in length
 * 172453 172552: gap of unknown length
 * 172553 174441: contig of 1889 bp in length
 * 174442 174541: gap of unknown length
 * 174542 177481: contig of 2940 bp in length
 * 177482 177581: gap of unknown length
 * 177582 180454: contig of 2873 bp in length
 * 180455 180554: gap of unknown length
 * 180555 183726: contig of 3072 bp in length
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 * 183727 186150: contig of 2424 bp in length
 * 186151 186250: gap of unknown length
 * 186251 189086: contig of 2836 bp in length
 * 189087 189186: gap of unknown length
 * 189187 191883: contig of 2697 bp in length
 * 191884 191983: gap of unknown length
 * 191984 193902: contig of 1919 bp in length
 * 193903 194002: gap of unknown length
 * 194003 195664: contig of 1662 bp in length
 * 195665 195764: gap of unknown length
 * 195765 198028: contig of 2264 bp in length
 * 198029 198128: gap of unknown length
 * 198129 199325: contig of 1197 bp in length
 * 199326 199425: gap of unknown length
 * 199426 200978: contig of 1553 bp in length
 * 200979 201078: gap of unknown length
 * 201079 202252: contig of 1174 bp in length
 * 202253 202352: gap of unknown length
 * 202353 203363: contig of 1011 bp in length
 * 203364 203463: gap of unknown length
 * 203464 205297: contig of 1834 bp in length
 * 205298 205397: gap of unknown length
 * 205398 206483: contig of 1086 bp in length
 * 206484 207966: contig of 1383 bp in length
 * 207967 208066: gap of unknown length
 * 208067 209182: contig of 1116 bp in length
 * 209183 209282: gap of unknown length
 * 209283 210285: contig of 1003 bp in length.

FEATURES
Source

Location/Qualifiers
 1. .210285

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 /db_xref="taxon:10116"
 /clone="CH230-4B10"

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/SID55/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAU3622 + 57.00 116.21 399.20 + 57.00 99.83 3.3e+03 +
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:AAH68456 + 57.00 115.50 437.56 + 57.00 98.68 3.8e+03 +
/SID55/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:ABU18899 + 57.00 115.20 454.26 + 57.00 97.88 4.2e+03 +

/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABL22106 - 57.00 97.58 4.4e+03 6
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:ABL3147 - 57.00 96.38 5.1e+03 72
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABL22628 + 57.00 94.86 6.2e+03 8
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABL08598 + 57.00 94.73 6.3e+03 8
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:ABL32462 - 57.00 94.00 6.9e+03 91
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABL03530 + 57.00 90.47 1.1e+04 1
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:AAV62176 - 57.00 67.50 2.0e+05 15
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:AAV25119 - 57.00 64.61 2.9e+05 15
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAH96431 - 57.00 56.13 7.8e+05 3
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAH68532 - 57.00 56.13 7.8e+05 3
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:AAV58840 + 57.00 50.98 1.4e+06 58
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAV20248 + 57.00 46.19 2.1e+06 91
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/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAI99682 + 57.00 29.79 3.5e+06 4
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/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAV34375 - 56.50 125.29 183.03 55
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/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAV5784 + 56.50 116.12 404.08 96
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAV65933 + 56.50 115.43 441.18 10
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/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAI3346 + 56.50 114.88 473.29 10
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:ABA05817 + 56.50 114.01 529.61 11
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:AAV29011 + 56.50 113.95 533.78 11
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAV54516 + 56.50 112.97 604.62 13
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAV51826 - 56.50 112.09 676.98 14
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:AAQ38917 - 56.50 112.09 676.98 14
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/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:AAV33228 + 56.50 110.95 783.96 15
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:AAV77058 + 56.50 110.38 843.56 16
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAH67644 + 56.50 110.23 859.63 16
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:AAV29669 + 56.50 110.12 871.74 17
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/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABL11637 + 56.50 109.71 918.54 17
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAV26704 + 56.50 109.66 924.68 18
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:AAV1110 + 56.50 109.54 939.07 18
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAV67752 + 56.50 109.51 943.19 18
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/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:AAV02471 + 56.50 109.01 1.0e+03 19
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAV221078 + 56.50 109.01 1.0e+03 19
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/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAV44843 + 56.50 109.01 1.0e+03 19
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAV37849 + 56.50 109.01 1.0e+03 19
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:AAV29678 + 56.50 108.80 1.0e+03 19
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/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAV09764 + 56.50 108.75 1.0e+03 19
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAV84394 + 56.50 108.75 1.0e+03 19
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAV26650 + 56.50 108.75 1.0e+03 19
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAV21818 + 56.50 108.75 1.0e+03 19
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAV09875 + 56.50 108.75 1.0e+03 19
/SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAV07037 + 56.50 108.75 1.0e+03 19


```

PS Disclosure; Fig 5A-K; 77pp; English.
XX A cDNA clone contg. the entire coding region of the large RNA
CC segment of infectious bursal disease virus serotype I strain GLS
CC has the sequence given in AAT05623, and encodes the structural
CC proteins VP2/4/3 (in that order). Chimeric immunogens in which
CC an epitopic determinant of a lethal IBDV strain is inserted
CC into GLS VP2 can be expressed in recombinant mammalian and poultry
CC host cells.
XX
SQ Sequence 3230 BP; 865 A; 908 C; 838 G; 619 T; 0 other;

alignment_scores:
  Quality: 77.00      Length: 125
  Ratio: 1.305       Gaps: 6
  Percent Similarity: 47.200      Percent Identity: 21.600

alignment_block:
US-09-528-682-3 x AAT05623 ..

Align seg 1/1 to: AAT05623 from: 1 to: 3230

16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
   :: ||||| ::|||
999 ATTCCAACCAACGAGATAACCCAG.....CCAAAT 1027

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
   : :: ::||| ::|||
1028 CACATCC.....ATCAAACTGGAGATAGTGACCTCCAAAGTGGTGC 1071

49 InAspGlyAsp.....LeuPheGlyThr 56
   ||::|||
1072 AGAAGGGGACCAAGATGTCATGTCGCGAAGTGGGACCTAGCAGTGACG 1121

57 ValAsnGlnSerAsnPhePro..... 63
   ::::: ::|||
1122 ATTCATGGTGGAACATATCCAGGGGCCCTCCGTCGTCACACTAGTAGC 1171

64 .....MetSert 66
1172 CTACGAAGAGAGTGGCAACAGGAGTCTGTGTTACGGTGGTGGGTGAGCA 1221

66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
   ::||| ::|||
1222 ACTTCGAGCTGATCCCAATCTCGAAGTACCAAGAACCTGGTTACAGAA 1271

83 AsnValLysTyrAsp.....MetAsnPheLysLysLeuLeuArgPh 96
   ::||| ::|||
1272 TACGGCGGATTTGACCCAGGAGGCATGACATACACAAAATTGATA...CT 1318

96 eMetGluAspAspPheIleGlyVal 104
   : ||| ||| ::|||
1319 GAGTGAGAGGGGACCGCTTGGGCATC 1343

seq_name: /SID85/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:AAT63065

seq_documentation_block:
ID AAT63065 standard; DNA; 3230 BP.
XX
AC AAT63065;
XX
DT 08-MAY-1997 (first entry)
XX
DE DNA sequence encompassing GLS-1, GLS-2, GLS-3 and GLS-4.
XX
KW Infectious bursal disease virus; IBDV; large segment; GLS 5 strain;
KW structural protein; VP2; VP3; VP4; Immunogen; vaccine;
KW Gumboro disease; ss.
XX
OS Infectious bursal disease virus.
XX
FH Key Location/Qualifiers

```

```

FT CDS 114..3152
FT misc_RNA /*tag= a
FT 1..348
FT /*tag= b
FT /note= "Represents clone GLS-1, see also AAT63066"
FT misc_RNA 283..1252
FT /*tag= c
FT /note= "Represents clone GLS-2, see also AAT63067"
FT misc_RNA 999..2620
FT /*tag= d
FT /note= "Represents clone GLS-4, see also AAT63069"
FT misc_RNA 1722..3230
FT /*tag= e
FT /note= "Represents clone GLS-3, see also AAT63068"
XX
XX US5595912-A.
PN
XX
PD 21-JAN-1997.
XX
XX 04-MAY-1990; 90US-0519202.
XX
XX 23-MAR-1994; 94US-0216276.
XX 04-MAY-1990; 90US-0519202.
XX 28-JUN-1993; 93US-0083784.
XX (UYMA-) UNIV MARYLAND BALTIMORE.
XX
XX Snyder D, Vakharina V;
XX
XX WPI; 1997-107584/10.
DR P-PSDB; AAW14737.
XX
XX Infectious bursal disease virus nucleic acids - for prodn. of
XX vaccines for poultry for protection against Gumboro disease
XX
XX Claim 4; Column 43-52; 41pp; English.
XX
XX This sequence represents a fragment of the infectious bursal disease
XX virus (IBDV) large segment from the GLS 5 strain. This sequence
XX encodes the structural proteins VP2, VP3 and VP4. The proteins
XX encoded by this sequence, esp. VP2 which is the major host protective
XX immunogen of IBDV, may be used to prepare vaccines against IBDV
XX infection/Gumboro disease.
XX
XX Sequence 3230 BP; 865 A; 909 C; 837 G; 619 T; 0 other;

```

```

alignment_scores:
  Quality: 77.00      Length: 125
  Ratio: 1.305       Gaps: 6
  Percent Similarity: 47.200      Percent Identity: 21.600

alignment_block:
US-09-528-682-3 x AAT63065 ..

Align seg 1/1 to: AAT63065 from: 1 to: 3230

16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
   :: ||||| ::|||
999 ATTCCAACCAACGAGATAACCCAG.....CCAAAT 1027

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
   : :: ::||| ::|||
1028 CACATCC.....ATCAAACTGGAGATAGTGACCTCCAAAGTGGTGC 1071

49 InAspGlyAsp.....LeuPheGlyThr 56
   ||::|||
1072 AGAAGGGGACCAAGATGTCATGTCGCGAAGTGGGACCTAGCAGTGACG 1121

57 ValAsnGlnSerAsnPhePro..... 63
   ::::: ::|||
1122 ATTCATGGTGGAACATATCCAGGGGCCCTCCGTCGTCACACTAGTAGC 1171

```



```

1319 GAGTGAAGAGGGACCGCCCTTGGCATC 134
      :  |||  |||  ::|||:::
1320 GAGGAGGAGGAGGAGGAGGAGGAGGAG

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Ratio: 1.177
Percent Similarity: 50.38

alignment block:

US-09-528-682-3 x AAS22655

Align seq 1/1 to: AAS2265

1 AspPhePheThrArgAlaLeuGlnGlnAlaTyrGluPr

379 GATTTCTTCTCAATTTCCTGGAGCATCGCTTTGGGCCCAGTGATGCCAT 428

17 nThrasnThrValthr.....GlnIleAsnGlySerAsnCg 29
::: ::: |||
429 GGCCTGGCGTTTATACTATTTTTGAATAATCAAGACTTCACCTACAACG 478

29 luVal.....ProLeuAspGlyArgTyrSerAsnPhe 39
|||||
479 AGGTATTGAGTCACGCTTCTATCGACTCCTTGATGGAAAGCGGAGTAGAAT 528

40 AlaLeuIle.....	42
-------------------	----

529 GTGTATGTCACCCAGAGGAGACAGTAGCCCCAGCTGCTGAAGGAGATGAC 578

43SerAlaGluGlyGlyMetGlnAspGlyVasPLeupheGlyT 56

579 A A A T G C T G A C A G T C A G A A C G A G G G C T A C T A A C C A T G G A G C A G T T C A A C A 628

56 hrValAsnGlnSerAsnGlnPheProMetSerThrPheGluGlnValProAsn 72

629 CTGTCCTCAAGAGTACCTTCCCTCTCAAGACAGAGCAATCCAGGAG 678

73 AsnLysGluPheLysGlyValIleSerAlaAsnValLysTyrAsp...Me 88

679 CTGATGGAGGCGAGGGGGCTGGCATCCCAGCAGCAGCAATGCAGACTTGCT 728

88 + Asn PheI.vsl.vsl.enI.enI.AraG PheMetG||AspAsp 100

729 CAACTACCGCTCACTG.....TTTATGGAGGATGAG 759

seq name: /SRPS5/qcadata/geneseq/geneseq-emb1/NA2001A.DAT:AAS22891

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seq_documentation_block:
ID   AAS22891 standard; cDNA; 2663 BP.
XX
XX
AC   AAS22891;
XX
XX   24-OCT-2001 (first entry)
XX
XX   Human cDNA encoding a novel human protein #457.
DE
XX
XX   Human; novel protein; ss: Antianaemic; osteopathic; antiinflammatory;
KW   immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;
KW   anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW   antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW   thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW   Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW   tissue regeneration; immune disorder.

```


XX OS Homo sapiens.
 XX PN WO200155437-A2.
 XX PD 02-AUG-2001.
 XX PF 25-JAN-2001; 2001WO-US02623.
 XX PR 25-JAN-2000; 2000US-0491404.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT;
 XX DR WPI: 2001-451939/48.
 XX DR P-PSDB; AAU14586.
 XX
 XX Isolated polypeptides useful for treating anti-inflammatory diseases,
 XX PT nervous system disorders, and for regenerating bone and cartilage -
 XX PS Claim 1; Page 776-777; 894pp; English.
 XX
 CC The invention relates to polynucleotides encoding novel human
 CC proteins or their active domains. The polypeptides, polynucleotides and
 CC antibodies raised against the polypeptides are used in a method of
 CC treatment of a mammal and prevention of disorders caused by the aberrant
 CC protein expression or activity. The polypeptides can be used as
 CC molecular weight markers, food supplements, and in antibody production.
 CC The polypeptides are used to identify compounds which bind to the
 CC polypeptides. Polynucleotides of the invention are used as probes and
 CC primers, for sequencing, for chromosome or gene mapping, in the
 CC production of recombinant proteins, and in generating anti-sense DNA or
 CC RNA and in gene therapy. Polypeptides of the invention can be used to
 CC target drugs to a tumour, in assays to determine biological activity, to
 CC raise antibodies/elicit an immune response, to determine quantitative
 CC protein levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.
 CC The present sequence encodes a protein of the invention.
 XX
 SQ Sequence 2663 BP; 510 A; 805 C; 667 G; 681 T; 0 other;

alignment_scores:
 Quality: 76.50 Length: 129
 Ratio: 1.177 Gaps: 5
 Percent Similarity: 50.388 Percent Identity: 26.357

alignment_block:

US-09-528-682-3 x AAS22891/rev ..

Align seg 1/1 to reverse of: AAS22891 from: 1 to: 2663

1 AspPheThrArgAlaLeuGlnAlaTyCluProIleGluValAs 17
 945 GATTCCTTCATTCCTGGAGCATCGCTTTGGCCCGAGTGATGCCAT 896
 17 nThrAsnThrValThr.....GlnIleAsnGlySerAsnG 29
 895 GGCCTGGCGCTATACTATTTTGAATAATACAGATCTTCCACTCCACG 846
 29 luVal.....ProLeuAspGlyArgTyrSerAsnPhe 39
 845 AGGTTTACGAGTCAGTTCTATGACAGTCTTGATGGGAAAGCGGAGTGAGAA 796

40 AlaLeuIle..... 42
 795 GTGTATGTCACCCAGAGGAGACAGTACCCAGAGTGTGAAGGAGATGAC 746
 43SerAlaGluGlyMetGlnAspGlyAspLeuPheGlyT 56
 745 AATGCTGACAGTACAGAGGAGGGCTACTAACCATGGAGCAGTTCACA 696
 56 hrValAsnGlnSerAsnPheProMetSerThrPheGluGlnValProAsn 72
 695 CTGTCTCAAGAGTACCTTCCTCTCAAGACAGAGCAATCCAGGAG 646
 73 AsnLysGluPheLysGlyValIleSerAlaAsnValLysTyrAsp...Me 88
 645 CTGATGGAGGAGGGGCTGGCATCCAGCAGCAGCAATGCAGACTTCCT 596
 88 tAsnPheLysLysLeuLeuArgPheMetGluAspAsp 100
 595 CAACCTACCGCTCACTG.....TTTATGGAGGATGAG 565
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 seq_documentation_block:
 ID AAQ14897 standard; DNA; 3228 BP.
 AC AAQ14897;
 DT 24-FEB-1992 (first entry)
 DE GLS clones 1 to 4.
 KW Infectious bursal disease virus; IBDV; vaccine; poultry; ss.
 OS Infectious bursal disease virus.
 FH Key Location/Qualifiers
 CDS 79..3150
 FT /tag= a
 FT /note= "Polypeptide encoded by GLS clones 1 to 4"
 FT misc_feature 1..348
 FT /tag= b
 FT /note= "GLS-1 clone"
 FT misc_feature 283..1252
 FT /tag= c
 FT /note= "GLS-2 clone"
 FT misc_feature 1722..3230
 FT /tag= d
 FT /note= "GLS-3 clone"
 FT misc_feature 999..2620
 FT /tag= e
 FT /note= "GLS-4 clone"
 XX WO9116925-A.
 XX 14-NOV-1991.
 XX 30-APR-1991; 91WO-US03056.
 XX 04-MAY-1990; 90US-0519202.
 XX (UYMA-) UNIV MARYLAND COL.
 XX Vakharia V;
 XX WPI; 1991-353531/48.
 XX P-PSDB; AAR15054.
 XX Infectious bursal disease virus nucleic acids - useful as
 XX vaccines against IBDV in poultry
 XX Example; Page 30; 45pp; English.

CC The sequence is made up of variant GLS clones 1 to 4 of infectious
 CC bursal disease virus (IBDV). It can be used in broad spectrum IBDV
 CC poultry vaccines, administration is ophthalmically, by injection,
 CC nasally or orally, at any time after hatching and as a booster at
 CC other times. Poultry treated include chickens, roosters, broilers,
 CC roasters, breeders, layers, turkeys and ducks. See also AAQ14896.
 XX
 SQ Sequence 3228 BP; 868 A; 907 C; 836 G; 617 T; 0 other;

alignment_scores:
 Quality: 74.00 Length: 125
 Ratio: 1.254 Gaps: 6
 Percent Similarity: 47.200 Percent Identity: 20.800

alignment_block:
 US-09-528-682-3 x AAQ14897 ..

Align seg 1/1 to: AAQ14897 from: 1 to: 3228

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16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
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997 ATTCCACCAACGAGATAACCCAG.....CCAAAT 1025

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
   : :: : : : : : : : : : : : : : : : : : : : : : : : :
1026 CACATCC.....ATCAAACTGGAGATAGTACCTCCAAAAGTGGTGTC 1069

49 InAspGlyAsp.....LeuPheGlyThr 56
||:||||| |||
1070 AGGAAGGGGACAGATGTCATGTGTCGCAAGTGGGAGCCCTAGCAGTGACG 1119

57 ValAsnGlnSerAsnPhePro..... 63
: : : : : : : : : : : : : : : : : : : : : : : : : :
1120 ATTCATGTGGCACTATCCAGGGGCCCTCCGTCCTCAGCTAGTAGC 1169

64 .....MetSert 66

1170 CTACGAAAGAGTGGCAACAGGATCTGCTGTACGTCGCTGGGTGAGCA 1219

66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
: : : : : : : : : : : : : : : : : : : : : : : : : :
1220 ACTACGAGCTGATCCCAATCTCTGAACCTAGCAAGAAGACCTGGTTACAGAA 1269

83 AsnValLysTyrAsp.....MetAsnPheLysLysLeuLeuArgPh 96
: : : : : : : : : : : : : : : : : : : : : : : : : :
1270 TACGGCCGATTGACCCAGGAGCCATGAACCTACACAAATTGATA...CT 1316

96 eMetGluAspPheLeGlyVal 104
: ||| ||| : : : : : : : : : :
1317 GAGTGAGAGGACCGCCTGGCATC 1341

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seq_name: /SIDS5/gcdata/geneseq/geneseqn-emb1/NA1996.DAT:AAAT43283

seq_documentation_block:

ID AAAT43283 standard; cDNA; 1362 BP.

XX AC AAAT43283;

XX DT 05-FEB-1997 (first entry)

XX DE Coding sequence for infective bursa protein.

XX DE Infective bursa; fabricius disease virus; poxvirus; vaccine;
 KW domestic fowl; ss.

XX OS Fabricius disease virus.

XX XX

XX key Location/Qualifiers

FT misc_difference 520..522

FT /*tag= a

FT /codon= seq:GAI, aa:ASP

XX

PN JP08242869-A.

XX

PD 24-SEP-1996.

XX

PF 16-JAN-1996; 96JP-0023125.

XX

PR 13-JAN-1995; 95JP-0021249.

XX

PA (JAPG) JAPANESE GEON CO LTD.

XX

DR WPI: 1996-479907/48.

XX

DR P-PSDB: AAW06086.

XX

PT Recombinant pox:virus containing Fabricius disease virus protein -

XX

XX used in a vaccine to immunise domestic fowl

XX

PS Claim 1; Page 10-12; 31pp; Japanese.

XX

CC This sequence represents the coding sequence for a protein derived from
 CC the infective bursa of Fabricius disease virus. This sequence was used
 CC to create a recombinant poxvirus of the invention. The recombinant
 CC poxvirus contains nucleotides 1-1359 of this sequence (i.e. the stop
 CC codon is removed), inserted into a genomic region of the poxvirus. The
 CC genomic region where this sequence is inserted is a region non-essential
 CC to the growth of the poxvirus. The recombinant virus can be used as the
 CC main component in an anti-infective bursa of Fabricius disease virus,
 CC recombinant virus vaccine. The recombinant poxvirus can also be used as
 CC a live vaccine for domestic fowls.

XX

SQ Sequence 1362 BP; 367 A; 365 C; 340 G; 289 T; 1 other;

alignment_scores:

Quality: 73.00 Length: 125
 Ratio: 1.259 Gaps: 6
 Percent Similarity: 46.400 Percent Identity: 21.600

alignment_block:

US-09-528-682-3 x AAAT43283 ..

Align seg 1/1 to: AAAT43283 from: 1 to: 1362

```

16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
   :: ||||| ::|||::
886 ATTCCAACCAACGAGATAACCCAG.....CCAAAT 914

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
   : : : : : : : : : : : : : : : : : : : : : : : : : :
915 CACATCC.....ATCAAACTGGAGATAGTACCTCCAAAAGTGGTGTC 958

49 InAspGlyAsp.....LeuPheGlyThr 56
||:||||| |||
959 AGCAGGGGATCAGATGTCATGTGTCGCAAGTGGGAGCCCTAGCAGTGACG 1008

57 ValAsnGlnSerAsnPhePro..... 63
: : : : : : : : : : : : : : : : : : : : : : : : : :
1009 ATCCATGGTGGCAACTATCCAGGGGCCCTCCGTCCTCAGCTAGTAGC 1058

64 .....MetSert 66

1059 CTACGAAAGAGTGGCAACAGGATCTGCTTACGTCGCTGGGTGAGCA 1108

66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
: : : : : : : : : : : : : : : : : : : : : : : : : :
1109 ACTTCGAGCTGATCCCAATCTCTGAACCTAGCAAGAAGACCTGGTTACAGAG 1158

83 AsnValLysTyrAsp.....MetAsnPheLysLysLeuLeuArgPh 96
: : : : : : : : : : : : : : : : : : : : : : : : : :
1159 TAGGGCCGATTGACCCAGGAGCCATGAACCTACACAAATTGATA...CT 1205

96 eMetGluAspPheIleGlyVal 104
: ||| ||| : : : : : : : : : :
1206 GAGTGAGAGGACCGCTTGGCATC 1230

```


seq_name: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV49345

seq_documentation_block:

ID AAV49345 standard; DNA; 1362 BP.

AC AAV49345;

DT 28-OCT-1998 (first entry)

DE Infectious bursal disease virus VP2 gene.

XX
XX
KW Multivalent vaccine; bird; pathogen; respiratory disease; MDV; NDV; IBDV;
KW digestive disease; Marek's disease virus; Newcastle disease virus; CAV;
KW infectious bursal disease virus; Gumboro disease virus; vaccine; IITV;
KW avian infectious bronchitis virus; IBV; chicken anaemia virus; AEV; PCR;
KW infectious laryngotracheitis virus; avian encephalomyelitis virus; TRTV;
KW turkey rhinotracheitis virus; influenza virus A avian; vector; primer;
KW amplification; glycoprotein; gallid herpesvirus; ss.

OS Infectious bursal disease virus of chickens.

FH Key Location/Qualifiers

FT CDS 1..1362

FT /*tag= a

FT /product= "VP2 protein"

XX FR2751225-A1.

XX 23-JAN-1998.

XX 19-JUL-1996; 96FR-0009339.

XX 19-JUL-1996; 96FR-0009339.

XX (INMR) RHONE MERIEUX SA.

XX Audonnet JCF, Bouchardon A, Riviere MEA;

XX WPI; 1998-112825/11.

XX P-PSDB; AAW44942.

XX Multi-valent polynucleotide vaccines against avian pathogens -

PT consist of at least 3 plasmids able to express protective antigens

PT from specified viruses

XX Example 11; Fig 8; 55pp; French.

XX The invention relates to a multivalent vaccine for protecting birds
CC against several pathogens, especially pathogens associated with
CC respiratory and digestive diseases. The pathogens are especially
CC selected from Marek's disease virus (MDV), Newcastle disease virus (NDV),
CC infectious bursal disease virus (IBDV), avian infectious bronchitis virus
CC (IBV), chicken anaemia virus (CAV), infectious laryngotracheitis virus
CC (IITV), avian encephalomyelitis virus (AEV), turkey rhinotracheitis virus
CC (TRTV) and influenza virus A avian (AIV). The vaccines are preferably
CC composed of polynucleotide sequences encoding 3 antigens, all as part
CC of vectors. This sequence represents the coding region of the IBDV
CC strain Faragher VP2 gene. The sequence was subcloned into the plasmid
CC pVR1012 to generate plasmid pAB048 for use in the vaccine.

XX Sequence 1362 BP; 370 A; 359 C; 341 G; 292 T; 0 other;

alignment_scores:

Quality: 73.00 Length: 125

Ratio: 1.259 Gaps: 6

Percent Similarity: 46.400 Percent Identity: 21.600

alignment_block:

US-09-528-682-3 x AAV49345 ..

Align seg 1/1 to: AAV49345 from: 1 to: 1362

16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
::: ||||| ::|||::|
886 ATTCCAACCAATGAGATAACCCAG.....CCAAT 914
32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
: ::::: :::::|
915 CACATCC.....ATCAAACTGGAGATAGTGACCTCCAAAAGTGGTGC 958
49 InAspGlyAsp.....LeuPheGlyThr 56
|| |||||
959 AGGCAGGGGATCAGATGTCTATGTCGGCAAGTGGGAGCCTAGCAGTGACG 1008
57 ValAsnGlnSerAsnPhePro..... 63
:::|:::|:::|
1009 ATCCATGGTGGCAACTATCCAGGGGCCCTCCGTCCTCACACTAGTAGC 1058
64MetSerT 66
:::|
1059 CTACGAAAGAGTGGCAACAGGATCCGTTACGGTCGCTGGGTGAGTA 1108
66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
::|||::|
1109 ACTTCGAGCTGATTCCAAATCCTGAACCTAGCAAGAACCTGGTTACAGAA 1158
83 AsnValLysTyrAsp.....MetAsnPheLysLysLeuLeuArgPh 96
:::|
1159 TACGGCCGATTTGCCAGGAGCCATGAACTACACAAATTTGATA...CT 1205
96 eMetGluAspAspPheIleGlyVal 104
: ||| ::|||
1206 GAGTGAGAGGGACCGCTTGGCATC 1230

seq_name: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:AAV43284

seq_documentation_block:

ID AAT43284 standard; cDNA; 2391 BP.

XX AAT43284;

XX 05-FEB-1997 (first entry)

XX Coding sequence for infective bursa protein #2.

XX Infective bursa; fabricius disease virus; poxvirus; vaccine;

XX domestic fowl; ss.

XX Fabricius disease virus.

XX JP08242869-A.

XX 24-SEP-1996.

XX 16-JAN-1996; 96JP-0023125.

XX 13-JAN-1995; 95JP-0021249.

XX (JAPG) JAPANESE GEON CO LTD.

XX WPI; 1996-479907/48.

XX P-PSDB; AAW08087.

XX Recombinant pox:virus containing Fabricius disease virus protein -

PT used in a vaccine to immunise domestic fowl

XX Claim 3; Page 13-16; 31pp; Japanese.

XX This sequence represents the coding sequence for a protein derived from
CC the infective bursa of Fabricius disease virus. This sequence was used
CC to create a recombinant poxvirus of the invention. The recombinant
CC poxvirus contains nucleotides 1-1359 of this sequence (i.e. the stop
CC codon is removed), inserted into a genomic region of the poxvirus. The
CC genomic region where this sequence is inserted is a region non-essential


```

XX AC AAQ31857;
XX DT 16-APR-1993 (first entry)
XX DE IBDV strain EDGAR segment A amplified by PCR.
XX KW Infectious Bursal Disease Virus; Gumboro's Disease; Birnaviridae;
XX KW chicken; Gallus; polymerase chain reaction; vaccine; ss.
XX OS Infectious Bursal Disease Virus.
XX FH Key
XX CDS Location/Qualifiers
XX     77..3115
XX     /*tag= a
XX     /product= 110kD-precursor
XX     /note= "VP2, VP3 and VP4 are generated by cleavage
XX           of the precursor encoded by ORF1"
XX CDS 43..480
XX     /*tag= b
XX     /label= ORF_2
XX     /note= "function as yet unknown"
XX CDS 11..43
XX     /*tag= c
XX     /label= ORF_3
XX     /note= "function as yet unknown"
XX     /*tag= d
XX     /label= Primer_0_binding_site
XX     complement (50..81)
XX     /*tag= e
XX     /label= Primer_1_binding_site
XX     574..604
XX     /*tag= f
XX     /label= Primer_1b_binding_site
XX     1147..1178
XX     /*tag= g
XX     /label= Primer_2_binding_site
XX     complement (1179..1208)
XX     /*tag= h
XX     /label= Primer_3_binding_site
XX     1817..1849
XX     /*tag= i
XX     /label= Primer_4_binding_site
XX     complement (1844..1883)
XX     /*tag= j
XX     /label= Primer_5_binding_site
XX EP517292-A.
XX PD 09-DEC-1992.
XX PF 19-MAY-1992; 92EP-0201406.
XX PR 27-MAY-1991; 91BE-0000507.
XX PA (SOLV ) SOLVAY SA.
XX PI Colau D, De Wannemaeker C, Malarne D, Thiry G, Malarne D;
XX WPI; 1992-408761/50.
XX DR P-PSDB; AAR29277, AAR29278, AAR29279.
XX PT New recombinant avipox virus for use in vaccines - contg.
XX PT sequence encoding heterologous antigen in inter-gene region of
XX PT terminal inverted repeat
XX PS Example 19; Fig 9; 53pp; French.
XX CC IBDV EDGAR strain viral RNA was isolated from infected chickens and
XX CC reverse transcribed to cDNA using four pairs of primers. The primer
XX CC sequences were designed based on known IBDV segment A sequences from
XX CC the Australian strain 002-73, the German strain CU-1 and the British

```

```

CC strain 52/70 (see AAQ31858-Q31865 for sequences of primers 0, 1, 1b,
CC 2, 3, 4, 5 and 6, respectively; the primer 6 binding site is not
CC shown in the Features Table as this primer binds immediately
CC downstream of the segment A sequence). The resulting ds cDNA fragments
CC were subcloned, sequenced and aligned to give the full-length sequence.
CC The EDGAR strain sequences which were replaced by using primers based
CC on other sequences were then determined using primers situated outside
CC them and based on the EDGAR sequence. Segment A contains 3 ORFs, of
CC which ORF1 is the most important. The PCR-amplified segment A fragment
CC was inserted into a non-coding region of a transfer vector derived from
CC an attenuated Fowlpox virus, esp, into one of the terminal inverted
CC Repeat regions. The recombinant vector was then used to vaccinate chicks
XX against Gumboro's disease.
XX SQ Sequence 3115 BP; 843 A; 856 C; 799 G; 617 T; 0 other;

alignment_scores:
    Quality: 73.00      Length: 125
    Ratio: 1.259        Gaps: 6
    Percent Similarity: 46.400      Percent Identity: 21.600

alignment_block:
US-09-528-682-3 x AAQ31857 ..
Align seg 1/1 to: AAQ31857 from: 1 to: 3115

16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
   ::: ||||| ::|||
962 ATTCCGACCAACGAGATAACCCAG.....CCAAAT 990

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetG 49
   :::: ::::: ::::: ::::: ::::: ::::: ::::: |||
991 CACATCC.....ATCAAACTGGAGATAGTACCTCCAAAAGTGGCGGTC 1034

49 InAspGlyAsp.....::: ::::: ::::: ::::: ::::: |||
   || |||||
1035 AGCGAGGGGACCAAGATGTCATGTGCGCAAGTGGGAGCCTAGCAGTGACA 1084

57 ValAsnGlnSerAsnPhePro.....MetSert 66
   ::::: ::|||::|||
1085 ATCCATGGTGGCAACTATCCAGGGGCCCTCCGTCGCTCACACTAGTAGC 1134

64 .....
1135 CTACGAAGAGTGGCAACAGGATCCGTCGTTACGGTAGCCGGGTGAGCA 1184

66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
   ::|||::: ::|||::: ::: ||::: :::::
1185 ACTTCGAGCTGATCCCAATCTCTGAAGTACGAAAGAACCTGGTTACAGAA 1234

83 AsnValLysTyrAsp.....MetAsnPheLysLysLeuLeuArgPh 96
   ::::: ||| ::|||::: |||||::: |||||::: ::
1235 TAGCGCCGATTTGACCCAGGAGGCATGACTACACAAAATTGATA...CT 1281

96 eMetGluAspPheIleGlyVal 104
   : ||| ||| ::|||:::
1282 GACTGAGAGGACCGCTCTGGCATC 1306

seq_name: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:AAQ42757
seq_documentation_block:
ID AAQ42757 standard; DNA; 3257 BP.
XX
XX AC AAQ42757;
XX DT 25-NOV-1993 (first entry)
XX DE IBDV gene sequence.
XX KW Attenuated; vaccine; herpes virus; non-primate; live; safer; IBR;
XX KW infectious bovine rhinotracheitis; MDV; Marek's disease virus; fowl;
XX KW pseudo-rabies; swine; infectious bursal disease virus; ss.

```


Ratio: 1.259 Gaps: 6
Percent Similarity: 46.400 Percent Identity: 21.600
alignment_block:
US-09-528-682-3 x AAV26605 ..
Align seg 1/1 to: AAV26605 from: 1 to: 3257
16 ValAsnThrValThrValThrGlnIleAsnGlySerAsnGluValProLe 32
::: ||||| ::|||
1014 ATTCCAAACACGAGATACCCAG.....CCAAAT 1042
32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
: ::::: ::|||
1043 CACATCC.....ATCAAACTGGAGATAGTGACCTCCAAAAGTGGTGTC 1086
49 lNaspGlyAsp.....LeuPheGlyThr 56
|| ||||| |||
1087 AGCAGGGGATCAGATGTTATGTCGGCAAGAGGGAGCCCTAGCAGTGACG 1136
57 ValAsnGlnSerAsnPhePro..... 63
1137 ATCCATGGTGGCAACTATCCAGGGGCCCTCCGTCCTCAGCTAGTGCG 1186
64MetSert 66
1187 CTACGAAAGAGTGGCAACAGGATCCGTCGTACGGTCGCTGGGTGAGCA 1236
66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
: ||||| ::|||
1237 ACTTCGAGCTGATCCCAATCTGAATAGCAAAAGACCTGGTTACAGAA 1286
83 AsnValLysTyrAsp.....MetAsnPheLysLysLeuLeuArgPh 96
: ::::: |||||
1287 TAGCGCGGATTTACCCAGGAGCCATGACACTACACAAATTTGATA...CT 1333
96 eMetGluAspPheIleGlyVal 104
: ||| ||| ::|||
1334 GAGTGAGGGGACCGCTTGGCATC 1358
seq_name: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV26605
seq_documentation_block:
ID AAV26605 standard; CDNA; 3261 BP.
XX
AC AAV26605;
XX
DT 28-AUG-1998 (first entry)
XX
DE Plasmid pUC19FLAD78 containing IBDV segment A CDNA.
XX
KW Plasmid pUC19FLAD78; IBDV; Gumboro disease; vaccine;
KW synthetic RNA transcript; reverse genetics; VP2; VP3; VP4; VP5;
KW ss; cyclic; circular.
XX
OS Infectious bursal disease virus strain D78.
XX
FH Key Location/Qualifiers
FT CDS 97..534
FT /tag= a
FT /product= vp5
FT 131..3169
FT CDS
FT /tag= b
FT /product= vp2-vp4-vp3
XX
PN WO9809646-A1.
XX
PD 12-MAR-1998.
XX
PF 31-JUL-1997; 97WO-US12955.
XX
PR 05-SEP-1996; 96US-0708541.
XX

(UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
Mundt E, Vakharlia VN;
WPI: 1998-193322/17.
DR P-PSDB; AAW54374-75.
XX
PT Generation of live birnavirus from synthetic RNA transcripts -
useful for vaccines against infectious bursal disease
XX
PS Example 1; Fig 5A-B; 84pp; English.
XX
CC Plasmid pUC19FLAD78 contains infectious bursal disease virus (IBDV)
strain D78 segment A CDNA that encodes the polyprotein VP2-VP4-VP3
CC (see AAW54375) and the newly identified non-structural protein VP5
CC (see AAW54374). It was obtained by RT-PCR amplification (see
CC AAV26592-95) of strain D78 RNA and cloning into vector pUC19. In a
CC new reverse genetics system for IBDV, 3 independent full-length
CC CDNA clones (see also AAV26604 and AAV26606) were constructed which
CC contain segment A of serotype I strain D78 or serotype II strain
CC 23/82 and segment B of the serotype I strain P2. Synthetic RNAs of
CC segments A and B were produced by in vitro transcription of
CC linearised plasmids with T7 RNA polymerase. Transfection of Vero
CC cells with combined plus strand transcripts of both segments
CC generated infectious virus. The development of a reverse genetics
CC system for double-stranded RNA viruses will facilitate studies of
CC the regulation of viral gene expression pathogenesis, and design of
CC a new generation of live and inactivated vaccines.
XX
SQ Sequence 3261 BP; 873 A; 909 C; 847 G; 632 T; 0 other;

alignment_scores:
Quality: 73.00 Length: 125
Ratio: 1.259 Gaps: 6
Percent Similarity: 46.400 Percent Identity: 21.600
alignment_block:
US-09-528-682-3 x AAV26605 ..
Align seg 1/1 to: AAV26605 from: 1 to: 3261
16 ValAsnThrValThrValThrGlnIleAsnGlySerAsnGluValProLe 32
::: ||||| ::|||
1016 ATTCCAAACACGAGATACCCAG.....CCAAAT 1044
32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
: ::::: ::|||
1045 CACATCC.....ATCAAACTGGAGATAGTGACCTCCAAAAGTGGTGTC 1088
49 lNaspGlyAsp.....LeuPheGlyThr 56
|| ||||| |||
1089 AGCAGGGGATCAGATGTCATGTCGGCAAGAGGGAGCCCTAGCAGTGACG 1138
57 ValAsnGlnSerAsnPhePro..... 63
1139 ATCCATGGTGGCAACTATCCAGGGGCCCTCCGTCCTCAGCTAGTGCG 1188
64MetSert 66
1189 CTACGAAAGAGTGGCAACAGGATCCGTCGTACGGTCGCTGGGTGAGCA 1238
66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
: ||||| ::|||
1239 ACTTCGAGCTGATCCCAATCTGAATAGCAAAAGACCTGGTTACAGAA 1288
83 AsnValLysTyrAsp.....MetAsnPheLysLysLeuLeuArgPh 96
: ::::: |||||
1289 TAGCGCGGATTTACCCAGGAGCCATGACACTACACAAATTTGATA...CT 1335
96 eMetGluAspPheIleGlyVal 104
: ||| ||| ::|||
1336 GAGTGAGGGGACCGCTTGGCATC 1360

CC programs other than by vaccination against very virulent strains of IBDV,
 CC as it allows separation of infected animals prior to commencing the
 CC program, to reduce spread of disease. This vaccine comprises the first
 CC birnavirus mutant with a mutation in a non-essential region, which is
 CC also able to elicit a major serological response. The present sequence
 CC represents a cDNA sequence of segment A of IBDV strain D78 encoding the
 CC VP5 protein. The mutant of the invention is derived from this sequence.
 XX
 SQ Sequence 3261 BP; 873 A; 909 C; 847 G; 632 T; 0 other;

alignment_scores:
 Quality: 73.00 Length: 125
 Ratio: 1.259 Gaps: 6
 Percent Similarity: 46.400 Percent Identity: 21.600

alignment_block:

US-09-528-682-3 x AAV99789 ..

Align seg 1/1 to: AAV99789 from: 1 to: 3261

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16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
   ::: ||||| ::: |||||
1016 ATTCCAACAACGAGATAACCCAG.....CCAAAT 1044

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetG 49
   ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
1045 CACATCC.....ATCAAACTGGAGTAGTGACCTCCAAAGAGTGTGGTC 1088

49 InAspGlyAsp.....LeuPheGlyThr 56
   || |||||
1089 AGCGAGGGATCATGATGTCGTGCGCAAGAGGAGCCCTAGCAGTGACG 1138

57 ValAsnGlnSerAsnPhePro.....MetSerT 66
   ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
1139 ATCCATGTTGGCAACTATCCAGGGGCCCTCCGTCGTCACGCTAGTGCG 1188

64 .....MetSerT 66
1189 CTACGAAAGAGTGGCAACAGGATCCGTCGTACGGTCGCTGGGTGAGCA 1238

66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
   ::: ||||| ::: ||||| ::: ||||| ::: ||||| ::: |||||
1239 ACTTCGAGCTGATCCAAATCTCTGAAGTACGAAAGAACCTGTTACAGAA 1288

83 AsnValLysTyrAsp.....MetAsnPheLysLysLeuLeuArgPh 96
   ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
1289 TACGCCCGATTTGACCCAGGAGCCATGAAGTACACAAAATTGATA...CT 1335

96 eMetGluAspAspPheIleGlyVal 104
   : ||| ||| ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
1336 GAGTGAGAGGGACCGCTCTGGGCATC 1360

```

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.AAV99790

seq_documentation_block:

ID AAV99790 standard; cDNA; 3261 BP.

AC AAV99790;

DT 26-MAR-1999 (first entry)

DE cDNA sequence of segment A of IBDV strain D78 encoding VP polypeptide.

XX Birnavirus; mutant; VP5 protein; vaccine; IBDV; Infection; IPNV;
 KW Infectious bursal disease virus; Infectious pancreatic necrosis virus;
 KW marker; polyprotein; ss.

OS Infectious bursal disease virus.

XX Key Location/Qualifiers

FT CDS 131..3169

FT /*tag= a

```

FT /product= "VP2-VP3-VP4 polypeptide"
PN EP887412-A1.
XX 30-DEC-1998.
XX 22-MAY-1998; 98EP-0201704.
XX 26-MAY-1997; 97EP-0201599.
XX (ALKU ) AKZO NOBEL NV.
XX Luetticken HD, Mundt E, Van Loon AAWM;
PI WPI; 1999-047879/05.
XX P-PSDB; AAW95395.
XX New recombinant birnavirus mutant containing a mutated VP5 gene -
PT useful as a vaccine against Infectious Bursal Disease Virus, and for
PT distinguishing between vaccinated and naturally infected animals
XX Disclosure; Pages 30-36; 53pp; English.
XX The invention provides a birnavirus mutant which has a mutation in the
CC VP5 gene. The new birnavirus mutant is useful as a vaccine against
CC birnavirus infections in animals, especially against infectious bursal
CC disease virus (IBDV) and infectious pancreatic necrosis virus (IPNV). The
CC lack of native VP5 protein expression in the recombinant VP5 mutant
CC vaccine is useful as a marker to distinguish vaccinated animals from
CC animals infected with naturally-occurring birnavirus. This is because the
CC anti-sera from naturally-occurring birnavirus has antibodies directed to
CC the non-structural VP5 protein. This method is useful for new eradication
CC programs other than by vaccination against very virulent strains of IBDV,
CC as it allows separation of infected animals prior to commencing the
CC program, to reduce spread of disease. This vaccine comprises the first
CC birnavirus mutant with a mutation in a non-essential region, which is
CC also able to elicit a major serological response. The present sequence
CC represents a cDNA sequence of segment A of IBDV strain D78 encoding the
CC VP2-VP3-VP4 polypeptide.
XX SQ Sequence 3261 BP; 873 A; 909 C; 847 G; 632 T; 0 other;

```

alignment_scores:

Quality: 73.00 Length: 125
 Ratio: 1.259 Gaps: 6
 Percent Similarity: 46.400 Percent Identity: 21.600

alignment_block:

US-09-528-682-3 x AAV99790 ..

Align seg 1/1 to: AAV99790 from: 1 to: 3261

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16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
   ::: ||||| ::: |||||
1016 ATTCCAACAACGAGATAACCCAG.....CCAAAT 1044

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetG 49
   : ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
1045 CACATCC.....ATCAAACTGGAGTAGTGACCTCCAAAGTGTGGTC 1088

49 InAspGlyAsp.....LeuPheGlyThr 56
   || |||||
1089 AGCGAGGGATCATGATGTCGTGCGCAAGAGGAGCCCTAGCAGTGACG 1138

57 ValAsnGlnSerAsnPhePro.....MetSerT 66
   ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
1139 ATCCATGTTGGCAACTATCCAGGGGCCCTCCGTCGTCACGCTAGTGCG 1188

64 .....MetSerT 66
1189 CTACGAAAGAGTGGCAACAGGATCCGTCGTACGGTCGCTGGGTGAGCA 1238

```


PT New method of expressing insecticidal proteins in plants transformed
 PT with a bacillus thuringiensis delta-endotoxin encoding gene resulting
 PT in effective control of susceptible target pests -
 XX
 PS
 PS Claim 12; Page 81; 104pp; English.
 XX
 XX The present sequence is the cry2Ab delta-endotoxin gene. Delta-endotoxins
 CC are produced by *Bacillus thuringiensis* during sporulation. These proteins
 CC are toxic to certain species of insect e.g. Lepidopteran and Coleopteran
 CC larvae. An insect-resistant transgenic plant has been constructed which
 CC contains the present sequence. The cry2Ab gene would be transferred into
 CC plants via expression vectors, which subsequently allow high expression
 CC of the cry2Ab gene. The present sequence lacks Dipteran inhibitory
 CC activity. Protection may be attained against insects such as *Ostrinia*
 CC spp., *Diatraea* spp., *Helicoverpa* spp., and *Spodoptera* spp., in *Zea*
 CC mays; *Heliothis virescens*, *Helicoverpa* spp., *Pectinophora* spp., in *Zea*
 CC mays; *Gossypium hirsutum*; *Anticarsa* spp., *Pseudoplusia* spp., *Epinotia* spp., in
 CC Glycine max; and *Scirpophaga incertulas* in *Oryza sativa*. Expression of
 CC the present sequence by a plant cell produces a fusion protein comprising
 CC an amino-terminal plastid transit peptide (PTP) covalently linked to the
 CC delta-endotoxin. The fusion protein functions to localise the
 CC delta-endotoxin to a subcellular organelle or compartment.
 XX
 SQ Sequence 1934 BP; 438 A; 678 C; 442 G; 376 T; 0 other;

alignment_scores:

Quality	71.00	Length:
Ratio: 1.690		Gaps: 4
Percent Similarity: 59.155	Percent Identity: 33.803	

alignment_block:

US-09-528-682-3 x AAA15556 ..

Align seg 1/1 to: AAA15556 from: 1 to: 1934

11 TyrGluProIleGluValAsnThrAsnThrValThrGlnIleAsnGly.. 26
 ||||| :|||||:|||||:||||| :||| :|||||
 894 TATTGGTTGTTCCAAAGTCAACTCCAACTACGTC.....CTCAACGGCTT 937

27SerAsnGluValPro.....LeuAspG 34
 ||||| ||| ||| |||
 938 CTCGGTCTCGCTCTCCACACCTTCCCAACATTGTTGGCTCCCG 987

34 IyArgTyfSerAsnPheAlaLeuIleSerAla.....GluCly 46
 || :|||: |||||:|||||:||||| :|||
 988 GCTCCACCACAACTCATGCTCTGCTTGTGCGCAGAGTCACTACTCCGGC 1037

47 GlyMetGlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPhePr 63
 |||||:|||||:|||||:||||| :|||:|||||
 1038 GGCAFTCTCGAGCGGACATTGGTGCAFTCCGCGTCAACACGAACTTCAA 1087

63 oMetSerThrPhe 67
 ||||| |||
 1088 CTGCTCCACCTTC 1100

seq_name: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAAC48833

seq_documentation_block:

ID AAC48833 standard; DNA; 2154 BP.

XX AAC48833;

AC AAC48833;

XX 18-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 58940.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

OS

XX

PN	EP1033405-A2.
XX	9905-0121825.
PD	9905-0123180.
XX	9905-0123548.
XX	9905-0125788.
XX	9905-0126264.
XX	9905-0126785.
XX	9905-0127462.
XX	9905-0128234.
XX	9905-0128714.
XX	9905-0129845.
XX	9905-0130077.
XX	9905-0130449.
XX	9905-0130510.
XX	9905-0130891.
XX	9905-0131449.
XX	9905-0132048.
XX	9905-0132407.
XX	9905-0132484.
XX	9905-0132485.
XX	9905-0132486.
XX	9905-0132487.
XX	9905-0132863.
XX	9905-0134256.
XX	9905-0134218.
XX	9905-0134219.
XX	9905-0134221.
XX	9905-0134370.
XX	9905-0134768.
XX	9905-0134941.
XX	9905-0135124.
XX	9905-0135353.
XX	9905-0135629.
XX	9905-0136021.
XX	9905-0136392.
XX	9905-0136782.
XX	9905-0137222.
XX	9905-0137528.
XX	9905-0137502.
XX	9905-0137724.
XX	9905-0138094.
XX	9905-0138540.
XX	9905-0138847.
XX	9905-0139119.
XX	9905-0139452.
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XX	9905-0139460.
XX	9905-0139461.
XX	9905-0139462.
XX	9905-0139463.
XX	9905-0139750.
XX	9905-0139763.
XX	9905-0139817.
XX	9905-0139899.
XX	9905-0140353.
XX	9905-0140354.
XX	9905-0140695.
XX	9905-0140823.
XX	9905-0140991.
XX	9905-0141287.
XX	9905-0141842.

PI Corblin DR, Romano CP;
 XX WPI; 2000-376130/32.
 XX
 XX
 PT New method of expressing insecticidal proteins in plants transformed
 PT with a Bacillus thuringiensis delta-endotoxin encoding gene resulting
 PT in effective control of susceptible target pests -
 XX
 XX
 XX Claim 26; Page 93-96; 104pp; English.
 PS
 XX
 CC Bacillus thuringiensis produce delta-endotoxins during sporulation. These
 CC proteins are toxic to certain insects e.g. Lepidopteran and Coleopteran
 CC larvae. An insect-resistant transgenic plant has been constructed which
 CC contains the delta-endotoxin cry2Ab gene. The present sequence would be
 CC used to transfer delta-endotoxin genes into plant cells and for
 CC subsequent high expression of the cry2Ab gene. Protection may be attained
 CC against insects such as Ostrina spp., Diatraea spp., Helicoverpa spp.,
 CC and Spodoptera spp., in Zea mays; Heliothis virescens, Helicoverpa spp.,
 CC Pectinophora spp., in Gossypium hirsutum; Anticarsia spp., Pseudoplusia
 CC spp., Epinotia spp., in Glycine max; and Scirpophaga incertulas in Oryza
 CC sativa. Expression of the endotoxin by a plant cell produces a fusion
 CC protein comprising an amino-terminal plastid transit peptide 2 (PTP2)
 CC covalently linked to the delta-endotoxin. The fusion protein functions to
 CC localise the delta-endotoxin to a subcellular organelle or compartment.
 XX
 SQ Sequence 10312 BP; 2391 A; 2853 C; 2577 G; 2363 T; 128 other;

alignment_scores:
 Quality: 71.00 Length: 71
 Ratio: 1.690 Gaps: 4
 Percent Similarity: 59.155 Percent Identity: 33.803

alignment_block:

US-09-528-682-3 x AAAL5564 ..

Align seg 1/1 to: AAAL5564 from: 1 to: 10312

11 TyrGluProIleGluValAsnThrValThrGlnIleAsnGly.. 26
 |||::: : : : : : |||::: ||| : : : : : :
 1860 TATTCTGTTGTTCAAGTCAACTCCCACTAGTC.....CTCAACGGCTT 1903
 CC
 27SerAsnGluValPro.....LeuAspG 34
 |||::: : : : : : ||| : : : : : :
 1904 CTCCTGGTGTCTGCTCTCCCAACACCTTCCCACTATTGTTGGCTCCCG 1953
 CC
 34 lyArgTyrSerAsnPheAlaLeuIleSerAla.....GluGly 46
 |||::: : : : : : |||::: : : : : :
 1954 GCTCCACCAACAACATCATGCTCTGCTGCTGCCAGAGTGAAGTACTCCGGC 2003
 CC
 47 GlyMetGlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPhePr 63
 |||::: : : : : : |||::: : : : : :
 2004 GGCATCTCGAGCGCGACATTGGTGTGATCGCCGTTCAACCAAGACTTCAA 2053
 CC
 63 oMetSerThrPhe 67
 |||::: : : : : :
 2054 CTGCTCCACCTTC 2066

seq_name: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAAL5562

seq_documentation_block:

ID AAAL5562 standard; DNA; 10339 BP.

XX

AC AAAL5562;

XX

DT 28-JUL-2000 (first entry)

XX

DE pMON33827 plasmid.

XX

KW Transgenic plant; insect resistance; cry2Aa delta-endotoxin; Coleopteran;

KW Lepidopteran; Dipteran; plastid transit peptide; ptp1; insecticidal;

KW plasmid targeting peptide; pMON33827 plasmid; expression vector; ds.

XX

OS Synthetic.
 XX
 XX WO200026371-A1.
 XX
 XX
 PD 11-MAY-2000.
 XX
 XX
 PF 04-NOV-1999; 99WO-US26086.
 XX
 XX
 PR 04-NOV-1998; 98US-0186002.
 XX
 XX
 PA (MONS) MONSANTO CO.
 XX
 XX Corblin DR, Romano CP;
 PI
 XX
 DR WPI; 2000-376130/32.
 XX
 XX
 PT New method of expressing insecticidal proteins in plants transformed
 PT with a Bacillus thuringiensis delta-endotoxin encoding gene resulting
 PT in effective control of susceptible target pests -
 XX
 XX
 PS Claim 24; Page 87-90; 104pp; English.

CC Bacillus thuringiensis produce delta-endotoxins during sporulation. These
 CC proteins are toxic to certain insects e.g. Lepidopteran and Coleopteran
 CC larvae. An insect-resistant transgenic plant has been constructed which
 CC contains the delta-endotoxin cry2Ab gene. The present sequence would be
 CC used to transfer delta-endotoxin genes into plant cells and for
 CC subsequent high expression of the cry2Ab gene. Protection may be attained
 CC against insects such as Ostrina spp., Diatraea spp., Helicoverpa spp.,
 CC and Spodoptera spp., in Zea mays; Heliothis virescens, Helicoverpa spp.,
 CC Pectinophora spp., in Gossypium hirsutum; Anticarsia spp., Pseudoplusia
 CC spp., Epinotia spp., in Glycine max; and Scirpophaga incertulas in Oryza
 CC sativa. Expression of the endotoxin by a plant cell produces a fusion
 CC protein comprising an amino-terminal plastid transit peptide (PTP1)
 CC covalently linked to the delta-endotoxin. The fusion protein functions to
 CC localise the delta-endotoxin to a subcellular organelle or compartment.
 XX
 SQ Sequence 10339 BP; 2393 A; 2877 C; 2579 G; 2362 T; 128 other;

alignment_scores:
 Quality: 71.00 Length: 71
 Ratio: 1.690 Gaps: 4
 Percent Similarity: 59.155 Percent Identity: 33.803

alignment_block:

US-09-528-682-3 x AAAL5562 ..

Align seg 1/1 to: AAAL5562 from: 1 to: 10339

11 TyrGluProIleGluValAsnThrValThrGlnIleAsnGly.. 26
 |||::: : : : : : |||::: ||| : : : : : :
 1887 TATTCTGTTGTTCAAGTCAACTCCCACTAGTC.....CTCAACGGCTT 1930
 CC
 27SerAsnGluValPro.....LeuAspG 34
 |||::: : : : : : ||| : : : : : :
 1931 CTCCTGGTGTCTGCTCTCCCAACACCTTCCCACTATTGTTGGCTCCCG 1980
 CC
 34 lyArgTyrSerAsnPheAlaLeuIleSerAla.....GluGly 46
 |||::: : : : : : |||::: : : : : :
 1981 GCTCCACCAACAACATCATGCTCTGCTGCTGCCAGAGTGAAGTACTCCGGC 2030
 CC
 47 GlyMetGlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPhePr 63
 |||::: : : : : : |||::: : : : : :
 2031 GGCATCTCGAGCGCGACATTGGTGTGATCGCCGTTCAACCAAGACTTCAA 2080
 CC
 63 oMetSerThrPhe 67
 |||::: : : : : :
 2081 CTGCTCCACCTTC 2093

seq_name: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:AAQ46181

seq_documentation_block:

CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 2937 BP; 1192 A; 480 C; 601 G; 664 T; 0 other;

alignment_scores:
 Quality: 70.00 Length: 117
 Ratio: 1.129 Gaps: 5
 Percent Similarity: 52.991 Percent Identity: 23.077

alignment_block:
 US-09-528-682-3 x AAS51819 ..

Align seg 1/1 to: AAS51819 from: 1 to: 2937

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13 ProfileGluValAsn.....ThrAsnThrValThrGlnIleAsnG1 26
||||| ||| :|||: :|||: |||
928 CCAATAGAATATAATCCAGGAGTAAGTAATAGCTATGCTAATGTAATGG 977

26 ySerAsnGluValProLeuAspGly.....ArgTyrSerAsnPheAlaL 41
||| |||: ||| |||: |||: |||
978 TTCATTGAACCTTCGATAAGGAATAATAGATCACTCATGTGGCTT 1027

41 euIleSerAlaGluGlyMetGlnAspGly.....AspLeuPheGly 55
|||: |||: |||: |||: |||: |||
1028 ACATAAACCCACAAATGGGCATAATCAGATAGCGTTTCAATTACTGGT 1077

56 ThrValAsnGln..... 59
|||: |||: |||: |||: |||: |||
1078 ACATTAACTCAAGGTAGTAAGCAGATGGGAGGCTCCTACTGTAAAGT 1127

60 .....SerAsnPheProMetSerThrPheGluG 69
||||| |||: |||: |||: |||: |||: |||
1128 ATATGAAGTTTAAAGGATGCTAATGAATACCAAAAGTGTATACGCAA 1177

69 InValProAsnAsnLysGluPheLysGlyVal..... 79
||| |||: |||: |||: |||: |||: |||
1178 ATGTATCAGATCTTCATGTTTAAAGATGTAAGTGAAGAAATGAAGAT 1227

80 .....IleSerAlaAsnValLysTyrAspMetAsnPheLysLysLe 93
||||| |||: |||: |||: |||: |||: |||
1228 AAATTTAAAGTAGAATAATGAAGTAAATAGATATATGATAATGAAAT 1277

93 u 93
|
1278 A 1278

```

seq_name: /SID5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:AAS54951

seq_documentation_block:
 ID AAS54951 standard; DNA; 3006 BP.

AC AAS54951;

XX 13-FEB-2002 (first entry)

DE Staphylococcus aureus DNA for cellular proliferation protein #1263.

XX Antisense; ds; prokaryotic cellular proliferation gene;
 KW antibiotic; antibacterial; drug design.

XX Staphylococcus aureus.

PN W0200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US09180.

XX 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

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PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR P-PSDB; AAU37092.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
PT
XX
PS Claim 27; Seq ID No 8588; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: the sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3006 BP; 1220 A; 490 C; 616 G; 680 T; 0 other;

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alignment_scores:

Quality: 70.00 Length: 117
 Ratio: 1.129 Gaps: 5
 Percent Similarity: 52.991 Percent Identity: 23.077

alignment_block:

US-09-528-682-3 x AAS54951 ..

Align seg 1/1 to: AAS54951 from: 1 to: 3006

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13 ProfileGluValAsn.....ThrAsnThrValThrGlnIleAsnG1 26
||||| ||| :|||: :|||: |||
997 CCAATAGAATATAATCCAGGAGTAAGTAATAGCTATGCTAATGTAATGG 1046

26 ySerAsnGluValProLeuAspGly.....ArgTyrSerAsnPheAlaL 41
||| |||: ||| |||: |||: |||
1047 TTCATTGAACCTTCGATAAGGAATAATAGATCACTCATGTGGCTT 1096

41 euIleSerAlaGluGlyMetGlnAspGly.....AspLeuPheGly 55
||||| |||: |||: |||: |||: |||: |||
1097 ACATAAAAGCCACAAATGGCATAATCAGATAGCGTTTCAATTACTGGT 1146

56 ThrValAsnGln..... 59
|||: |||: |||: |||: |||: |||
1147 ACATTAACTCAAGGTAGTAAGCAGATGGGAGGCTCCTACTGTAAAGT 1196

60 .....SerAsnPheProMetSerThrPheGluG 69
||||| |||: |||: |||: |||: |||: |||
1197 ATATGAAGTTTAAAGGATGCTAATGAATACCAAAAGTGTATACGCAA 1246

69 InValProAsnAsnLysGluPheLysGlyVal..... 79

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alignment_block:
  US-09-528-682-3 x AAZ60605      ..
  Align seg 1/1 to: AAZ60605 from: 1 to: 5398

  21 ValThrGlnIleAsnGlySerAsnGluValProLeuAspGlyArg..... 35
  |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
  2044 GTAGATAGTGTCATCATCTAGTTTCAGTTCCTGTCGGTAAACGTAA 2093

  36 .....TyrSerAsnPhea 40
  |||:||||:||||:||||:||||:||||:||||:||||:||||:

  2094 TGTAAGTACCCAGTACAACGGATACATTGACTCCAATGAGATCATCATTC 2143

  40 IaLeuIleSerAlaGluGlyGlyMetGlnAspGlyAspLeuPheGlyThr 56
  |||:||||:||||:||||:||||:||||:||||:||||:||||:

  2144 GTACAGTCAAT...GAGACGATATGGAAAATTTCTCAGTCTTAGGTCCA 2190

  57 ValAsnGlnSerAsn.....PheProMetSe 65
  |||:||||:||||:||||:||||:||||:||||:||||:||||:

  2191 AGAAATAGTGGTTAAATTCGTCTGTACACCAAGGACTTCAATCAAAATTC 2240

  65 rThrPheGluGlnVal...ProAsnAsnLysGluPheLysGlyValIles 81
  |||:||||:||||:||||:||||:||||:||||:||||:||||:
  2241 TACTTTGGGAAGATTTTTCACCGCTCCCAACAAAAATTTTAAAGTCAGCTAAAT 2290

  81 erAlaAsnValLysTyrAspMetAsnPheLysLysLeuLeuArgPheMet 97
  |||:||||:||||:||||:||||:||||:||||:||||:||||:

  2291 CGATTTCAGAAATGGTTGATGGGAATTCCTGANAATTTTAAAGGCATGTT 2340

  98 Glu 98
  ::
  2341 CAG 2343

```

seq_name: /SIDS5/qcadata/qeneseq-emb1/NA2000.DAT:AAA81463

seq_documentation_block:

AC AAA81463:

XXXX

DT 04-DEC-2000 (first entry)

04 DEC 2000 (1130 energy) YY

DE Nominativus masculinus singularis

DE N. MENTIGLIANI PARCERAI DN
vv[illegible]

MY
NETSSTP

KW antigen; vaccine; diagnosis

KW Meningococcus B; MenB; as:

[illegible]OS *Neisseria meningitidis*.

XX

PN WO200022430-A2.

XX

PD 20-APR-2000.

XX

PF 08-OCT-1999; 99WO-US2357

XX

PR 09-OCT-1998; 98US-010379

PR 30-APR-1999; 99US-013206

XX

PA (CHIR) CHIRON CORP.

XX

PI Frazer CM. Hickey E. Pet

PT Masignani V. Galeotti C.

PT Rappuoli R. pizza M:

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 11-10-34
 11-10-34

WPT: 2000-318079/27

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NET, 2000 310013/21.

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used in the development and
 of a program to protect
 and maintain the
 integrity of the
 system.

PI Used in the diagnosis and

Other Neisserial infection

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PS Claim 7; Page 330-353; 176

XX

CC The present invention describes methods of obtaining immunogenic
 CC proteins from *Neisseria* genomic sequences. AAA81453 to AAA82414
 CC represent specifically claimed *Neisseria meningitidis* genomic DNA
 CC sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
 CC *Neisseria* DNA sequences and their corresponding proteins; AAA81254 to
 CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
 CC isolation of *Neisseria meningitidis* DNA sequences; and AAA81322 to
 CC AAA81452 represent *Neisseria meningitidis* MenB polynucleotide ORF
 CC sequences, which are all used in the exemplification of the present
 CC invention. The nucleic acid sequences, protein sequences, and antibodies
 CC against them, can be used in the manufacture of a composition. The
 CC composition can be used as a medicament (or in the manufacture of a
 CC medicament) for treating, preventing or diagnosing infection due to
 CC *Neisseria* bacteria. For example, some of the identified proteins could
 CC be components of vaccines against *Meningococcus* B; against all serotypes;
 CC and/or against all pathogenic *Neisseriae*. Identification of sequences
 CC from the bacterium will also facilitate production of biological probes,
 CC particularly organism-specific probes. Attempts to make efficacious
 CC *Meningococcus* B vaccines have failed mainly due to antigen tolerance.
 CC Multivalent vaccines have also been tried but none have successfully
 CC overcome antigenic variability. The provision of further, complete
 CC sequences may provide an opportunity to identify secreted or surface
 CC exposed proteins that may be presumed targets for the immune system and
 CC which are not antigenically variable or at least more conserved than
 CC other more variable regions.

XX
 SQ Sequence 78845 BP; 19372 A; 21111 C; 19042 G; 19318 T; 2 other;

alignment_scores:
 Quality: 70.00 Length: 123
 Ratio: 1.111 Gaps: 6
 Percent Similarity: 51.220 Percent Identity: 26.829

alignment_block:

US-09-528-682-3 x AAA81463 ..

Align seg 1/1 to: AAA81463 from: 1 to: 78845

```

9 GlnAlaTyrgluProileGluValAsnThrAsnThrValThrGlnIleAs 25
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
8732 :AAGCGCAGTAGATCCGATTGTCTTCCCTCACCGCGCCTACCGCATCAA 8781
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:
25 nGlySerAsnGluValProLeuAspGlyArgTyr.....SerAsnPheA 40
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:
8782 :CGCGACGAAACCCCTTTCAGAGCGCATCCGCTACAAATCGGGCACTACC 8831
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:
40 IaLeu.....IleSerAla 44
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:
8832 :TGCTGCTCAACCCCAACATCTCAATTGTGTCACAGCAGAAATCAGCCTG 8881
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:
45 GluGlyGlyMetGln.....AspGlyAs 52
  :|||:|||||:|||||:|||||:|||||:|||||:|||||:
8882 :ACCGAGGACATCCAAATGCTGGCAGGAGCGCCGACGCGACGCGACAA 8931
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
52 pLeuPheGlyThrValAsnGlnSerAsnPhe.ProMetSerThrPheGlu 68
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
8932 :ACGGGAATCCTCCAGAAACATCCACCTACGCGCATTCGCGCAGGTT 8981
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
69 GlnVal.....ProAsnAsnLysGluPh 76
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
8982 :TCGGTTCACCAAAACACCGGCTTTAAACGCATCGCACGTTTCAACGTT 9031
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
76 eIysGly.....ValIleSerAlaAsnValLysTyrAspMetAsnPheL 91
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
9032 :TCAGGGCAACAGAGTCCGAACCTGAAATTTGGGTACAGCATACATTTTA 9081
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
91 ysLysLeuLeuArgPhe 96
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
9082 :ACGAGGTTTGTGATTC 9098
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

seq_name: /STD55/gcdata/genesec/geneseqn-emb1/NA2000.DAT:AAF21608

seq_documentation_block:

ID AAF21608 standard; DNA; 349980 BP.
 XX
 AC AAF21608;
 DT 13-MAR-2001 (first entry)
 DE *Neisseria meningitidis* B nucleotide sequence SEQ ID NO:109.
 XX
 KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; immunogenic; vaccine;
 KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
 KW ds.
 OS *Neisseria meningitidis*.
 PN WO2000066791-A1.
 XX
 PD 09-NOV-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05928.
 XX
 PR 30-APR-1999; 99US-0132068.
 PR 08-OCT-1999; 99WO-US23573.
 PR 28-FEB-2000; 2000GB-0004695.
 XX
 XX (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX
 XX Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC, Masignani V;
 PI Galeotti C, Mora M, Ratti G, Scarselli M, Scariato V, Rappuoli R;
 PI Frazer CM, Grandi G;
 XX
 DR WPI; 2000-647603/62.
 XX
 PT *Neisseria meningitidis* B full length genome sequence and open reading
 PT frames are used to detect, treat and prevent *Neisseria* infections -
 XX
 PS Claim 7; Appendix A; 692pp; English.
 CC The present invention describes the full length genome of
 CC *Neisseria meningitidis* B (NMB). The sequences in AAF21544 and AAF21607
 CC to AAF21613 represent fragments of the NMB genomic sequence, as the
 CC sequence was too long to go in a record on its own it was split into 8
 CC sequences which overlap each other at the beginning and end of each
 CC sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at
 CC the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated at
 CC the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the
 CC *Neisseria* proteins given in AAB58550 to AAB58593, and AAF21589 to
 CC AAF21606 represent PCR primers which are used in the exemplification of
 CC the present invention. The NMB genome and fragments from it have
 CC antibacterial activity, and can be used in vaccines and gene therapy.
 CC *Neisseria* nucleic acids, proteins and/or antibodies which binds to the
 CC proteins can be used in compositions for treating or preventing infection
 CC due to *Neisseria* bacteria or as a diagnostic reagent for detecting the
 CC presence of *Neisseria* bacteria or of antibodies raised to *Neisseria*
 CC bacteria. Computers, computer memory, computer storage medium or computer
 CC databases can be used in a search to identify open reading frames (ORFs)
 CC or coding sequences within the NMB genome. The DNA sequences provide
 CC further opportunities to find antigenic or immunogenic proteins which are
 CC more effective in vaccines than the outer membrane proteins currently
 CC used.
 XX
 SQ Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 other;

alignment_scores:

Quality: 70.00 Length: 123
 Ratio: 1.111 Gaps: 6
 Percent Similarity: 51.220 Percent Identity: 26.829

alignment_block:

US-09-528-682-3 x AAF21608/rev ..


```

seq_documentation_block:
ID AAI99683 standard; DNA; 4403765 BP.
XX
XX AAI99683;
XX
XX
XX 15-JAN-2002 (first entry)
XX
XX
XX Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
DE
XX Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
KW variation; epidemiology; patient treatment; epidemic monitoring; ds.
XX
XX Mycobacterium tuberculosis.
OS
XX
XX US6294328-B1.
XX
XX 25-SEP-2001.
PD
XX
XX 24-JUN-1998; 98US-0103840.
PF
XX
XX 24-JUN-1998; 98US-0103840.
PR
XX
XX (GENO-) INST GENOMIC RES.
PA
XX
XX Fleischmann RD, White OR, Fraser CM, Venter JC;
PI
XX
XX WPI; 2001-647261/74.
XX
XX
XX Evaluating strain variation of Mycobacterium tuberculosis, comprises
PT determining the nucleotide sequence of the strain at positions in the
PT genome corresponding to positions where M. tuberculosis strains CDC
PT 1551 and H37Rv differ
XX
XX
XX Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
XX
XX The invention relates to evaluating strain variation within and between
XX different populations of the tuberculosis bacterial pathogen, and
XX Mycobacterium tuberculosis or related Mycobacterium by determining the
XX nucleotide sequence of the first strain at positions in the complete
XX sequence of the genome that correspond to positions that differ in the
XX nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
XX H37Rv (AAI99682). The method is useful for evaluating strain variation of
XX M. tuberculosis and has valuable application in the fields of
XX tuberculosis genetics, epidemiology, patient treatment and epidemic
XX monitoring.
XX
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from USPTO
XX at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
XX
XX
XX Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
XX

alignment_scores:
Quality: 70.00 Length: 75
Ratio: 1.489 Gaps: 4
Percent Similarity: 62.667 Percent Identity: 28.000

alignment_block:
US-09-528-682-3 x AAI99683/rev ..
Align seg 1/1 to reverse of: AAI99683 from: 1 to: 4403765
9 GlnAlaTyrGluProIleGluValAsnThrAsnThrValThrGlnIleAs 25
4044858CGGGGTACAAGCCGGTGTACTCGGGT...GCATACACAGATCAA 4044812
25 nGlySerAsn.....GluValProLeuAspGlyArgTyrSerAsnPheA 40
|||||:||||:||||:||||:||||:||||:||||:||||:||||:
4044811|CGGCGCACACGTCAGAGCCGACAGATCGACGATCCGAGCAACAGCTGC 4044762
40 laLeuSerAlaGluGlyGlyMetGln...AspGly..... 51
|||||:||||:||||:||||:||||:||||:||||:||||:

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4044761GGCTGATCCTGAAGAGGGTACACACGACGACCGACGGTCCGAGAGGTC 4044711
52 .....AspLeuPheGlyThrValas 58
|||||||:|||||:
4044711ATCACCAAGTACCCACCGGGTACGCGCTGACGCTGTTCTTCAACGCGCTCAG 4044662

58 nClnSerAsnPhePrometSerThr 66
: |||||:|||||
4044661CGCCAAAACGCGAAGGTCAGCACG 4044637

seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAI99682
seq_documentation_block:
ID AAI99682 standard; DNA; 4411529 BP.
XX AAI99682;
XX AC
XX AC
XX DT
XX 15-JAN-2002 (first entry)
XX Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
DE
XX
XX Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; gen
KW variation; epidemiology; patient treatment; epidemic monitorin
XX OS
XX Mycobacterium tuberculosis.
XX US6294328-B1.
XX 25-SEP-2001.
XX
XX 24-JUN-1998; 98US-0103840.
XX 24-JUN-1998; 98US-0103840.
XX (GENO-) INST GENOMIC RES.
XX
XX Fleischmann RD, White OR, Fraser CM, Venter JC;
XX WPI; 2001-647261/74.
XX
XX Evaluating strain variation of Mycobacterium tuberculosis, com
PT determining the nucleotide sequence of the strain at positions
PT genome corresponding to positions where M. tuberculosis strain
PT 1551 and H37Rv differ
XX
XX Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
XX
XX The invention relates to evaluating strain variation within an
CC different populations of the tuberculosis bacterial pathogen,
CC Mycobacterium tuberculosis or related Mycobacterium by determi
CC nucleotide sequence of the first strain at positions that corre
CC sequence of the genome that correspond to positions that differe
CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI9
CC H37Rv (AAI99682). The method is useful for evaluating strain v
CC M. tuberculosis and has valuable application in the fields of
CC tuberculosis genetics, epidemiology, patient treatment and epi
CC monitoring.
CC Note: The sequence data for this patent did not form part of t
CC specification, but was obtained in electronic format directl
CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
XX
XX Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T;
SQ

alignment_scores:
Quality: 70.00 Length: 75
Ratio: 1.489 Gaps: 4
Percent Similarity: 62.667 Percent Identity: 28.000

alignment_block:
US-09-528-682-3 x AAI99682/rev
Align seq l/1 to reverse of: AAI99682 from: 1 to: 4411529

```


PT isomylase activity - and related vectors, transformed cells and
 PT plants, proteins and antibodies, used to generate starch with
 XX altered properties, for use in foods, as thickeners etc.

PS Claim 3; Fig 3; 78pp; English.

XX This sequence encodes a Solanum tuberosum isomylase of the invention.
 CC Fragments of the isomylase coding sequence are used to identify and
 CC clone isomylases from other plant species, by standard hybridisation
 CC or amplification methods. Expression of the isomylase DNA in host cells
 CC is used to produce the isomylase which is used: (i) to raise antibodies
 CC (Ab) for identification, isolation and localisation of isomylases; and
 CC (ii) for synthesis of branched polysaccharides. The DNA, proteins
 CC and Ab (or related peptides) are used to alter the quality and
 CC quantity of polysaccharides in a host cells, specifically to alter
 CC branching in amylopectin. The modified starches produced are useful in
 CC human or animal foods; as biodegradable plastic; as food or paint
 CC thickener; in starch-coated films, paper and textiles; in mining
 CC explosives; in pharmaceuticals and glues. Manipulation of debranching
 CC activity in a plant allows control of starch properties, e.g. increased
 CC gel strength; formation of paste rather than gel, changed physical
 CC characteristics etc.

XX SQ Sequence 2634 BP; 854 A; 496 C; 573 G; 711 T; 0 other;

alignment_scores:
 Quality: 69.50 Length: 96
 Ratio: 1.363 Gaps: 5
 Percent Similarity: 53.125 Percent Identity: 28.125

alignment_block:

US-09-528-682-3 x AAX27062 ..
 Align seg 1/1 to: AAX27062 from: 1 to: 2634
 14 lIeGluValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluVa 30
 2039 ATTCAGAAGACGACATTACTTGGCTCGAGGACAACTGGTACAATGAA... 2086
 30 lProLeuAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyG 47
 2087GAGAGTAGATTCTCTGCTTATGCTCCATGATGGGAATGGA... 2128
 47 lYMetGlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPhePro 63
 2129GGAGATATTTACTTGGCATTTAATGCACACCACTTCTCC 2167
 64 MetSerThr...PheGluGlnValProAsnAsnLysGluPheLysGlyVa 79
 2168 ATCAAAACAGCAATACCTTACCACCAACAGCAATAGAAATGGTACCGAGT 2217
 79 lIleSerAlaAsnValLysTyrAspMetAsnPheLysLysLeuLeuArgp 96
 2218 GGTGGACACTAATCTGAAA.....GlyValHisGly 106
 2237 ..TCACAGATGATTTGTACTGAGGAGTGCTGTGT 2272

seq_name: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA1999.DAT: AAX13013

seq_documentation_block:

ID AAX13013 standard; DNA; 6399 BP.
 XX AC AAX13013;
 XX DT 19-MAR-1999 (first entry)
 XX DE Enterococcus faecalis genome contig SEQ ID NO:76.
 XX KW Enterococcus faecalis; contig; detection; Enterococcal infection;
 KW vaccine; attenuation; computer readable medium; ds.

XX Enterococcus faecalis.
 XX WO9850555-A2.
 XX 12-NOV-1998.
 XX 04-MAY-1998; 98WO-US08985.
 XX 14-NOV-1997; 97US-0066009.
 XX 06-MAY-1997; 97US-0044031.
 XX 16-MAY-1997; 97US-0046655.
 XX (HUMA-) HUMAN GENOME SCI INC.

XX Barash SC, Dillon PJ, Kunsch CA;
 WPI; 1999-045171/04.
 XX New isolated Enterococcus faecalis polynucleotides and polypeptides
 PT - used to develop products for the detection of Enterococcus and for
 PT use in vaccines for prevention or attenuation of Enterococcus
 PT infection.

XX Claim 1; Page 549-552; 2084pp; English.
 XX A computer readable medium has been developed which has recorded on it
 CC 982 nucleotide sequences isolated from the Enterococcus faecalis genome.
 CC AAX12938 to AAX13919 represent these nucleotide sequences which are
 CC primary nucleotide sequences, also known as contigs. The computer-based
 CC system can identify fragments of the Enterococcus faecalis genome with
 CC commercial importance. The products can be used to detect the presence
 CC of Enterococcus faecalis in samples. They can also be used for
 CC diagnosing Enterococcal infection in an animal and monitoring
 CC progression of disease, and for identifying agents which can be used to
 CC modulate the growth or pathogenicity of Enterococcus faecalis, or
 CC another related organism, in vivo or in vitro. In particular the
 CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences
 CC can be used in vaccines to prevent or attenuate an Enterococcal
 CC infection.

XX SQ Sequence 6399 BP; 2102 A; 1048 C; 1356 G; 1889 T; 4 other;

alignment_scores:

Quality: 69.50 Length: 97
 Ratio: 1.264 Gaps: 5
 Percent Similarity: 56.701 Percent Identity: 25.773

alignment_block:

US-09-528-682-3 x AAX13013 ..
 Align seg 1/1 to: AAX13013 from: 1 to: 6399
 19 AsnThrValThrGlnIleAsnGlySerAsnGluValPro..... 31
 787 ATCAAAATCAATGAATGAAGCTACTGAAGAGTTTACAGCTATAGAACA 836
 32LeuAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyG 47
 837 TAATTACTCTCGGT...TATCTTAATGTACAAGTTTGTATTGGGAATACG 883
 47 lYMetGlnAspGlyAspLeuPheGlyThrValAsnGln...SerAsnPhe 62
 884 GTATT.....GCCCTATCAGGATTAGCTAATGAGCAACAGGTCTA 924
 63 PrometSerThrPheGluGlnValProAsnAsnLysGluPheLysGlyVa 79
 925 GCGGGTAGCAATGTGAAAAGATTCTCACAGGTAGATAATATCTTGATT 974
 79 lIleSerAlaAsnValLysTyrAspMetAsnPheLys..... 91
 975 ATTACGTTTCAAAGTTAAAGTGCCAAATGAACCTTAAATGGTAAATCCAA 1024


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44 laGluGlycylMetClnAspGlyLeuPheGlyThrValAsnGlnSer 60
   || :||:||||| |||:||||| :||
1037 CA.....AGTGGGAGCCTAGCAGTGCAGCATCCAGTGGGC 1071
      61 AsnPhePro..... 63
      |||:|||||
1072 AAATATCCAGGAGCCCTCCGTCCGTCACACTAGTGGCCTACGAAAGAGT 1121
      64 .....MetSerThrPheGluGlnV 70
      :||:|||||
1122 GCCAACAGGACTGTCTGTACGTCGTGGGGTGAGCAACTTCGAGCTGA 1171
      70 aIProAsnAsnLysGluPheLysGlyValIleSerAlaAsnValLysTyr 86
      ||||| :||:||||| :||:|||||
1172 TCCCAAATCCTGAACATACCAAGAACCCTGGTTACAGAAATATGCGCGATT 1221
      87 Asp.....MetAsnPheLysLeuLeuArgPheMetGluAspAs 100
      ||||| :||:||||| :||:|||||
1222 GACCCAGGAGGCATGAACATACACGAAATTGATA...CTGCTGTAGAGGGA 1368
      100 pHeileGlyVal 104
      | :||:|||||
1269 CGCGGTGGGCATC 1281

```

seq_documentation_block:

XX
AC
AAN60874;

DT 29-OCT-1991 (first entry)

DE Large RNA segment of infectious bursal disease virus.
XX

XX
XX

XX	Key	Location/Qualifiers
EH		

$$F_T / \text{tag} = a$$
XX
DN
1308507050-2

PD 04-DEC-1986.

PF 30-MAY-1986;

PR 30-MAY-1985: 85AU-0000815:
PR 30-MAY-1985: 85AU-0000815:
PR 30-MAY-1985: 85AU-0000815:
PR 30-MAY-1985: 85AU-0000815:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
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xx Azad AA. Hudson P.J. Fahey K.J.

DR WPI; 1986-332075/50.

XX	Recombinant DNA	cor
DT		

infectious bursal di

PS Claim 10; Fig 10; 78

CC
CC
CC

CC of the sequence.

SQ Sequence 3129 BP; 845 A; 882 C; 799 G; 603 T; 0 other;

alignment_scores:

Quality: 69.00 Length: 128
Ratio: 1.211 Gaps: 5
Percent Similarity: 44.531 Percent Identity: 21.094

alignment_block:

US-09-528-682-3 x AAN60874 ..

Align seg 1/1 to: AAN60874 from: 1 to: 3129

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13 ProIleGluValAsnThrValThrGlnIleAsnGlySerAsnG1 29
   |||   ::   |||:::  |||||:::||||
917 CCAACCAAGTGAGTAACCCAGCCAGTTAGATCCATT..... 952

29 uValProLeuAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluG 46
   :::::  :::::  :::::  :::::  :::::  :::::
953 .....AAACTGGAGATAGTAACCTCCAAA 977

46 LyGlyMetGlnAspGlyAsp.....Leu 53
   ::|||  |||  |||||
978 GTGGAGGTCAGGCTGGAGATCAGATGCTCTGTTGGCAAGTGGGAACCTA 1027

54 PheGlyThrValAsnGlnSerAsnPhePro..... 63
   |||:::  ::|||:::
1028 GCAGTGACAATTCATGGTGGAAACTACCCAGGTGCCCTCCGCCCGTCAC 1077

63 ..... 63

1078 ACTAGTAGCCTATGAAGAGTGGCAACAGGATCTGTGTACGGTCGCTG 1127

64 ..MetSerThrPheGluGlnValProAsnAsnLysGluPheLysGlyVal 79
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
1128 GGTGAGCAACTTCGAGCTGATCCCGCAATCCTGAGCTAGCCCAAGAACCTA 1177

80 IleSerAlaAsnValIlyTyrAsp.....MetAsnPheLysLysLe 93
   :::::  :::::  |||
1178 GTCACAGATATGGCCGATTTCACCCAGGAGCCATGAACTACACAAACT 1227

93 uLeuArgPheMetGluAspPheIleGlyVal 104
   ::::  ::  |||  ::|::|::|
1228 AATC...CTGAGTGAGAGGACCGCTTGGTATC 1258
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OM of: US-09-528-682-3 to: EST:* out_format : pfs

Date: Jun 18, 2002 6:26 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=framet.p2n.model -DEV=xlp
-O=/cgn2_1/USPTO_seq/LUS09528682/runat_18062002_082443_7797/app_query.fasta_1.689
-DB=EST -OPMT=fastap -SUFFIX=p2n.rst -GAPOP=12,000 -GAPEXT=4,000
-MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000 -GAPOP=4,500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6,000
-FGAPEXT=7,000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6,000
-DELEXT=7,000 -START=1 -MATRIX=blosom62 -TRANS=human40.cdi
-LIST=1000 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=50 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZ=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09528682_@CGN1_1_5309
-NCPUP=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-528-682-3

Query length: 107

Database: EST:*

Database sequences: 13736207

Database length: 1841457050

Search time (sec): 4056.470000

score_list:

Sequence	Strd	Orig	ZScore	Escore	Len	Documentation
gb_est2:Bj030418	+	79.00	175.34	1.61	621	Bj030418 BJ030418 NIBB Moch11
gb_gss:BH298334	+	76.50	169.69	3.32	596	BH298334 CH230-1012.TJ CHORI-23
gb_gss:BH324419	+	76.50	168.64	3.80	660	BH324419 CH230-189M18.TJ CHORI-23
gb_est2:BH316490	+	76.00	169.49	3.41	540	BH316490 saf03h08.y1 Gm-cl085 C
gb_est2:BM270616	+	76.00	169.23	3.52	554	BM270616 sak15011.y1 Gm-cl075 G
gb_est1:BM636005	+	76.00	166.48	5.01	723	BM636005 ALG36005 XGC-neurula S
gb_gss:BH157168	+	76.00	164.12	6.78	909	BH157168 ENTL34TR Entamoeba hj
gb_gss:BH266151	+	75.00	172.40	2.35	322	BH266151 CH230-55LA.TV CHORI-23
gb_est1:AI134063	+	75.00	166.28	5.15	583	AI134063 GH11413.Sprime GH bro
gb_gss:AZ986197	+	74.50	164.15	6.76	637	AZ986197 SMOVL3CAN1G04 Onchoce
gb_est1:AA917243	+	74.00	166.05	5.30	471	AA917243 SMOVL3CAN1G04 Onchoce
gb_est1:AA333548	+	73.50	169.69	3.32	548	AA333548 EST37697 Embryo, 8 wee
gb_gss:BH413108	+	73.50	163.27	7.56	294	BH413108 CH230-101K19.TV CHORI-
gb_est1:AUI18471	+	73.50	158.72	13.56	852	AUI18471 AUI18471 HEMBA1 Homo
gb_est2:BH316465	+	73.00	162.92	7.91	504	BH316465 saf03f02.y1 Gm-cl085 C
gb_est2:BE590377	+	73.00	161.74	9.20	565	BE590377 SB117 Sugar Beet germi
gb_est1:AW309153	+	73.00	160.92	10.23	612	AW309153 sf94h02.y1 Gm-cl019 G
gb_gss:AZ2339485	+	73.00	160.43	10.90	642	AZ2339485 RPCI-23-73L24.TJ RPCI-
gb_gss:BH417892	+	73.00	157.97	14.94	815	BH417892 MusIt801-255 MuTAIL-PC
gb_gss:BH373734	+	72.50	167.81	4.23	279	BH373734 AG-ND-126H18.TF ND-TAM
gb_gss:BH313283	+	72.50	164.07	6.83	401	BH313283 CH230-196N15.TJ CHORI-
gb_gss:BH319283	+	72.50	159.60	12.11	508	BH319283 kq47a07.y1 TBN95TM-SSR
gb_est2:BE581518	+	72.50	159.60	12.11	508	BE581518 RPCI-23-366D18.TJ RPCI-
gb_gss:BH218768	+	72.50	159.29	12.60	637	BH218768 CH230-108N7.TV CHORI-2
gb_est2:BG524649	+	72.50	159.20	12.76	643	BG524649 5-44 Stevia field grow
gb_gss:AZ735738	+	72.50	157.59	15.67	731	AZ735738 RPCI-24-70J5.TJB RPCI-
gb_gss:AZ678077	+	72.50	156.63	17.74	835	AZ678077 ENTPX25TF Entamoeba hj
gb_gss:AZ2336242	+	72.50	156.50	18.03	825	AZ2336242 ENTPX25TF Entamoeba hj
gb_gss:AZ693407	+	72.50	155.57	20.32	914	AZ693407 ENTPIT84TF Entamoeba hj
gb_gss:AZ441996	+	71.50	160.52	10.77	447	AZ441996 LM0234P21F Mouse 10kb
gb_gss:AZ293665	+	71.50	159.47	12.33	495	AZ293665 4908.gf21m18.s1 Sacche
gb_est2:BE536132	+	71.50	155.94	19.38	697	BE536132 601061788F1 NIH_MGC_10
gb_gss:BH096764	+	71.50	155.17	21.40	731	BH096764 RPCI-24-287C31F.TJ RPCI-
gb_gss:CN5034250	+	71.50	152.16	31.45	1005	AL320217 Tetraodon nigroviridi
gb_gss:AZ2329571	+	71.00	158.46	14.02	485	AZ2329571 LM0054F14F Mouse 10kb
gb_gss:AZ515059	+	71.00	158.46	14.02	485	AZ515059 LM0054F14F Mouse 10kb
gb_gss:BH600950	+	71.00	158.11	14.67	502	BH600950 BOC2V06TR BOC2 Brassic
gb_est2:BE442965	+	71.00	157.20	16.48	548	BE442965 WHEI108_G02_N04Z5 Whea
gb_est2:BM050293	+	71.00	153.75	25.66	766	BM050293 603632513F1 NIH_MGC_43
gb_gss:AZ672583	+	71.00	152.42	30.42	871	AZ672583 ENTPJL17TR Entamoeba hj

gb_est1:AW587961	+	70.50	158.30	14.32	438	AW587961 kp10c06.y1 TBN95TM-
gb_est1:AA823163	+	70.50	158.07	14.75	448	AA823163 v41e03.r1 Soares_m
gb_gss:BH295572	+	70.50	156.63	17.74	515	BH295572 CH230-187A17.TV CHO
gb_gss:AZ423995	+	70.50	156.24	18.65	535	AZ423995 LM0203B13F Mouse 10
gb_est2:BG804725	+	70.50	155.05	21.71	600	BG804725 0271-56 Mouse E14.5
gb_est2:BG808959	+	70.50	155.05	21.71	600	BG808959 2144-54 Mouse E14.5
gb_gss:BH061596	+	70.50	153.61	26.12	690	BH061596 RPCI-24-269B12.TJ R
gb_est2:BF295592	+	70.50	153.32	27.12	710	BF295592 025PB002 PB CDNA #1
gb_gss:BH665274	+	70.50	152.43	30.40	774	BH665274 602784057F1 NCI_CGA
gb_est2:BI695125	+	70.50	151.68	33.45	832	BI695125 603345846F1 NCI_CGA
gb_est2:BM454164	+	70.50	148.39	51.03	1145	BM454164 AGENCOURT_6419302
gb_est2:BM170235	+	70.50	153.32	27.11	631	BM170235 EST572758 PYBS Plas
gb_gss:AZ915388	+	70.00	151.89	32.58	725	AZ915388 RPCI-24-165I13.TV R
gb_est2:BI302215	+	69.50	155.87	19.55	438	BI302215 UI-R-D10-clip-j-20.0
gb_gss:BH288978	+	69.50	153.35	26.99	559	BH288978 CH230-171N12.TVC CH
gb_est2:BE888235	+	69.50	150.42	39.32	743	BE888235 601511755F1 NIH_MGC
gb_gss:BH354216	+	69.50	150.05	41.23	770	BH354216 CH230-221H9.TJ CHOR
gb_gss:AZ549155	+	69.50	148.23	52.09	919	AZ549155 ENTCW48TR Entamoeba
gb_est1:AO69704	+	69.00	154.04	24.72	412	AO69704 AO069704 Rice panic
gb_est2:BF871591	+	69.00	154.04	24.72	465	BF871591 QVO-ET0148-O11100-4
gb_gss:BH354762	+	69.00	152.77	29.10	526	BH354762 CH230-199F18.TJ CHO
gb_gss:AZ944352	+	69.00	150.71	37.88	642	AZ944352 2M0205B19F Mouse 10
gb_gss:BH272068	+	69.00	148.69	49.08	781	BH272068 CH230-21K14.TV CHOR
gb_gss:BH132334	+	69.00	146.33	66.45	982	BH132334 ENTNY27TR Entamoeba
gb_est1:AI982549	+	68.50	153.85	25.33	421	AI982549 WT21H01.x1 NCI_CGAP
gb_est2:BM273517	+	68.50	150.41	39.40	588	BM273517 PFESToaa51g08.y1 Pl
gb_gss:BH322134	+	68.50	149.01	47.11	673	BH322134 CH230-116C10.TV CHO
gb_gss:BH191484	+	68.50	149.00	47.20	674	BH191484 TC3-37A13.TR TC3 TJ
gb_gss:BH357297	+	68.50	148.02	53.50	741	BH357297 CH230-33E6.TV CHORI
gb_gss:AZ698722	+	68.50	147.90	54.36	750	AZ698722 RPCI-23-232G24.TJ R
gb_gss:AZ671779	+	68.50	146.29	66.76	876	AZ671779 ENTJL09TF Entamoeba
gb_gss:AZ549109	+	68.50	146.04	68.98	898	AZ549109 ENTPB95TR Entamoeba
gb_gss:AZ682869	+	68.50	145.73	71.74	925	AZ682869 ENTMS27TR Entamoeba
gb_gss:CN5071MR	+	68.50	145.07	78.06	986	CLONE BA0AB003D06.0
gb_est1:AO95147	+	68.00	153.01	28.21	406	AO95147 OY19A04.s1 Soares_s
gb_est2:BF016298	+	68.00	149.96	38.14	510	BF016298 u41c005.y1 NCI_CGAP
gb_est2:BF0162810	+	68.00	149.96	38.14	510	BF0162810 u41c005.y1 NCI_CGAP
gb_est2:BM274810	+	68.00	149.66	41.74	546	BM274810 PFESToaa51g08.y1 Pl
gb_est2:BM274074	+	68.00	149.66	43.37	562	BM274074 PFESToaa51g08.y1 Pl
gb_est1:AV835454	+	68.00	148.48	50.44	630	AV835454 AV835454 K. Sato un
gb_gss:AZ702601	+	68.00	148.40	50.97	635	AZ702601 RPCI-23-227G7.TJC R
gb_gss:AZ68577	+	68.00	147.92	54.18	665	AZ68577 RPCI-23-131H11.TJ R
gb_est2:BI088610	+	68.00	147.39	57.98	700	BI088610 602853163F1 NIH_MGC
gb_gss:BH296443	+	68.00	146.00	69.30	801	BH296443 CH230-123H12.TV CHO
gb_est2:BG023860	+	68.00	144.01	89.51	972	BG023860 602303507F1 NIH_MGC
gb_est1:AL514310	+	68.00	143.51	95.40	1020	AL514310 AL514310 LTI_NFL00
gb_est2:BM330986	+	67.50	150.05	41.25	481	BM330986 PC1_68.B03.g1 A002
gb_est1:BE019434	+	67.50	149.92	41.93	487	BE019434 bb55e12.y1 NIH_MGC
gb_est1:AA786963	+	67.50	149.61	43.64	502	AA786963 m7308a1.f1 Aspergill
gb_gss:BH310216	+	67.50	148.59	49.72	554	BH310216 CH230-3H2.TV CHORI-
gb_est1:BB625755	+	67.50	146.85	62.18	656	BB625755 BB625755 RIKEN full
gb_gss:BH191621	+	67.50	146.36	66.22	688	BH191621 TC3-37K13.TR TC3 TJ
gb_gss:BH256660	+	67.50	145.44	74.49	749	BH256660 CH230-286G11.TJ CHO
gb_est2:BI856252	+	67.50	145.25	76.33	755	BI856252 603382985F1 NIH_MGC
gb_est2:BM041968	+	67.50	145.24	76.46	767	BM041968 603615846F1 NIH_MGC
gb_est2:BG120604	+	67.50	145.10	77.78	777	BG120604 602436739F1 NIH_MGC
gb_est2:BE253581	+	67.50	144.38	85.28	833	BE253581 601109009F1 NIH_MGC
gb_est2:BG245099	+	67.50	143.78	92.11	883	BG245099 602358943F1 NCI_CGA
gb_gss:BH159129	+	67.50	143.73	92.80	888	BH159129 ENTSG95TF Entamoeba
gb_gss:BH160705	+	67.50	143.67	93.50	893	BH160705 ENTPX64TF Entamoeba
gb_est2:BG420284	+	67.50	143.40	96.28	913	BG420284 60248302F1 NIH_MGC
gb_est2:BM73346	+	67.50	142.95	102.46	957	BM73346 60248302F1 NIH_MGC
gb_hlc:BC004160	+	67.50	142.44	124.37	1108	BC004160 AGENCOURT_6466598
gb_est2:D75662	+	67.00	151.82	32.85	360	D75662 CELK108DAF.Yu1 Kohar
gb_est1:BM458341	+	67.00	151.13	35.90	385	BM458341 sh86g05.y1 Gm-cl016
gb_est2:BG4292365	+	67.00	149.75	42.84	440	BG4292365 EST422365 MGW Med1
gb_est2:BG730370	+	67.00	146.92	49.53	491	BG730370 df43a06.y1 Wellcome
gb_est2:BI448086	+	67.00	146.68	61.17	576	BI448086 dah91g01.y1 NICHX
gb_gss:AZ007727	+	67.00	146.68	62.72	587	AZ007727 RPCI-23-246J3.TV RP
gb_est2:BI42651	+	67.00	146.61	64.14	597	BI42651 fq47h01.y1 Zebrafis
gb_est2:BI475809	+	67.00	146.55	64.56	600	BI475809 fq72h07.y3 Zebrafis
gb_est2:BI075556	+	67.00	146.55	64.56	600	BI075556 fsq4e09.y1 Zebrafis
gb_est2:BI841035	+	67.00	146.55	64.56	600	BI841035 fsq5d00.y1 Zebrafis

gb_est2:BI841074	67.00	146.55	64.56	600	1	BI841074	fq50h06.y1 zebrafish a	gb_est1:AJ273964	572	1000	144.62	82.75	572	1	AJ273964	AJ273964 Metarhiziu
gb_est2:BI841136	67.00	146.55	64.56	600	1	BI841136	fq51f07.y1 zebrafish a	gb_gss:BH069552	587	383	66.00	144.35	587	1	BH069552	RPCI-24-389M1.TVC R
gb_est2:BI841165	67.00	146.55	64.56	600	1	BI841165	fq52a06.y1 zebrafish a	gb_est1:BG815729	591	385	66.00	144.28	591	1	BG815729	BD472e01.y1 Wellcom
gb_est2:BI841250	67.00	146.55	64.56	600	1	BI841250	fq53b04.y1 zebrafish a	gb_est1:BG815729	598	389	66.00	144.16	598	1	BG815729	AL649913 XGC-gastru
gb_est2:BI842618	67.00	146.55	64.56	600	1	BI842618	fq47d07.y1 zebrafish a	gb_est2:BE942684	598	434	66.00	144.16	598	1	BE942684	EST4222632 MGHG Medi
gb_est2:BI844454	67.00	146.55	64.56	600	1	BI844454	fq34c07.y1 zebrafish a	gb_gss:AZ227993	626	503	66.00	143.69	626	1	AZ227993	RPCI-23-79F21.TV RP
gb_est2:BI865153	67.00	146.55	64.56	601	1	BI865153	fq98a09.y1 zebrafish a	gb_gss:AL631463	646	507	66.00	143.69	646	1	AL631463	EST431463 XGC-gastru
gb_est2:BI844464	67.00	146.55	64.71	601	1	BI844464	fs34d05.y1 zebrafish a	gb_est1:AZ568742	660	514	66.00	143.14	660	1	AZ568742	251Pvc10.y1 MBN #30
gb_est2:C84717	67.00	146.43	65.56	607	1	C84717	C84717 Dictyostellum dis	gb_gss:AQ250262	672	700	66.00	142.96	672	1	AQ250262	TK17-Sp6 TAMU Arabi
gb_est2:BI475552	67.00	146.40	65.85	609	1	BI475552	fq67d08.y3 zebrafish a	gb_est1:AL628084	676	704	66.00	142.90	676	1	AL628084	AL628084 XGC-gastru
gb_est2:BI705474	67.00	146.40	65.85	609	1	BI705474	fq73g11.y3 zebrafish a	gb_est1:AL6406154	695	737	66.00	142.61	695	1	AL6406154	AV406154 Bombyx mor
gb_est2:BI841170	67.00	146.40	65.85	609	1	BI841170	fq52a11.y1 zebrafish a	gb_gss:BH319624	739	901	66.00	141.98	739	1	BH319624	CH230-119P18.TVB CH
gb_est2:BI845949	67.00	146.40	65.85	609	1	BI845949	fq75c04.y1 zebrafish a	gb_est2:BG868866	752	906	66.00	141.80	752	1	BG868866	602388366F1 NIH_MGC
gb_est2:BI841264	67.00	146.35	66.88	612	1	BI841264	fq53d12.y1 zebrafish a	gb_est2:BG868866	756	906	66.00	141.74	756	1	BG868866	CH230-79F21.TV RP
gb_gss:AQ928098	67.00	146.28	66.85	616	1	AQ928098	RPCI-23-258H6.TV RPCI	gb_gss:CNS07CGJ	761	906	66.00	141.68	761	1	CNS07CGJ	T7 end of clone BD0
gb_est2:BI475579	67.00	146.27	67.00	617	1	BI475579	fq67g03.y3 zebrafish a	gb_gss:AQ855490	774	906	66.00	141.50	774	1	AQ855490	CQ61764B CPTOWAGDNA
gb_est2:BI475662	67.00	146.27	67.00	617	1	BI475662	fq68g12.y3 zebrafish a	gb_est1:AI331122	803	906	66.00	141.12	803	1	AI331122	AI331122 NT2RP4 Hom
gb_est2:BI475702	67.00	146.27	67.00	617	1	BI475702	fq69d07.y3 zebrafish a	gb_est2:BF256770	836	906	66.00	139.54	836	1	BF256770	HVSMERF0010P12f Hord
gb_est2:BI845909	67.00	146.27	67.00	617	1	BI845909	fq74f12.y1 zebrafish a	gb_gss:BG290505	938	906	66.00	139.09	938	1	BG290505	602388366F1 NIH_MGC
gb_gss:AZ447600	67.00	146.22	67.43	620	1	AZ447600	IM0244P14R Mouse 10kb	gb_gss:BH266991	978	906	66.00	148.83	978	1	BH266991	CH230-6636.TV CHORI
gb_est2:BE060308	67.00	146.17	67.86	623	1	BE060308	HVSMER0011019f Hordem	gb_est1:AU177894	978	906	66.00	148.27	978	1	AU177894	AU177894 UV Irradia
gb_est2:BI842687	67.00	146.12	68.29	626	1	BI842687	fq48c12.y1 zebrafish a	gb_est1:AW636061	978	906	66.00	148.04	978	1	AW636061	BI42C06.y1 Blacksha
gb_est2:BG160282	67.00	145.99	69.45	634	1	BG160282	df32c08.y1 Wellcom CR	gb_gss:BH305635	993	906	66.00	148.94	993	1	BH305635	CH230-37121.TV CHOR
gb_gss:AZ417456	67.00	145.97	69.59	635	1	AZ417456	IM0193F11f Mouse 10kb	gb_gss:AZ936889	993	906	66.00	148.81	993	1	AZ936889	AU036816 Cryptomeri
gb_est1:AU0123386	67.00	145.84	70.75	643	1	AU0123386	AU123386 NT2RM2 Homo	gb_est2:BG290505	993	906	66.00	148.81	993	1	BG290505	602388366F1 NIH_MGC
gb_est2:BJ065577	67.00	145.54	73.53	662	1	BJ065577	BJ065577 NIBB Mochii	gb_gss:BH266991	978	906	66.00	148.83	978	1	BH266991	CH230-6636.TV CHORI
gb_gss:BH176803	67.00	145.39	75.01	672	1	BH176803	007_H-20-rev Mochii	gb_est1:AI469952	978	906	66.00	148.27	978	1	AI469952	T7 end of clone BD0
gb_gss:CNS073HS	67.00	145.39	75.01	672	1	CNS073HS	T3 end of clone 007DDI	gb_gss:BH266991	978	906	66.00	148.27	978	1	BH266991	CH230-6636.TV CHORI
gb_est2:BM183613	67.00	145.36	75.30	674	1	BM183613	fv65e09.y1 Sugano SUD	gb_est1:AW636061	978	906	66.00	148.04	978	1	AW636061	BI42C06.y1 Blacksha
gb_est1:AW18120	67.00	144.86	80.22	707	1	AW18120	f108a09.y1 Sugano Kawa	gb_gss:BH305635	993	906	66.00	148.94	993	1	BH305635	CH230-37121.TV CHOR
gb_gss:AZ006893	67.00	144.39	85.20	740	1	AZ006893	RPCI-23-24612.TV RPCI	gb_gss:BH029809	993	906	66.00	148.81	993	1	BH029809	AU036816 Cryptomeri
gb_est1:AU091198	67.00	143.57	94.62	801	1	AU091198	AU091198 lambda ZAPII	gb_est2:BG290505	993	906	66.00	148.81	993	1	BG290505	602388366F1 NIH_MGC
gb_est1:AU005267	67.00	143.46	96.02	810	1	AU005267	AU005267 Bombyx mori	gb_est1:AW245971	993	906	66.00	142.84	993	1	AW245971	2822950.3prime NIH
gb_gss:AZ536055	67.00	143.35	97.44	819	1	AZ536055	ENTIC022fR Entamoeba h	gb_est2:BG160282	819	906	66.00	142.84	819	1	BG160282	fq48c12.y1 Wellcom CR
gb_gss:AG672258	67.00	142.88	103.46	857	1	AG672258	ENTIC022fR Entamoeba h	gb_gss:BH266991	978	906	66.00	148.83	978	1	BH266991	CH230-6636.TV CHORI
gb_gss:BH148797	67.00	142.70	105.86	872	1	BH148797	ENTPE74fT Entamoeba h	gb_est1:AW636061	978	906	66.00	148.04	978	1	AW636061	BI42C06.y1 Blacksha
gb_gss:AZ540419	67.00	142.48	108.93	891	1	AZ540419	ENTPC57fT Entamoeba h	gb_gss:AZ936889	993	906	66.00	148.81	993	1	AZ936889	AU036816 Cryptomeri
gb_gss:BH148098	67.00	142.43	109.57	895	1	BH148098	ENTPD95fT Entamoeba h	gb_est2:BG290505	993	906	66.00	148.81	993	1	BG290505	602388366F1 NIH_MGC
gb_gss:BH136250	67.00	142.41	109.50	897	1	BH136250	ENTNH55fT Entamoeba h	gb_est1:AW245971	993	906	66.00	142.84	993	1	AW245971	2822950.3prime NIH
gb_gss:BH155062	67.00	141.94	116.75	939	1	BH155062	ENTSP09fT Entamoeba h	gb_est2:BG160282	819	906	66.00	142.84	819	1	BG160282	fq48c12.y1 Wellcom CR
gb_gss:AZ672390	67.00	141.89	117.41	943	1	AZ672390	ENTII07fT Entamoeba h	gb_gss:AQ950992	993	906	66.00	141.32	993	1	AQ950992	Sheared DNA-52G22.T
gb_gss:AZ675984	67.00	141.16	128.91	1012	1	AZ675984	AGENC002fR Entamoeba h	gb_est1:AW18120	1012	906	66.00	141.26	1012	1	AW18120	f108a09.y1 Sugano Kawa
gb_est2:CO6692	66.50	150.00	41.52	382	1	CO6692	CO6692 Rat pancreatic is	gb_gss:BH266991	978	906	66.00	148.83	978	1	BH266991	CH230-6636.TV CHORI
gb_est1:AW383214	66.50	148.73	48.86	432	1	AW383214	QV2-LR0051-130400-134	gb_gss:AZ543858	901	906	66.00	138.72	901	1	AZ543858	ENTHE04fT Entamoeba
gb_gss:AZ249188	66.50	148.49	51.37	442	1	AZ249188	RPCI-23-43C15.TJ RPCI	gb_gss:AZ689972	906	906	66.00	138.66	906	1	AZ689972	ENTH44fT Entamoeba
gb_gss:AZ523113	66.50	148.31	51.57	450	1	AZ523113	215PbE01 Pb MBN #21 P	gb_gss:CNS073HS	993	906	66.00	148.94	993	1	CNS073HS	AU036816 Cryptomeri
gb_gss:AQ442332	66.50	147.45	57.56	489	1	AQ442332	HS_5117_B1_C12_77A R	gb_gss:CNS071V6	993	906	66.00	137.69	993	1	CNS071V6	T3 end of clone AV0
gb_gss:AZ444932	66.50	147.39	58.03	492	1	AZ444932	IM0240624fR Mouse 10kb	gb_est1:AI987127	993	906	66.00	146.33	993	1	AI987127	rS22A05.y1 Sommer P
gb_gss:BH306907	66.50	146.60	64.19	531	1	BH306907	CH230-37M21.TJ CHORI-2	gb_est1:AW290550	993	906	66.00	146.27	993	1	AW290550	NNV031B06f NSF xy1
gb_gss:BH267401	66.50	145.91	70.17	568	1	BH267401	CH230-82K21.TJ CHORI-2	gb_gss:AZ272800	993	906	66.00	146.17	993	1	AZ272800	RPCI-23-161C17.TJ R
gb_gss:AZ264780	66.50	145.89	70.33	569	1	AZ264780	RPCI-23-156M11.TV RPCI	gb_gss:AQ090230	993	906	66.00	145.04	993	1	AQ090230	HS_3009.A1_H09.T7 C
gb_gss:BH332692	66.50	145.80	72.13	574	1	BH332692	CH230-201C13.TV CHORI	gb_est2:BF198880	993	906	66.00	144.83	993	1	BF198880	248865 MARC 2PIG Su
gb_est2:BI21214025	66.50	145.69	72.13	580	1	BI21214025	RE19713.Sprime RE dros	gb_est1:AA227827	993	906	66.00	144.42	993	1	AA227827	2566f12.r1 Soares_N
gb_gss:BH278694	66.50	145.36	75.28	589	1	BH278694	CH230-17119.TV CHORI-2	gb_est2:W72291	993	906	66.00	144.33	993	1	W72291	yc68e08.r1 Stratogens
gb_gss:BH060138	66.50	145.17	77.28	611	1	BH060138	RPCI-24-268L12.TJ #30 P	gb_est1:AA087068	993	906	66.00	143.94	993	1	AA087068	UI-HF-BM0-awg-h-11
gb_gss:AZ572565	66.50	144.37	85.41	659	1	AZ572565	307PvD12 Pb MBN #30 P	gb_gss:BH322157	993	906	66.00	143.52	993	1	BH322157	CH230-15A12.TV CHOR
gb_est1:AA440960	66.50	144.26	86.61	666	1	AA440960	LD12777.Sprime LD dros	gb_est2:BE461585	993	906	66.00	143.44	993	1	BE461585	UI-HF-BM0-awg-h-11
gb_est1:AA260343	66.50	144.03	89.20	681	1	AA260343	LP04144.Sprime LP dros	gb_est2:BI774580	993	906	66.00	143.29	993	1	BI774580	466755 MARC 1BOV B
gb_gss:BH318347	66.50	143.90	90.76	690	1	BH318347	CH230-119M20.TV CHORI	gb_est2:BE614138	993	906	66.00	142.86	993	1	BE614138	601503882F1 NIH_MGC
gb_gss:AZ859451	66.50	143.74	92.68	701	1	AZ859451	2M0165M08F Mouse 10kb	gb_est2:BI791429	993	906	66.00	142.65	993	1	BI791429	au053004.y1 Melton N
gb_gss:BH335860	66.50	143.39	96.90	725	1	BH335860	CH230-99H5.TV CHORI-23	gb_est1:AI929659	993	906	66.00	142.52	993	1	AI929659	au053005.y1 Schneide
gb_est1:BB597490	66.00	155.00	21.85	209	1	BB597490	BE597490 RIKEN full-le	gb_est2:BG041546	993	906	66.00	142.45	993	1	BG041546	sv359g06.y1 Gm-cl057
gb_est1:AV529706	66.00	150.74	37.75	316	1	AV529706	AV529706 Arabidopsis t	gb_est2:BE251981	993	906	66.00	142.19	993	1	BE251981	601107670F1 NIH_MGC
gb_est2:BE597537	66.00	147.51	57.09	432	1	BE597537	P11.70.G09.y1 A002 Pat	gb_est2:BE940929	993	906	66.00	141.82	993	1	BE940929	EST420508 MGHG Medi
gb_est1:AL902872	66.00															

gb_est2:BF103873	65.00	140.48	140.65	675	1	BF103873	601647380F1	NIH_MGC_61	+	64.50	136.41	237.27	891	1	BH151875	ENTPV13TR	Entamoeba	
gb_est2:BG499732	65.00	140.45	141.20	677	-	BG499732	602545149F1	NIH_MGC_60	-	64.50	134.92	349.06	1029	-	BH151735	AGNCSOURT	6394897	
gb_gss:BG298526	65.00	140.40	141.29	686	-	BG298526	CH230-84G12	TV CHORI-2	-	64.50	133.40	287.07	1193	-	BI2500	F18D4-Sp6	IGF Arabid	
gb_est1:AW689230	65.00	140.26	144.80	690	+	AW689230	NF016H08S91F1000	Devel	+	64.00	147.78	55.20	263	+	AV077298	AV077298	Mus muscul	
gb_est2:BI763780	65.00	140.26	144.80	690	+	BI763780	603049723F1	NIH_MGC_11	+	64.00	147.78	55.20	263	+	AV077298	AV077298	Mus muscul	
gb_est1:BB400791	65.00	139.86	152.34	717	-	BB400791	BB400791	RIKEN full-1e	-	64.00	143.56	94.85	396	-	AG062286	LO550C11-5	NIA Mous	
gb_gss:BIH13568	65.00	139.58	167.99	737	-	BIH13568	RPCI-24-386E1	TV RPCI	-	64.00	143.17	99.64	411	-	AW207979	M111000e	DSIR Medic	
gb_est2:BI332091	65.00	139.29	163.97	758	+	BI332091	602981426F1	NCI_CGAP_1	+	64.00	142.85	103.82	424	+	BI326857	NF034D06EC1F058	El	
gb_est2:BI7913538	65.00	139.23	165.12	762	-	BI7913538	603179137F1	NIH_MGC_12	-	64.00	141.79	118.98	470	-	BE943242	EST422821	MGHG Medi	
gb_est2:BE791195	65.00	139.11	167.70	771	-	BE791195	601584063F1	NIH_MGC_7	-	64.00	141.74	119.65	472	-	AL386987	MEBC93C01F1	MLBC Me	
gb_est1:AV762790	65.00	138.93	171.74	785	+	AV762790	AV762790	MDS Homo sapi	+	64.00	141.72	119.98	473	+	BI073353	kt23h05.y1	Strongyl	
gb_est1:AV762790	65.00	138.84	173.77	792	+	AV762790	AU020992	HEMIB1 Homo sa	+	64.00	141.49	123.69	484	+	AL446996	paramecium	tetreaure	
gb_est2:BG330853	65.00	138.71	176.68	801	-	BG330853	602431491F1	NIH_MGC_18	-	64.00	141.05	130.84	505	-	BI749607	ro80b09.y1	Heterode	
gb_gss:AG1910892	65.00	138.59	179.30	811	-	AG1910892	603067665F1	NIH_MGC_11	-	64.00	140.91	137.24	512	-	AQ449743	50000403.x1	CpiOwa	
gb_gss:AG1910892	65.00	138.30	186.06	834	-	AG1910892	ENTPMG61TR	Entamoeba hi	-	64.00	140.69	133.04	523	-	BM285475	524108 MARC	3BOV Bra	
gb_est2:BF794797	65.00	138.14	189.90	847	+	BF794797	602256640F1	NIH_MGC_85	+	64.00	140.49	140.52	533	+	BF649673	NF082B08EC1F1063	El	
gb_est1:AL556518	65.00	137.99	193.77	860	+	AL556518	ALS56518	LTI_NFL006.pl	+	64.00	140.47	140.86	534	+	BF631721	NF007A10DEC1F1070	Dr	
gb_gss:AG686076	65.00	137.96	194.37	862	+	AG686076	ENTIN13TR	Entamoeba hi	+	64.00	140.45	141.21	535	+	BF647076	NF007A10DEC1F1070	Dr	
gb_gss:AG686076	65.00	137.56	204.57	896	+	AG686076	ENTLV61TR	Entamoeba hi	+	64.00	140.26	144.71	545	+	BH049123	RPCI-24-39G120	TV R	
gb_gss:AG669951	65.00	137.55	204.87	897	+	AG669951	ENTFW26TR	Entamoeba hi	+	64.00	139.76	154.27	572	+	BG448038	NF105B02EC1F1015	El	
gb_gss:AG6711401	65.00	137.36	210.02	914	+	AG6711401	ENTIB51TR	Entamoeba hi	+	64.00	139.66	155.70	576	+	BJ095260	BJ095260	NIIBB Mochi	
gb_gss:AG6711832	65.00	137.34	210.63	916	+	AG6711832	ENTPS50TR	Entamoeba hi	+	64.00	139.66	156.42	578	+	BI512963	da64h09.y1	Wellcom	
gb_est2:BG823010	65.00	137.26	212.76	923	+	BG823010	602728030F1	NIH_MGC_15	+	64.00	139.62	157.13	580	+	BG447794	NF070D03EC1F1079	El	
gb_gss:AG686785	65.00	137.22	213.68	926	+	AG686785	ENTIC71TR	Entamoeba hi	+	64.00	139.48	160.01	588	+	BG452134	NF077A04LF1F1033	De	
gb_est2:BI912052	65.00	137.16	215.51	932	+	BI912052	601663229F1	NCI_CGAP_1	+	64.00	139.34	162.89	596	+	BE941470	EST421049	MGHG Medi	
gb_gss:CN8068519	65.00	137.09	217.35	938	+	CN8068519	601508248F1	NIH_MGC_71	+	64.00	139.32	163.25	597	+	BH443219	BOGNI25TR	BOGN Bras	
gb_gss:CN8068519	65.00	136.83	224.73	962	+	AL418814	T3 end of clone	AX0AAC	+	64.00	139.05	169.06	613	+	BE941610	EST421189	MGHG Medi	
gb_est2:BM139227	65.00	136.29	240.94	1014	+	BF139227	601783383F1	NCI_CGAP	+	64.00	139.03	169.43	614	+	BE941945	EST421461	MGHG Medi	
gb_est2:BM156645	65.00	135.73	258.69	1070	+	BM156645	AGNCSOURT_6408876	NIH	+	64.00	139.03	169.43	614	+	BE941945	EST421461	MGHG Medi	
gb_est2:BE876066	65.00	135.71	259.33	1072	+	BE876066	601485749F1	AGNCSOURT_6408876	NIH	+	64.00	139.03	169.43	614	+	BE941945	EST421461	MGHG Medi
gb_est2:BM462173	65.00	135.62	262.54	1082	+	BM462173	AGNCSOURT_6424373	NIH	+	64.00	138.95	171.26	619	+	BE875866	601487134F1	NIH_MGC	
gb_est2:BM465712	65.00	135.35	271.56	1110	+	BM465712	AGNCSOURT_6484795	NIH	+	64.00	138.51	181.21	646	+	BF649328	NF087A06EC1F1040	El	
gb_est2:BM458555	65.00	135.15	278.70	1132	+	BM458555	AGNCSOURT_6414130	NIH	+	64.00	138.41	181.24	652	+	BF649328	NF087A06EC1F1040	El	
gb_est2:BG339650	65.00	135.12	278.68	1135	+	BG339650	602437219F1	NIH_MGC_4	+	64.00	138.33	185.30	657	+	BG453541	NF097F08LF1F1064	De	
gb_est2:BI489462	65.00	134.95	285.89	1154	+	BI489462	603021023F1	NIH_MGC_1	+	64.00	138.13	190.16	670	+	BG586640	EST488408	MHAM Medi	
gb_htc:BC017057	65.00	130.93	479.09	3174	+	BC017057	Homo sapiens, Similar		+	64.00	137.87	196.47	682	+	BF645768	NF017C04EC1F1033	El	
gb_est2:BG508200	64.50	146.04	68.95	350	+	BM278924	Nb_ad1.196	M113 Nippo	-	64.00	137.52	205.70	711	-	AW331983	S1D11	AGS-1 Pneumoc	
gb_est1:BB761684	64.50	143.16	99.82	463	+	BB761684	BB761684	RIKEN full-1e	-	64.00	137.49	206.47	713	-	BH062681	RPCI-24-279P14	TV R	
gb_est2:BG347730	64.50	143.09	100.68	466	+	BE347730	sp0f12.y1	Gm-cl041	+	64.00	137.11	216.87	767	+	BH482871	BOH1T37TR	BOHI Bras	
gb_gss:AG5000175	64.50	142.36	110.51	500	+	AG5000175	V41D6 mtn-3xHA/lac2	Inf	+	64.00	136.74	220.94	767	+	BG589073	EST490882	MHRP- Med	
gb_gss:AG295038	64.50	142.02	115.50	517	+	AG295038	CH230-104A17	TV CHORI	+	64.00	136.62	230.94	776	+	BG585311	EST487075	MHAM Medi	
gb_gss:AG2912250	64.50	141.63	121.45	537	+	AG2912250	RPCI-24-167D24	TV RPCI	+	64.00	136.58	232.12	779	+	AL045777	DKF2p434F066_x1	434	
gb_gss:BM350930	64.50	141.55	122.65	541	+	BM350930	MEST270-G11	T3 ISUMS-F	+	64.00	136.28	241.23	802	+	BH284739	CH230-192C8	TV CHOR	
gb_gss:BM106317	64.50	141.44	124.45	547	+	BM106317	RPCI-24-306A13	TV RPCI	+	64.00	136.26	241.62	803	+	BF788917	602104648F1	NCI CGA	
gb_gss:BM065271	64.50	141.20	128.38	560	+	BM065271	RPCI-24-285H24	TV RPCI	+	64.00	136.24	242.42	805	+	BG776404	602563482F1	NIH_MGC	
gb_gss:AG394444	64.50	141.05	130.81	568	+	AG394444	1M0158G04F	Mouse 10kb	+	64.00	136.05	248.41	820	+	BH513370	BOGPK32TR	BOGP Bras	
gb_gss:AG796671	64.50	140.92	132.94	575	+	AG796671	CH230-160B7	TV CHORI-2	+	64.00	135.51	266.19	864	+	BG580865	602559407F1	NIH_MGC	
gb_gss:AG796671	64.50	140.71	136.63	587	+	AG796671	2M0052804R	Mouse 10kb	+	64.00	134.64	297.60	940	+	AL539727	AL539727	LTI_FLO13	
gb_gss:AG796671	64.50	140.68	137.24	589	+	AG796671	RPCI-23-225D23	TV RPCI	+	64.00	134.14	317.43	987	+	AL415369	T7 end of clone	AX0	
gb_gss:AG796671	64.50	140.64	137.86	591	+	BH341635	CH230-183G21	TV CHORI	+	64.00	134.10	319.14	991	+	AL422944	T3 end of clone	AX0	
gb_gss:AG796671	64.50	140.62	138.17	592	+	AQ158181	nbxd0010D18f	CUGI Rice	+	63.50	145.20	86.77	300	+	AU113726	AU113726	unpublishe	
gb_gss:AG796671	64.50	140.31	143.75	610	+	BH279391	CH230-166E1f	TJCB CHORI	+	63.50	144.25	76.77	329	+	BF425363	su55907.y1	Gm-cl069	
gb_gss:AG2824153	64.50	140.28	144.37	612	+	AG2824153	2M0098C08R	Mouse 10kb	+	63.50	141.78	119.18	418	+	AI213805	z5e10a1.f1	Aspergill	
gb_gss:AG947374	64.50	140.26	144.69	613	+	AG947374	RPCI-23-331010	TJ RPCI	+	63.50	141.21	128.05	442	+	AU008876	AU008876	Schizosacc	
gb_gss:AG2601985	64.50	140.08	148.13	624	+	AG2601985	1M0420C06R	Mouse 10kb	+	63.50	141.14	129.33	445	+	R2088471	AU088471	Sugano Mal	
gb_gss:AG2004955	64.50	140.06	148.44	625	+	AZ004955	RPCI-23-375A1	TV RPCI	+	63.50	140.55	139.42	471	+	R20111	yg18b02.r1	Soares Inf	
gb_est2:BG929257	64.50	140.05	148.76	626	+	BG929257	HNC60-1C11	R HNC (Hum	+	63.50	140.34	143.34	481	+	AZ052421	RPCI-23-40102	TV RP	
gb_gss:AG394444	64.50	140.05	148.76	626	+	BF645902	NF042D04EC1F041	Ellic	+	63.50	139.90	151.68	502	+	AI283316	AU183316	Rice cdna	
gb_gss:BM037806	64.50	139.90	151.59	635	+	BH037806	RPCI-24-387L7	TV RPCI	+	63.50	139.49	159.72	522	+	AZ700477	RPCI-23-233N23	TV R	
gb_gss:BM067137	64.50	139.80	153.49	641	+	BH067137	RPCI-24-371C9	TJ RPCI	+	63.50	139.22	165.41	536	+	AZ414879	LM0189A05R	Mouse 10	
gb_gss:BM092858	64.50	139.72	155.08	646	+	BH092858	RPCI-24-357C10	TJ RPCI	+	63.50	139.16	166.64	539	+	BE067807	MR4-BTO358	-050500-0	
gb_est1:AW574242	64.50	139.69	155.71	648	+	AW574242	EST316833	GVN Medicag	+	63.50	139.03	169.51	546	+	AW832449	sm10f03.y1	Gm-cl027	
gb_est1:BM127885	64.50	139.36	162.42	669	+	BH127885	BB127885	RIKEN full-1e	+	63.50	138.86	173.21	555	+	AZ111390	RPCI-23-472C4	TV RP	
gb_est2:BF006345	64.50	139.32	163.39	672	+	BF006345	EST434843	DSLIC Medicag	+	63.50	138.30	186.12	586	+	AZ368393	LM0118N21F	Mouse 10	
gb_gss:AG2040313	64.50	138.43	182.95	732	+	BH257513	CH230-243J20	TV CHORI	+	63.50	138.09	191.18	598	+	AZ884461	RPCI-23-203L3	TJ RP	
gb_gss:AG2040313	64.50	138.36	184.61	737	+	AZ040313	RPCI-23-243E17	TV RPCI	+	63.50	138.04	192.45	601	+	BM168394	EST570917	PYBS Plas	

63.50	137.20	214.34	-	63.50	137.07	217.83	652	! AW9211289	EST355293	Rat gene ind	qb_gss: A0766307	62.50	139.53	158.96	411	! A0766307	HS_5489_B2_D06_T7A
63.50	137.07	217.83	660	! AA056151	ZF55E09	Pv MBN #30	660	! AA056151	ZF55E09	Pv MBN #30	qb_est1: BG405800	62.50	139.50	159.47	412	! BG405800	SBC238h11.y1 Gm-cl05
63.50	137.07	217.83	660	! AA056151	ZF55E09	Pv MBN #30	660	! AA056151	ZF55E09	Pv MBN #30	qb_est1: BB725933	62.50	139.36	162.55	418	! BB725933	BAB725933 RIKEN full
63.50	137.00	220.01	664	! BB175228	BPI75228	RIKEN full-1e	664	! BB175228	BPI75228	RIKEN full-1e	qb_est1: BBG53982	62.50	139.36	162.55	431	! BBG53982	sad63901.y2 Gm-cl05
63.50	136.86	220.01	675	! AA050992	RPCI-23-461D5	TV RPCI-	675	! AA050992	RPCI-23-461D5	TV RPCI-	qb_est2: BG663435	62.50	139.04	169.27	431	! BG663435	DRAA9JA12 Rat DRG L
63.50	136.74	224.40	675	! A2824897	2M00959117R	Mouse 10kb	675	! A2824897	2M00959117R	Mouse 10kb	qb_est1: AW605378	62.50	138.53	180.79	431	! AW605378	UI-HF-BN0-alu-e-06-
63.50	136.75	227.04	681	! BF165454	601777345F1	NCI_CGAP_I	681	! BF165454	601777345F1	NCI_CGAP_I	qb_est1: BE0509860	62.50	138.35	185.03	461	! BE0509860	sn38b02.y1 Gm-cl016
63.50	136.73	227.48	682	! BF137660	601783189F1	NCI_CGAP_I	682	! BF137660	601783189F1	NCI_CGAP_I	qb_est2: H93030	62.50	138.19	188.75	468	! H93030	yv06b04.sl Soares fct
63.50	136.69	228.81	685	! AA260356	1M0103N04R	Mouse 10kb	685	! AA260356	1M0103N04R	Mouse 10kb	qb_gss: BH313433	62.50	138.19	188.75	468	! BH313433	CH230-101M12.TJ CHO
63.50	136.64	230.13	688	! BB135427	BB135427	RIKEN full-1e	688	! BB135427	BB135427	RIKEN full-1e	qb_gss: A2321786	62.50	137.93	195.18	480	! A2321786	CH242H08R Mouse 10
63.50	136.61	230.13	688	! A2876142	2M0191H06F	Mouse 10kb	688	! A2876142	2M0191H06F	Mouse 10kb	qb_gss: BH296566	62.50	137.93	195.18	480	! BH296566	CH230-92N14.TJ BJB CHO
63.50	136.61	231.02	690	! A2936570	2M0193M13F	Mouse 10kb	690	! A2936570	2M0193M13F	Mouse 10kb	qb_gss: BH2909362	62.50	137.70	201.12	491	! A2909362	1M043A002F Mouse 10
63.50	136.54	233.24	695	! A2958916	2M0226G22F	Mouse 10kb	695	! A2958916	2M0226G22F	Mouse 10kb	qb_gss: BH366225	62.50	137.70	201.12	491	! BH366225	CH230-28K9.TJ CHORI
63.50	136.42	236.79	703	! BH381735	AG-ND-164G6	TR ND-TAM	703	! BH381735	AG-ND-164G6	TR ND-TAM	qb_gss: A2927844	62.50	137.55	203.83	496	! A2927844	RPCI-23-262A4.TV RP
63.50	136.38	238.13	706	! BG858389	EST487153	MHAM Medica	706	! BG858389	EST487153	MHAM Medica	qb_gss: A2663209	62.50	137.55	204.92	498	! A2663209	1M05421A18R Mouse 10
63.50	136.15	245.29	722	! BH311576	CH230-72GK6	TV CHORI-23	722	! BH311576	CH230-72GK6	TV CHORI-23	qb_gss: A2767099	62.50	137.32	210.93	509	! A2767099	RPCI-23-409P8.TV RP
63.50	136.15	245.29	722	! BH322664	CH230-7071L	TVB CHORI-23	722	! BH322664	CH230-7071L	TVB CHORI-23	qb_gss: BH258587	62.50	137.22	213.67	514	! BH258587	CH230-75K9.TJ CHORI
63.50	136.05	248.44	729	! BH382673	AG-ND-143318	TF ND-TAM	729	! BH382673	AG-ND-143318	TF ND-TAM	qb_est1: AA942620	62.50	137.14	215.87	521	! AA942620	LD26942.5prime LD D
63.50	135.34	272.51	781	! A1660780	60330382F1	NIH_CGAP_I	781	! A1660780	60330382F1	NIH_CGAP_I	qb_gss: A2451320	62.50	137.08	217.53	521	! A2451320	1M0520H08R Mouse 10
63.50	135.30	272.53	784	! AV384514	HALOCYNTHA	Mouse 10kb	784	! AV384514	HALOCYNTHA	Mouse 10kb	qb_est2: B1362580	62.50	136.77	226.41	537	! B1362580	RE47178.5prime RE D
63.50	134.55	301.09	843	! BH4354354	BOGTJ35TR	TJ CHORI-	843	! BH4354354	BOGTJ35TR	TJ CHORI-	qb_gss: A26551247	62.50	136.53	233.69	550	! AW851407	IL3-CT0220-170200-0
63.50	134.52	302.03	845	! BH437532	BOGTJ35TR	BOGTJ35TR	845	! BH437532	BOGTJ35TR	BOGTJ35TR	qb_est1: AW851407	62.50	136.53	233.69	550	! AW851407	IL3-CT0220-170200-0
63.50	134.19	315.34	873	! A2683120	ENTIG9ATF	Entamoeba hi	873	! A2683120	ENTIG9ATF	Entamoeba hi	qb_gss: A2591483	62.50	136.47	235.37	553	! A2591483	1M0401A11R Mouse 10
63.50	133.93	325.89	895	! AL290055	Tetraodon nigroviridis	Mouse 10kb	895	! AL290055	Tetraodon nigroviridis	Mouse 10kb	qb_gss: A2238114	62.50	136.17	244.42	569	! A2328114	RPCI-23-84T23.TV RP
63.50	133.75	325.89	911	! AL526887	LTI_NFL003	NE	911	! AL526887	LTI_NFL003	NE	qb_gss: A2949436	62.50	136.16	244.99	570	! A2949436	2M0212L19R Mouse 10
63.50	133.73	334.59	913	! B5542931	GVSMER006F1	NH1_MGC_10	913	! B5542931	GVSMER006F1	NH1_MGC_10	qb_gss: A2579605	62.50	136.12	246.13	572	! A2579605	1M03616A02R Mouse 10
63.50	133.73	334.59	913	! B5542931	GVSMER006F1	NH1_MGC_10	913	! B5542931	GVSMER006F1	NH1_MGC_10	qb_gss: A2579605	62.50	136.12	246.13	572	! A2579605	1M03616A02R Mouse 10
63.50	134.52	302.03	845	! BH437532	BOGTJ35TR	BOGTJ35TR	845	! BH437532	BOGTJ35TR	BOGTJ35TR	qb_est1: AW851407	62.50	136.53	233.69	550	! AW851407	IL3-CT0220-170200-0
63.50	134.19	315.34	873	! A2683120	ENTIG9ATF	Entamoeba hi	873	! A2683120	ENTIG9ATF	Entamoeba hi	qb_gss: A2591483	62.50	136.47	235.37	553	! A2591483	1M0401A11R Mouse 10
63.50	133.93	325.89	895	! AL290055	Tetraodon nigroviridis	Mouse 10kb	895	! AL290055	Tetraodon nigroviridis	Mouse 10kb	qb_gss: A2238114	62.50	136.17	244.42	569	! A2328114	RPCI-23-84T23.TV RP
63.50	133.75	325.89	911	! AL526887	LTI_NFL003	NE	911	! AL526887	LTI_NFL003	NE	qb_gss: A2949436	62.50	136.16	244.99	570	! A2949436	2M0212L19R Mouse 10
63.50	133.73	334.59	913	! B5542931	GVSMER006F1	NH1_MGC_10	913	! B5542931	GVSMER006F1	NH1_MGC_10	qb_gss: A2579605	62.50	136.12	246.13	572	! A2579605	1M03616A02R Mouse 10
63.50	133.73	334.59	913	! B5542931	GVSMER006F1	NH1_MGC_10	913	! B5542931	GVSMER006F1	NH1_MGC_10	qb_gss: A2579605	62.50	136.12	246.13	572	! A2579605	1M03616A02R Mouse 10
63.50	134.52	302.03	845	! BH437532	BOGTJ35TR	BOGTJ35TR	845	! BH437532	BOGTJ35TR	BOGTJ35TR	qb_est1: AW851407	62.50	136.53	233.69	550	! AW851407	IL3-CT0220-170200-0
63.50	134.19	315.34	873	! A2683120	ENTIG9ATF	Entamoeba hi	873	! A2683120	ENTIG9ATF	Entamoeba hi	qb_gss: A2591483	62.50	136.47	235.37	553	! A2591483	1M0401A11R Mouse 10
63.50	133.93	325.89	895	! AL290055	Tetraodon nigroviridis	Mouse 10kb	895	! AL290055	Tetraodon nigroviridis	Mouse 10kb	qb_gss: A2238114	62.50	136.17	244.42	569	! A2328114	RPCI-23-84T23.TV RP
63.50	133.75	325.89	911	! AL526887	LTI_NFL003	NE	911	! AL526887	LTI_NFL003	NE	qb_gss: A2949436	62.50	136.16	244.99	570	! A2949436	2M0212L19R Mouse 10
63.50	133.73	334.59	913	! B5542931	GVSMER006F1	NH1_MGC_10	913	! B5542931	GVSMER006F1	NH1_MGC_10	qb_gss: A2579605	62.50	136.12	246.13	572	! A2579605	1M03616A02R Mouse 10
63.50	133.73	334.59	913	! B5542931	GVSMER006F1	NH1_MGC_10	913	! B5542931	GVSMER006F1	NH1_MGC_10	qb_gss: A2579605	62.50	136.12	246.13	572	! A2579605	1M03616A02R Mouse 10
63.50	134.52	302.03	845	! BH437532	BOGTJ35TR	BOGTJ35TR	845	! BH437532	BOGTJ35TR	BOGTJ35TR	qb_est1: AW851407	62.50	136.53	233.69	550	! AW851407	IL3-CT0220-170200-0
63.50	134.19	315.34	873	! A2683120	ENTIG9ATF	Entamoeba hi	873	! A2683120	ENTIG9ATF	Entamoeba hi	qb_gss: A2591483	62.50	136.47	235.37	553	! A2591483	1M0401A11R Mouse 10
63.50	133.93	325.89	895	! AL290055	Tetraodon nigroviridis	Mouse 10kb	895	! AL290055	Tetraodon nigroviridis	Mouse 10kb	qb_gss: A2238114	62.50	136.17	244.42	569	! A2328114	RPCI-23-84T23.TV RP
63.50	133.75	325.89	911	! AL526887	LTI_NFL003	NE	911	! AL526887	LTI_NFL003	NE	qb_gss: A2949436	62.50	136.16	244.99	570	! A2949436	2M0212L19R Mouse 10
63.50	133.73	334.59	913	! B5542931	GVSMER006F1	NH1_MGC_10	913	! B5542931	GVSMER006F1	NH1_MGC_10	qb_gss: A2579605	62.50	136.12	246.13	572	! A2579605	1M03616A02R Mouse 10
63.50	133.73	334.59	913	! B5542931	GVSMER006F1	NH1_MGC_10	913	! B5542931	GVSMER006F1	NH1_MGC_10	qb_gss: A2579605	62.50	136.12	246.13	572	! A2579605	1M03616A02R Mouse 10
63.50	134.52	302.03	845	! BH437532	BOGTJ35TR	BOGTJ35TR	845	! BH437532	BOGTJ35TR	BOGTJ35TR	qb_est1: AW851407	62.50	136.53	233.69	550	! AW851407	IL3-CT0220-170200-0
63.50	134.19	315.34	873	! A2683120	ENTIG9ATF	Entamoeba hi	873	! A2683120	ENTIG9ATF	Entamoeba hi	qb_gss: A2591483	62.50	136.47	235.37	553	! A2591483	1M0401A11R Mouse 10
63.50	133.93	325.89	895	! AL290055	Tetraodon nigroviridis	Mouse 10kb	895	! AL290055	Tetraodon nigroviridis	Mouse 10kb	qb_gss: A2238114	62.50	136.17	244.42	569	! A2328114	RPCI-23-84T23.TV RP
63.50	133.75	325.89	911	! AL526887	LTI_NFL003	NE	911	! AL526887	LTI_NFL003	NE	qb_gss: A2949436	62.50	136.16	244.99	570	! A2949436	2M0212L19R Mouse 10
63.50	133.73	334.59	913	! B5542931	GVSMER006F1	NH1_MGC_10	913	! B5542931	GVSMER006F1	NH1_MGC_10	qb_gss: A2579605	62.50	136.12	246.13	572	! A2579605	1M03616A02R Mouse 10
63.50	133.73	334.59	913	! B5542931	GVSMER006F1	NH1_MGC_10	913	! B5542931	GVSMER006F1	NH1_MGC_10	qb_gss: A2579605	62.50	136.12	246.13	572	! A2579605	1M03616A02R Mouse 10
63.50	134.52	302.03	845	! BH437532	BOGTJ35TR	BOGTJ35TR	845	! BH437532	BOGTJ35TR	BOGTJ35TR	qb_est1: AW851407	62.50	136.53	233.69	550	! AW851407	IL3-CT0220-170200-0
63.50	134.19	315.34	873	! A2683120	ENTIG9ATF	Entamoeba hi	873	! A2683120	ENTIG9ATF	Entamoeba hi	qb_gss: A2591483	62.50	136.47	235.37	553	! A2591483	1M0401A11R Mouse 10
63.50	133.93	325.89	895	! AL290055	Tetraodon nigroviridis	Mouse 10kb	895	! AL290055	Tetraodon nigroviridis	Mouse 10kb	qb_gss: A2238114	62.50	136.17	244.42	569	! A2328114	RPCI-23-84T23.TV RP
63.50	133.75	325.89	911	! AL526887	LTI_NFL003	NE	911	! AL526887	LTI_NFL003	NE	qb_gss: A2949436	62.50	136.16	244.99	570	! A2949436	2M0212L19R Mouse 10
63.50	133.73	334.59	913	! B5542931	GVSMER006F1	NH1_MGC_10	913	! B5542931	GVSMER006F1	NH1_MGC_10	qb_gss: A2579605	62.50	136.12	246.13	572	! A2579605	1M03616A02R Mouse 10
63.50	133.73	334.59	913	! B5542931	GVSMER006F1	NH1_MGC_10	913	! B5542931	GVSMER006F1	NH1_MGC_10	qb_gss: A2579605	62.50	136.12	246.13	572	! A2579605	1M03616A02R Mouse 10
63.50	134.52	302.03	845	! BH437532	BOGTJ35TR	BOGTJ35TR	845	! BH437532	BOGTJ35TR	BOGTJ35TR	qb_est1: AW851407	62.50	136.53	233.69	550	! AW851407	IL3-CT0220-170200-0
63.50	134.19	315.															

gb_gss:AQ411905	132.88	372.84	783	1	AQ411905	CpG0901A	CpIOWagDNaI	C	62.00	127.74	721.02	1146	1	B1600453	603246492F1	NH_MGC_1	
gb_gss:BH283394	132.87	373.47	784	1	BH283394	CH230-206A23	TJ	CHOR_1	61.50	142.74	105.37	238	1	BE1704533	2M00044N06F	Mouse	10
gb_gss:BG755427	132.78	377.89	791	1	BG755427	602713990F1	NTH	MGC_48	61.50	141.21	128.18	276	1	AZ700855	UI-R-BU1-atx-4	h1-10	0
gb_gss:A2675661	132.04	415.61	850	1	A2675661	ENTH057R	Entamoeba	h1	61.50	140.95	132.49	283	1	AE698531	g326	glabularid-hair	1
gb_gss:BH164326	131.29	457.50	914	1	BH164326	ENTH071R	Entamoeba	h1	61.50	140.52	139.97	295	1	BE024048	sm96a08.y1	Gm-c1015	5
gb_gss:A2669831	130.78	488.20	960	1	A2669831	ENTKM57F	Entamoeba	h1	61.50	138.44	182.82	361	1	A2325587	LM0048C08F	Mouse	10
gb_gss:CN806294	130.46	508.47	990	1	AL422546	T7	end of clone	AZ0A0A	61.50	137.72	200.43	387	1	BZ165807	EST568330	PyBS	Plas
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end of clone	AZ0A0A	61.50	137.48	206.62	396	1	AZ803117	2M063318F	Mouse	10
gb_gss:CN806294	130.24	523.47	1012	1	ALJ97982	T3	end										

gb_gss:BU036363	61.50	131.74	431.49	691	! BH036363	RPCI-24-295A15.TV RPCI	gb_gss:AZ843321	61.00	131.75	431.26	614	! AZ843321	2M01422G08F Mouse 10
gb_est2:BG593493	61.50	131.71	433.15	693	! BG593493	EST492171 CSTS Solanum	gb_gss:AZ007704	61.00	131.73	432.18	615	! AZ007704	RPCI-23-246123.TV R
gb_gss:AZ557685	61.50	131.68	434.80	695	! AZ557685	RPCI-23-21/EF.TV RPCI	gb_gss:AZ007704	61.00	131.73	432.18	615	! AZ007704	RPCI-24-222K19.TJ R
gb_est2:BI697769	61.50	131.65	436.46	697	! BI697769	60334663F1 NCI_CGAP_M	gb_est2:BE356393	61.00	131.61	438.70	622	! BE356393	DGL_124_D03.g1_A002
gb_gss:BU072341	61.50	131.60	439.77	701	! BU072341	RPCI-24-286GJ23.TV RPCI	gb_est2:BE445098	61.00	131.56	444.31	625	! BE445098	SP49606.y1_Gm-cl043
gb_est1:BB646819	61.50	131.54	443.10	705	! BB646819	BB646819 RIKEN Full-1e	gb_est2:BE445098	61.00	131.52	444.31	628	! BE445098	SP49606.y1_Gm-cl043
gb_gss:BU060549	61.50	131.46	447.26	710	! BU060549	60330363F1 NCI_CGAP_M	gb_gss:AZ908712	61.00	131.40	449.93	634	! AZ908712	VVA008F09_53005.TJ R
gb_gss:BU0605870	61.50	131.42	449.76	713	! BU0605870	RPCI-24-361B21.TJ RPCI	gb_hic:AK007129	61.00	131.40	450.87	635	! AK007129	MUS musculus adult
gb_gss:BU344418	61.50	131.32	455.61	720	! BU344418	CH230-52A1F1.TV CHORI-2	gb_gss:BU361369	61.00	131.35	453.69	638	! BU361369	CH230-95M6.TJ CHORI
gb_gss:BU369794	61.50	131.21	462.31	728	! BU369794	60334048F1 NCI_CGAP_M	gb_gss:AW309264	61.00	131.27	458.40	643	! AW309264	CH230-95M6.TJ CHORI
gb_gss:BU164641	61.50	131.19	463.16	729	! BU164641	BMJ16461 unpublished	gb_est1:AW913444	61.00	131.26	459.34	644	! AW913444	AV913444 K. Sato un
gb_gss:BU164641	61.50	131.16	464.84	731	! BU164641	BMJ16461 unpublished	gb_est1:AW913444	61.00	130.96	477.35	663	! AW913444	AV913444 K. Sato un
gb_gss:BU222880	61.50	131.02	473.27	741	! BU222880	CH230-5318.TV CHORI-2	gb_gss:AZ367264	61.00	130.96	477.35	663	! AZ367264	AV913444 K. Sato un
gb_est1:AL046546	61.50	131.00	474.96	743	! AL046546	DKFZP434Q1729.r1_434	gb_gss:AZ367264	61.00	130.86	483.86	669	! AZ367264	AV913444 K. Sato un
gb_gss:BU434800	61.50	130.94	478.34	747	! BU434800	BOGDY88TR BOGD Brassic	gb_est1:AL046546	61.00	130.79	487.86	674	! AL046546	DKFZP434Q1729.r1_434
gb_gss:BU434800	61.50	130.83	485.13	755	! BU434800	BOGDY88TR BOGD Brassic	gb_est1:AL046546	61.00	130.79	487.86	674	! AL046546	DKFZP434Q1729.r1_434
gb_gss:BU151429	61.50	130.75	490.23	761	! BU151429	2M0087D04F Mouse 10kb	gb_est1:AI225192	61.00	130.68	494.57	681	! AI225192	U332604.y1 Soares m
gb_gss:BU151429	61.50	130.63	497.92	770	! BU151429	2M0087D04F Mouse 10kb	gb_est1:AI225192	61.00	130.68	494.57	681	! AI225192	U332604.y1 Soares m
gb_gss:BU383802	61.50	130.59	500.48	773	! BU383802	CH230-130G15.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.51	505.63	779	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.43	507.92	789	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.38	514.23	789	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.35	522.87	799	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.32	531.54	809	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.29	545.49	825	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.25	574.54	858	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.21	602.15	889	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.17	629.17	919	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.13	645.52	937	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.10	687.77	983	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.07	810.57	1113	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.04	880.57	1285	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.01	905.63	1389	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	935.03	1485	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	965.03	1581	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	995.03	1677	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1025.03	1773	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
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gb_gss:BU383802	61.50	130.00	1085.03	1965	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1115.03	2061	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1145.03	2157	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
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gb_gss:BU383802	61.50	130.00	1205.03	2349	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1235.03	2445	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
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gb_gss:BU383802	61.50	130.00	1385.03	2925	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1415.03	3021	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1445.03	3117	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
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gb_gss:BU383802	61.50	130.00	1595.03	3597	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
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gb_gss:BU383802	61.50	130.00	1655.03	3789	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1685.03	3885	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1715.03	3981	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1745.03	4077	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1775.03	4173	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1805.03	4269	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1835.03	4365	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1865.03	4461	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
gb_gss:BU383802	61.50	130.00	1895.03	4557	! BU383802	CH230-57EA.TV CHORI-2	gb_gss:BU434800	61.00	130.43	510.96	698	! BU434800	BOGDY88TR BOGD Brassic
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 gb_gss:AZ314727 355.86 133.25 + 60.50
 gb_est2:BF1594837 358.85 133.18 + 60.50
 gb_gss:BF285313 358.85 133.18 + 60.50
 gb_gss:AZ296159 361.85 133.12 + 60.50
 gb_est1:AW639704 372.91 132.88 + 60.50
 gb_est1:AV533558 372.91 132.88 + 60.50
 gb_gss:BF309875 382.01 132.69 + 60.50
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 gb_est1:AV1897681 403.46 132.27 + 60.50
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 gb_gss:CN507053 932.98 125.57 994 +
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DEFINITION CH230-189M18-TV CHORI-230 Segment-1 Rattus norvegicus genomic clone
ACCESSION BH332419 DNA sequence.
VERSION BH332419.1 GI:17263133
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 660)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M

TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment

JOURNAL Unpublished (1999)
COMMENT Other_GSSs: CH230-189M18.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources.
page: http://www.chori.org/bacpac/or ering_information.htm). BAC end
plate: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 189 row: M column: 18
Seq primer: T7
Class: BAC ends.

FEATURES Location/Qualifiers
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/note="Vector: pTABAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"

BASE COUNT 268 a 114 c 117 g 161 t

ORIGIN

alignment_scores:
Quality: 76.50 Length: 41
Ratio: 2.638 Gaps: 2
Percent Similarity: 70.732 Percent Identity: 43.902

alignment_block:
US-09-528-682-3 x BH332419

Align seg 1/1 to: BH332419 from: 1 to: 660

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seq_documentation_block:
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DEFINITION saf03h08.y1 Gm-cl065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl065-4576 5' similar to TR:Q92W71 Q92W71 F14B2.18 PROTEIN.
; mRNA sequence.

ACCESSION BI316490
VERSION BI316490.1 GI:14990817
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE 1 (bases 1 to 540)

AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpellding,J., Coryell,V., Khanna
A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Stappier,M., Theising,B., Allen,M., Bowers
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
R., Waterston,R. and Willson,R.
Public Soybean EST Project
Unpublished (1999)

TITLE Public Soybean EST Project
JOURNAL Contact: Shoemaker R/Public Soybean EST Project
COMMENT Public Soybean EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 418.

FEATURES Location/Qualifiers
1..540

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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl065-4576"
/clone_lib="Gm-cl065"
/tissue_type="germinating shoots"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
germinating shoots of the cultivar Williams. The seeds
were allowed to germinate for 24 hours prior to being
cold stressed for 2 days at 4C. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."

BASE COUNT 122 a 133 c 104 g 181 t
ORIGIN

alignment_scores:
Quality: 76.00 Length: 99
Ratio: 1.357 Gaps: 6
Percent Similarity: 56.566 Percent Identity: 29.293

alignment_block:
US-09-528-682-3 x BI316490/rev ..
Align seg 1/1 to reverse of: BI316490 from: 1 to: 540
14 lIeGluValAsnThrAsnThrValThrGlnTleAsnGlySerAsnGluVa 30
:|||||:|||||:|||||:|||||: |||
462 CTGAAGCAACTAGTACACAACTACCAACGACCAAAAGACGTTGAGTG 413
30 lProLeuAspGlyArgTyrSerAsnPheAlaLeuIle..... 42
||| ||||| ||||| ||||| ||||| |||
412 CACGTTGCTTGGACGATATCTCTTTGTGGCATCATAAAGCCCTTGAT 363
43 ..SerAlaGluGlyMetGlnAspGlyAspLeuPheGlyThrValAsn 58
||| ||||| ||||| ||||| ||||| |||
362 ATAGTTTGGCGGAGG.....GGAAACCAATTGGATGCGCAAC 322
59 GlnSer...AsnPhePro.....MetSerTh 66
::: ||||| ||||| ||||| ||||| |||
321 ACTGCATTCATATCCGGTTCTTCATGATATATCCTCCACACATCAGG 272
66 rPheGluGlnValProAsnAsn.....LysGluPheLysGlyValI 80
:|||||:|||||:|||||:|||||: |||
271 GTATGAAGAACTCGATATAAATGAGTCCAGAAAGACGATTCGGGT.... 226
80 leSerAlaAsnValLysTyrAspMetAsnPheLysLysLeuLeuArg 95
:|||||:|||||:|||||:|||||: |||
225GAACTCGATGTCATCTGCAGCTGAGCGGACGATTCGA 187
seq_name: gb_est2:BM270616
seq_documentation_block:
LOCUS BM270616 554 bp mRNA linear EST 20-DEC-2001
DEFINITION Sak15d11.v1 Gm-c1075 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1075-3237 5' similar to TR:Q92W71 Q92W71 F14B2.18 PROTEIN. ; mRNA sequence.
BM270616 GI:17963872
VERSION EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
1 (bases 1 to 554)
Shoenaker,R., Keim,P., Vodkin,L., Erpelidg,J., Corryell,V., Khanna ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann ,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco

High quality sequence stop: 425.
Location/Qualifiers
1..554
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1075-3237"
/clone_lib="Gm-c1075"
/tissue_type="differentiating somatic embryos cultured on MSMGAC"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site1: EcoRI; Site2: XhoI; The cDNA library was constructed from mRNA isolated from differentiating somatic embryos cultured on MSMGAC. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. Tissue culture and library construction were performed by Francoise Thibaud-Nissen and Anu Khana (Lila Vodkin lab, University of Illinois)."
BASE COUNT 127 a 135 c 106 g 186 t
ORIGIN
alignment_scores:
Quality: 76.00 Length: 99
Ratio: 1.357 Gaps: 6
Percent Similarity: 56.566 Percent Identity: 29.293
alignment_block:
US-09-528-682-3 x BM270616/rev ..
Align seg 1/1 to reverse of: BM270616 from: 1 to: 554
14 lIeGluValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluVa 30
:|||||:|||||:|||||:|||||: |||
461 CTGAAGCCCACTAGAACACAACTACCAACGACCAAAAGACGTTGAGTG 412
30 lProLeuAspGlyArgTyrSerAsnPheAlaLeuIle..... 42
||| ||||| ||||| ||||| ||||| |||
411 CACGTTGCTTGGACGATATCTCTTTGTGGCATCATAAAGCCCTTGAT 362
43 ..SerAlaGluGlyMetGlnAspGlyAspLeuPheGlyThrValAsn 58
||| ||||| ||||| ||||| ||||| |||
361 ATAGTTTGGCGGAGG.....GGAAACCAATTGGATGCGCAAC 321
59 GlnSer...AsnPhePro.....MetSerTh 66
::: ||||| ||||| ||||| ||||| |||
320 ACTGCATTCATATCCGGTTCTTCATGATATATCCTCCACACATCAGG 271
66 rPheGluGlnValProAsnAsn.....LysGluPheLysGlyValI 80
:|||||:|||||:|||||:|||||: |||
270 GTATGAAGAACTCGATCTAAATCGAGTCCAGAAAGACGATTCGGGT.... 225
80 leSerAlaAsnValLysTyrAspMetAsnPheLysLysLeuLeuArg 95
:|||||:|||||:|||||:|||||: |||
224GAACTCGATGTCATCTGCAGCTGAGCGGACGATTCGA 186
seq_name: gb_est1:AL636005
seq_documentation_block:
LOCUS AL636005 723 bp mRNA linear EST 12-DEC-2001
DEFINITION AL636005 XGC-neurula silurana tropicalis cDNA clone tNeu015014 5', mRNA sequence.
AL636005
ACCESSION AL636005
VERSION AL636005.1 GI:16787984
KEYWORDS EST.
SOURCE western clawed frog.


```

|||||||
270 GTAATTTTCACTACCGACTTAATGCTTTTAAACATATCTCTCAGAAATGTA 319
|||||||
67 PheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAlaAs 83
|||||||
320 TTTTATATTGATCTCTCAAAAATGAATACCAGATTA.....AA 360
|||||||
83 nValLysTyrAspMetAsnPhe 90
|||||||
361 TTTAGATTATGACTATACTAT 382
|||||||

seq_name: gb_gss:BH266151

seq_documentation_block:
LOCUS BH266151 322 bp DNA linear GSS 30-NOV-2001
DEFINITION CH230-55L4_TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION BH266151
VERSION BH266151.1 GI:17176966
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 322)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: CH230-55L4.TJ
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 55 row: L column: 4
Seq primer: T7
Class: BAC ends.
FEATURES
source Location/Qualifiers
1..322
/organism="Rattus norvegicus"
/strain="BN/SSNhsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-55L4"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/notes="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNhsd/MCW) BAC library produced by
Pieter de Jong"
BASE COUNT 80 a 56 c 55 g 131 t
ORIGIN

alignment_scores:
Quality: 75.00 Length: 51
Ratio: 2.273 Gaps: 3
Percent Similarity: 64.706 Percent Identity: 39.216

alignment_block:
US-09-528-682-3 x BH266151/rev ..
Align seg 1/1 to reverse of: BH266151 from: 1 to: 322

|||||||
64 MetSerThrPheGluGlnValProAsnAsnLysGluPheLysGlyVal.. 79
|||||||
290 ATGACACCCCTTCAAAATAGTCCCAATAATATAAATACCTTGGTGTGAG 241
|||||||
80 IleSerAlaAsnValLys.....TyrAspMetAsnPheLysLysLeuL 94
|||||||
240 TTTAACCAAGGAAGTGAAGATCTGTATGATAAGAACTTCAAGCCTCTGA 191
|||||||
94 euArgPheMetGluAspAspPhe.....IleGlyValHis 105
|||||||
190 AGAAGAAATTGAAGAGATCTCAGAAGGTGGAAAGATCTCCATGCTCAT 141
|||||||
106 Gly 106
|||||||
140 GGA 138

seq_name: gb_est1:A1134063

seq_documentation_block:
LOCUS A1134063 583 bp mRNA linear EST 19-APR-2001
DEFINITION GH11413.5prime GH Drosophila melanogaster head pOT2 Drosophila
melanogaster cDNA clone GH11413 5prime similar to X61209: Top2
FBgn0003732 PID:98711 SWISS-PROT:P15348, mRNA sequence.
ACCESSION A1134063
VERSION A1134063.1 GI:3626621
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 583)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd. Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence DS05231
Plate: 114 row: B column: 1
High quality sequence stop: 534.
FEATURES
source Location/Qualifiers
1..583
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH11413"
/clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/notes="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. plasmid cDNA library."
BASE COUNT 150 a 140 c 124 g 169 t
ORIGIN

alignment_scores:
Quality: 75.00 Length: 118
Ratio: 1.230 Gaps: 5
Percent Similarity: 51.695 Percent Identity: 25.424

alignment_block:
US-09-528-682-3 x A1134063/rev ..
Align seg 1/1 to reverse of: A1134063 from: 1 to: 583

11 TyrGluProIleGluValAsnThrAsnThrValThrGlnIleAsnGlySe 27

```


Schurk, R., Ritter, E., Kohn, S., Underwood, K. and Marra, M.
Molecular Parasitology OvL3
Unpublished (1998)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genomesmith.edu

The library was constructed by Wenhong Lu. The library is available
from Dr. S.A. Williams, email genomesmith.edu when requesting this
clone from Dr. Williams, please reference the Williams lab clone id
- SMOVL3CAN1G04

Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 458.

FEATURES

1. .471
Location/Qualifiers

/organism="Onchocerca volvulus"
/strain="Sierra Leone"
/db_xref="taxon:6282"
/clone="onch556"
/clone_lib="Onchocerca volvulus infective larva cdna
(SAW94WL-OvL3)"
/lab_host="XLI-Blue MRF"
/note="Vector: lambda Unizap XR; Site.1: EcoR I; Site.2:
Xho I; Cutaneous filarial nematode parasite of humans.
mRNA was prepared from third stage infective larvae of
Onchocerca volvulus isolated from mosquitoes 10 days after
infection and converted to double stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNasep I. The library had 1.8 x 10E5 independent
recombinants and average insert size was 900 base pairs.
The library was constructed by Wenhong Lu. The library is
available from Dr. S.A. Williams, email genomesmith.edu."

BASE COUNT 159 a 92 c 118 g 102 t
ORIGIN

alignment_scores:
Quality: 74.00 Length: 102
Ratio: 1.321 Gaps: 7
Percent Similarity: 54.902 Percent Identity: 33.333

alignment_block:

US-09-528-682-3 x AA917243 ..

Align seg 1/1 to: AA917243 from: 1 to: 471

12 GluProIleGluValAsnThrAsnThrValThrGlnIleAsnGlySerAs 28
||||| : : : : : ||| ||| : : : : : |||
190 GAAAGATGGATGTCGATTAAT...GTTTCTCAGCTCAACACCATAA 236
28 nglu...ValProLeuAspGlyArgTyrSerAsnPheAlaLeuIleSerA 44
||||| : : : : : ||| : : : : : ||| : : : : :
237 CGAAGGAATGAGCTGGGATGTTTATGCTCAACAAGTGAGTGTGCTACT 286
44 laGluGlyGlyMetGlnAspGly.....Asp 52
: : : : : ||| : : : : : ||| : : : : :
287 CTGAACCTGCACCTCGATGCTGTCGAGCGGACGATGACGATCAGATC 336
53 LeuPheGlyThrValAsnGln...SerAsnPheProMet.....Se 65
||||| : : : : : ||| : : : : : ||| : : : : :
337 TGGGTTGGCCCTGTAATGAAGACCAAAATTTTCTCTTCGCAACATC 386
65 rThrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerA 82
||||| : : : : : ||| : : : : : ||| : : : : :
387 AACGAAACAGCAG.....CGCTTTATTAAAGAGCGGTACTG 421
82 laAsnValLysTyrAspMetAsnPhelLysLysLeuLeuArgPheMetGlu 98
||||| : : : : : ||| : : : : : ||| : : : : :
422 CATCAGCAGCTCTCAG.....CGGAACCTTGAAGATTTTATTTCGA 462

99 AspAsp 100
|||||
463 GATGAT 468

seq_name: gb_est1:AA333548

seq_documentation_block:

LOCUS AA333548 294 bp mRNA linear EST 21-APR-1997
DEFINITION EST37697 Embryo, 8 week I Homo sapiens cdna 5' end similar to
aggrecan 1, mRNA sequence.

ACCESSION AA333548

VERSION AA333548.1 GI:1985843

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 294)

AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult
, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White
, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,
Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,
Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinkar, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,
, Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
Kunsch, C., Hunglun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L.,
Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon
, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
Venter, J.C.

TITLE

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

COMMENT

Other_ESTs: THCL66485

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlavetigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse

FEATURES

Location/Qualifiers

1. .294

/organism="Homo sapiens"

/db_xref="ATCC (inhost):135261"

/db_xref="taxon:9606"

/clone_lib="Embryo, 8 week I"

/dev_stage="embryo, 8 wks"

/note="Organ: Embryo, 8 weeks; Vector: pBluescript SK-"

Site_1: ECORI; Site_2: XhoI"

BASE COUNT 69 a 62 c 86 g 74 t 3 others

ORIGIN

alignment_scores:

Quality: 73.50 Length: 70

Ratio: 1.670 Gaps: 2

Percent Similarity: 62.857 Percent Identity: 34.286

alignment_block:

US-09-528-682-3 x AA333548 ..

Align seg 1/1 to: AA333548 from: 1 to: 294

```

14 IleGluValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluVa 30
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
44 GTTGAAGTGGCCCTACTACATTTAAAGAAAGAAAGGCTTAGGGTCTGT 93
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
30 lProLeuAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGly 47
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
94 GGAACACAGTGGCCCTCCCTCCGGAGAGCAGATCTGTCCAGCAATCTG 143
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
47 lYMetGlnAsp.....GlyAspLeuPheGlyThrValAsnGlnSerAsn 61
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
144 GGATGTGGATGTGTCAGTGGACAGATTTTGGACAGTCGATTCAGTGGG 193
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
62 PheProMetSerThrPheGluGlnValProAsnAsnLysGluPheLysG 78
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
194 TTTACATCCAGACT.....CCGGAATTCAGTGG 222
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
78 yValIleSer 81
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
223 CCTACCAAGT 232

```

seq_name: gb_gss:BH313108

seq_documentation_block:

LOCUS BH313108 548 bp DNA linear GSS 03-DEC-2001
 DEFINITION CH230-101K19_TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
 CH230-101K19, DNA sequence.

ACCESSION BH313108

VERSION BH313108.1 GI:17241916

KEYWORDS GSS.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 548)
 Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
 ,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
 Jong,P. and Fraser,C.M

Rat BAC End Sequences from Library CHORI-230 EcoRI segment

Unpublished (1999)

Other_GSS: CH230-101K19.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(<http://www.chori.org/bacpac/rat230.htm>). For BAC library

availability, please contact Pieter de Jong (pdejong@email.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/orering_information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

Plate: 101 row: K column: 19

Seq primer: T7

Class: BAC ends.

FEATURES Location/Qualifiers

```

1..548
   /organism="Rattus norvegicus"
   /strain="BN/SSNHsd/MCW"
   /db_xref="taxon:10116"
   /clones="CH230-101K19"
   /clone_lib="CHORI-230 Segment 1"
   /sex="Female"
   /cell_type="Brain"
   /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"

```

BASE COUNT 124 a 102 c 107 g 215 t

ORIGIN

```

alignment_scores:
  Quality: 73.50 Length: 40
  Ratio: 2.625 Gaps: 2
  Percent Similarity: 70.000 Percent Identity: 45.000

alignment_block:
US-09-528-682-3 x BH313108/rev ..

Align seg 1/1 to reverse of: BH313108 from: 1 to: 548

64 MetSerThrPheGluGlnValProAsnAsnLysGluPheLysGlyVal.. 79
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
192 ATGACACCCCTTCACATAGTCCCAATAACATAAATATCTTGGTGTGAC 143
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
80 .lIleSerAlaAsnValLys.....TyrAspMetAsnPheLysLysLeuL 94
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
142 TTTAACCAAGCAAGTGAAGATCTGTATGACAAAGAACTTCAAGTCTCTGA 93
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
94 euArgPheMetGluAspAsp 100
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|
92 CGAAAGAAATTTGAGGAAGAT 73

```

seq_name: gb_est1:AUI18471

seq_documentation_block:

LOCUS AUI18471 852 bp mRNA linear EST 19-OCT-2000
 DEFINITION AUI18471 HEMBAI Homo sapiens cDNA clone HEMBAI003666 5', mRNA
 sequence.

ACCESSION AUI18471

VERSION AUI18471.1 GI:10933523

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 852)

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
 Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
 Isogai,T.

TITLE HRI human cDNA project

JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3951

Fax: 81-438-52-3952

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- 3'-end one pass sequencing; Helix

Research Institute; cDNA library construction; Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

FEATURES Location/Qualifiers

```

1..852
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="HEMBAI003666"
   /clone_lib="HEMBAI"
   /tissue_type="whole embryo, mainly head"
   /dev_stage="embryo, 10 weeks"
   /note="Vector: pME18SFL3"

```

BASE COUNT 198 a 194 c 248 g 210 t 2 others
 ORIGIN

alignment_scores:

```

  Quality: 73.50 Length: 74
  Ratio: 1.531 Gaps: 2
  Percent Similarity: 64.865 Percent Identity: 32.432

```

alignment_block:

SOURCE
ORGANISM
Stevia rebaudiana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
Heliantheae; Stevia.
1 (bases 1 to 643)
Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in
diterpene synthesis
Unpublished (2001)
Contact: Jim Brandle
Genomics and Biotechnology
Agriculture and Agri-Food Canada - SCPFRC
1391 Sandford St., London, Ontario, CANADA, N5V 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: brandleje@agr.ca
Seq primer: T3 promoter primer.

FEATURES
source
1..643
/organism="Stevia rebaudiana"
/strain="751/1501"
/cultivar="Landrace"
/db_xref="taxon:55670"
/clone_lib="Stevia field grown leaf cDNA"
/tissue_type="leaf"
/dev_stage="field grown, mid-size"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This
cDNA library was constructed from polyA+ enriched mRNA
from field grown leaves. Mid-size actively growing leaves
were collected and pooled from several plants and frozen
immediately after harvesting in liquid nitrogen. The cDNA
was prepared using an xhoi-poly(dT) linker-primer. An
EcoRI adapter was ligated to the blunt end cDNA and the
products were digested with EcoRI and XhoI enabling
directional cloning into the lambda ZAP Express vector.
The library was amplified using the host strain XL1-Blue
MRP'. Mass excision of the library was performed to
obtain pBK-CMV phagemid clones in the host strain XLOLR.
Single pass DNA sequencing was performed using the T3
promoter primer: 5' ATTACCCCTCAATAAGGGA 3'. This library
was constructed by Alex Richman."

BASE COUNT 212 a 112 c 149 g 170 t
ORIGIN
alignment_scores:
Quality: 72.50 Length: 90
Ratio: 1.450 Gaps: 3
Percent Similarity: 55.556 Percent Identity: 25.556
alignment_block:
US-09-528-682-3 x BG524649 ..
Align seg 1/1 to: BG524649 from: 1 to: 643

24 IleAsnGlySerAsnGluValProLeuAspGlyArgTyrSerAsnPheAl 40
103 GTTAATCTTGAACACATCATGCTATTGCTGTGCTGAATCGGC 152
40 AleuIleSerAlaGluGlyMetGlnAspGlyAspLeuPheGlyThrV 57
153 CCATGCTGCTATTGAAACGGGTCCAAAGAACGCTTAACGGTCATG 202
57 AlaAsnGln.....SerAsnPhe 62
203 TTGGTGAAATGAATCAGTTTCATGTAGAAAAAGCACACGACCATGTTT 252
63 ProMetSerThrPheGluGlnValProAsnAsnLysGluPheLysGlyVa 79
253 CCAAAGGATGCTGTGACGAGTGGCCCTGAAGCCAAAAGTTTCATCGGT 302

79 IleSerAlaAsnValLysTyrAspMetAsnPheLysLysLeuLeuArgp 96
303 TTATTTT.....GTAAATATC.....CGAA 322
96 heMetGluAspAspPheIle 102
323 CAGTTGAAGACCAAGATCTG 342
seq_name: gb_gss:AZ735738

seq_documentation_block:
LOCUS AZ735738 751 bp DNA linear GSS 25-JAN-2001
DEFINITION RPCI-24-70J5.TJB RPCI-24 Mus musculus genomic clone RPCI-24-70J5,
DNA sequence.
ACCESSION AZ735738
VERSION AZ735738.1 GI:12502115
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 751)
AUTHORS Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-24
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: RPCI-24-70J5.TVB
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igir.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/orderingframe.html>). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 70 row: J column: 5
Seq primer: SP6
Class: BAC ends.

FEATURES
Location/Qualifiers
1..751
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-70J5"
/clone_lib="RPCI-24"
/sex="Male"
/cell_type="Spleen/Brain"
/note="Vector: pRABAC1; Site_1: BamHI; Site_2: BamHI;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pRABAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."

BASE COUNT 311 a 128 c 125 g 187 t
ORIGIN

alignment_scores:
Quality: 72.50 Length: 73
Ratio: 1.576 Gaps: 4
Percent Similarity: 63.014 Percent Identity: 34.247

alignment_block:
US-09-528-682-3 x AZ735738 ..

Align seg 1/1 to: AZ735738 from: 1 to: 751

37 SerAsnPheAlaLeuIleSerAlaGlu.....GlyGlyMetGlnAspG1 51

alignment_block:

US-09-528-682-3 x AZ329751/rev ..

Align seg 1/1 to reverse of: AZ329751 from: 1 to: 485

```

57 ValAsnGlnSerAsnPhePrometSerThr..... 66
:|||||:|||||:|||||:|||||:
465 CTCAACAAGTCAATGGCTTCTCTACACAAGATAAACAGGCTGAG 416
77 .....PheGluGlnValProAsnAsnLysG 75
|||||:|||||:|||||:
415 AAAGAAATTAGGGAACAACCCCTTCTCAATAGTCCCAATAATATAA 366
75 luPheLysGlyVal...IleSerAlaAsnValLys.....TyrAspMet 88
:|||||:|||||:|||||:
365 AATACCTTGGAGTGACTCTAACTAAGCAACTGAAGATCTGTATGATAAG 316
89 AsnPhelLysLysLeuLeuArgPheMetGluAspAsp 100
|||||:|||||:|||||:
315 AACTTCAAGTCTCTGAAGAAAGAAATTAAGAAGAT 280

```

seq_name: gb_gss:AZ515059

seq_documentation_block:

LOCUS AZ515059 485 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0054F14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0054F14 F, DNA sequence.

ACCESSION AZ515059

VERSION AZ515059.1 GI:10696375

KEYWORDS

SOURCE house mouse.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 485)
Dunn,D., Aoyagi,A., Barber,M., Bescorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0054 row: F column: 14
Seq primer: CGTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 485.

Location/Qualifiers

1. .485

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0054F14"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

FEATURES

source

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 113 a 83 c 94 g 195 t

ORIGIN

alignment_scores:

Quality: 71.00 Length: 62

Ratio: 1.919 Gaps: 3

Percent Similarity: 59.677 Percent Identity: 32.258

alignment_block:

US-09-528-682-3 x AZ515059/rev ..

Align seg 1/1 to reverse of: AZ515059 from: 1 to: 485

57 ValAsnGlnSerAsnPhePrometSerThr..... 66

```

:|||||:|||||:|||||:|||||:
465 CTCAACAAGTCAATGGCTTCTCTACACAAGATAAACAGGCTGAG 416

```

67PheGluGlnValProAsnAsnLysG 75

```

|||||:|||||:|||||:|||||:
415 AAAGAAATTAGGGAACAACCCCTTCTCAATAGTCCCAATAATATAA 366

```

75 luPheLysGlyVal...IleSerAlaAsnValLys.....TyrAspMet 88

```

:|||||:|||||:|||||:|||||:
365 AATACCTTGGAGTGACTCTAACTAAGCAACTGAAGATCTGTATGATAAG 316

```

89 AsnPhelLysLysLeuLeuArgPheMetGluAspAsp 100

```

|||||:|||||:|||||:|||||:
315 AACTTCAAGTCTCTGAAGAAAGAAATTAAGAAGAT 280

```

seq_name: gb_gss:BH600950

seq_documentation_block:

LOCUS BH600950 502 bp DNA linear GSS 15-DEC-2001
DEFINITION BOGZV06TR BOGZ Brassica oleracea genomic clone BOGZV06, DNA

sequence.

ACCESSION BH600950

VERSION BH600950.1 GI:17853396

KEYWORDS

SOURCE GSS.

ORGANISM Brassica oleracea.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 502)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Other GSSs: BOGZV06TF

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1. .502

/organism="Brassica oleracea"

/strain="T0100DH3"

/db_xref="taxon:3712"


```

/clone="BOGZV06"
/clone_lib="BOGZ"
/note="vector: pHOsl; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOsl using BstXI linkers"
BASE COUNT      170 a  110 c  121 g  101 t
ORIGIN

```

```

alignment_scores:
  Quality: 71.00      Length: 102
  Ratio: 1.543        Gaps: 5
  Percent Similarity: 45.098  Percent Identity: 27.451

alignment_block:
US-09-528-682-3 x BH600950 ..
Align seg 1/1 to: BH600950 from: 1 to: 502
20 ThrValThrGlnIleAsnGlySerAsnGlu..... 29
||||| :|||:||||| |||
221 ACGTCCAGAACATTAAATGACCGCGCGAGCCGACCGTCGAGCC 270
30 .....ValProLeuAspGlyArgTyrSerAsnPheAlaLeuI 42
:||||| |||
271 AAGTGAGCGCGGCATGCCAAATGATCCGACCGTTCCAAT..... 310
42 leSerAlaGluGlyGlyMetGlnAspGlyAspLeuPheGlyThrValAsn 58
|||||:|||||:|||||:|||||
311 .....GTTGGGGTTCGGAGCGCGCAACTTCATGGGACA..... 343
59 GlnSerAsnPheProMetSerThrPheGluGlnValProAsnAsnLysG1 75
||| |||:|||||:|||||
344 .....CAAGGCGCGAACAATCAAGA 363
75 uPheLys....GlyValIleSerAlaAsnValLysTyrAspMetAsn.... 89
||||| :|||:|||||:|||||
364 GATCTCTATAAACTATATAATGTTCTTGGAAACGAAATGGAACAGAAATGATA 413
90 .....PheLysLysLeuLeuArgPheMetGlu 98
|||||:|||||:|||||:|||||
414 TCGACCTCGATGATATATTTTGGTTTATAAAGTAGCACTTGAGATCATGGAA 463
99 AspAsp 100
|||
464 AAAGAT 469

```

```
seq_name: gb_est2:BE442965
```

```

seq_documentation_block:
LOCUS      BE442965              548 bp    mRNA    linear    EST 25-JUL-2000
DEFINITION WHE1108_G02_N042S wheat etiolated seedling root normalized cDNA
            library Triticum aestivum cDNA clone WHE1108_G02_N04, mRNA
            sequence.

```

```

ACCESSION  BE442965
VERSION    BE442965.1  GI:9442489
KEYWORDS   EST.
SOURCE     bread wheat.
ORGANISM   Triticum aestivum

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Triticum.

```

```
REFERENCE  1 (bases 1 to 548)

```

```

AUTHORS    Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
            Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

```

```

TITLE       The structure and function of the expressed portion of the wheat
            genomes - Normalized root cDNA library

```

```
JOURNAL    Unpublished (2000)
```

```
COMMENT     Contact: Olin Anderson
```

```

US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105959773

```

```

Fax: 5105959818
Email: oanders@nps.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.

```

FEATURES

source

```

1..548
Location/Qualifiers
  /organism="Triticum aestivum"
  /cultivar="Chinese Spring"
  /db_xref="taxon:4565"
  /clone="WHE1108_G02_N04"
  /clone_lib="Wheat etiolated seedling root normalized cDNA
  library"
  /tissue_type="Root"
  /dev_stage="Five day old etiolated seedling"
  /lab_host="E. coli DH10B"
  /note="Vector: Lambda Uni-ZAP XR, excised phagemid
  pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
  surface-sterilized, germinated and grown aseptically in
  the dark at room temperature on filter paper with water,
  nystatin and cefotaxime in covered crystallization
  dishes. Roots were harvested. The tissue, total RNA, and
  poly(A) RNA were prepared, a cDNA library was made in the
  TJ Close lab (Choi, Close, Fenton) at the University of
  California, Riverside. The cDNA clones were in vivo
  excised to give pBluescript phagemids before
  normalization was carried out. The mass excision of
  phagemid library and normalization were done in HT Nguyen
  lab by D. Zhang at Texas Tech University. Normalization
  protocol used was that of Soares. Plasmid DNA
  preparations and DNA sequencing were performed in the OD
  Anderson lab (all other authors)."

```

```

BASE COUNT      125 a  148 c  115 g  160 t
ORIGIN

```

```

alignment_scores:
  Quality: 71.00      Length: 111
  Ratio: 1.420        Gaps: 2
  Percent Similarity: 45.045  Percent Identity: 23.423

alignment_block:
US-09-528-682-3 x BE442965 ..
Align seg 1/1 to: BE442965 from: 1 to: 548

```

```

8 GlnGlnAlaTyrGluProIleGluValAsnThrAsnThrValThrGlnI1 24
||||| :|||:|||||
126 CAGCAACCATTTACAGCCTGCATATTTAGGCTCTCTACTCCCGT 175
24 easn....GlySerAsnGluValProLeuAspGlyArgTyrSerAsnPheA 40
:|||||:|||||:|||||:|||||
176 ATCACAGGGGTGAGACAATGATGCCAATTTGACCAACAAGTCTTTTA 225
40 la.....
226 TCGCTGACACTCTGAGTCCAAACAGCTTCCTTTTGGACCAAGACCAGAA 275
41 .....LeulleSerAlaGluG1 46
|||||
276 TGGTTTATAGTCGTCACAAGGAAGTGGTTCTGTTCTATATCCTGCAACTTC 325
46 yGlyMetGlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheP 63
:|||||:|||||:|||||:|||||
326 ACCTCAACCTTTTGGTGATGTTTCAGGGGGCATTCGGACAAGCAACTTTC 375
63 roMetSerThrPheGluGlnValProAsnAsnLysGluPheLysGlyVal 79
|||||:|||||:|||||:|||||
376 CTATGCTCTCTGGGATGATGCCCTTCAGCAGAGAGTCTTCTATGTTT 425
80 IleSerAlaAsnValLysTyrAspMetAsnPhe 90
:|||||
426 GGAACCCCTAGTGACTCTTACGGAAGAAGGTTTC 458

```


Ratio: 1.392 Gaps: 3
Percent similarity: 68.919 Percent Identity: 27.027

alignment_block:

US-09-528-682-3 x A2672583 ..

Align seg 1/1 to: A2672583 from: 1 to: 871

```

20 ThrValThrGlnIleAsnGlySerAsnGluValProLeuAspGlyArgTy 36
   :::::||||| :::::||||| :::::||||| :::::|||||
375 TCATCACTCTCCACTGCGATGATGATGATTAACATGATGCTGCTATT 424
   :::::||||| :::::||||| :::::||||| :::::|||||
36 rSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetGlnAspGlyAspL 53
   :::::||||| :::::||||| :::::||||| :::::|||||
425 CACA...ATTACTAAATCCACTAGATTAAACAATAGAGATGAAATG 471
   :::::||||| :::::||||| :::::||||| :::::|||||
53 euPheGlyThrValAsnGlnSerAsnPheProMetSerThrPheGluGln 69
   :::::||||| :::::||||| :::::||||| :::::|||||
472 TTATTGGTACAATTACTCAATCTAGT...GATGTTTCAACA..... 509
   :::::||||| :::::||||| :::::||||| :::::|||||
70 ValProAsnAsnGlyGluPheGlyValIleSerAlaAsnValLysTy 86
   :::::||||| :::::||||| :::::||||| :::::|||||
510 ...CCATCAATTAATGTTGAAAAGGTACATTCACGATTACCAACA 556
   :::::||||| :::::||||| :::::||||| :::::|||||
86 rAspMetAsnPheLysLeu 93
   :::::||||| :::::||||| :::::||||| :::::|||||
557 AGACATAACTCTTACATCAATT 578
   :::::||||| :::::||||| :::::||||| :::::|||||

```

seq_name: gb_estl:AW587961

seq_documentation_block:

LOCUS AW587961 438 bp mRNA linear EST 09-MAY-2001
DEFINITION kp10c06.y1 TBN95TM-SSFH Strongyloides stercoralis cDNA 5', mRNA
sequence.
ACCESSION AW587961
VERSION AW587961.1 GI:7274991
KEYWORDS EST.
SOURCE Strongyloides stercoralis.
ORGANISM Strongyloides stercoralis.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimodea; Strongyloidea; Strongyloides.

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.,
Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.,
Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R.,
Ronko, I., Kennedy, S., McGuire, L., Beck, C., Underwood, K., Steptoe,
M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.,
Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
Wilson, R.

The Washington Univ. Nematode EST Project, 1999

Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

The library was constructed by Dr. Thomas Nutman and colleagues of
NIH, NIH (nutman@nih.gov). DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.

Seq primer: T3 ET from Amersham

High quality sequence stop: 418.

Location/Qualifiers

1..438

/organism="Strongyloides stercoralis"

/strain="Filariform larvae obtained from humans"

/db_xref="taxon:6248"

/clone_lib="TBN95TM-SSFH"

/lab_host="XL-1 Blue MRF" (Stratagene)"

/note="Vector: Lambda Uni-ZAP XR (Stratagene); Site_1:

ECORI; Site_2: XhoI; mRNA was purified from 4 x 10E5

filariform larvae which had been isolated from infected

humans. cDNA was constructed and, using adaptors, was
cloned unidirectionally into the vector from the EORI
site to the XhoI site. The library has an unamplified
titer of 1.5 x 10E6 pfu/ml and an amplified, undiluted
titer of 7 x 10E9 pfu/ml. The average insert size of the
unamplified library is 975 bp (range, 500-1500)."

BASE COUNT 211 a 37 c 53 g 137 t
ORIGIN

alignment_scores:

Quality: 70.50 Length: 92
Ratio: 1.195 Gaps: 3
Percent Similarity: 64.130 Percent Identity: 25.000

alignment_block:

US-09-528-682-3 x AW587961 ..

Align seg 1/1 to: AW587961 from: 1 to: 438

```

17 AsnThrAsnThrValThrGlnIleAsnGlySerAsnGlu.....ValPr 31
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
77 AATAATAATACACGAAAGATAAATTTGAGAACACAGAATATATCA 126
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
31 OLeuAspGlyArgTyrSerAsnPheAlaLeuIle.....SerA 44
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::
127 TTTCCCGCAGCGCATGTCAATACTTCAATAATAAAGATTGGATGATA 176
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::
44 laGluGlyGlyMetGlnAspGlyAspLeuPheGlyThrValAsnGlnSer 60
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::
177 AAAAGAGAAAAATCGGTGAAAAACAACTTTTAAATAAGTAAAAAATAA 226
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::
61 AsnPheProMetSerThrPheGluGlnValProAsnAsnLysGluPheLy 77
   :::|||||:::|||||:::|||||:::|||||:::|||||:::
227 AGTTTAAAAATAATATTTTAAAAAATGTTAATAATAATAAAGAC...AA 273
   :::|||||:::|||||:::|||||:::|||||:::|||||:::
77 sGlyValIleSerAlaAsnValLysTyrAspMetAsnPheLysLeuL 94
   |:::|||||:::|||||:::|||||:::|||||:::|||||:::
274 AACTATAATCTCGAATAATATATAGGAAGAATTTCTTACTTCAAAATAGTT 323
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::
94 euArgPheMetGluAspPheLe 102
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::
324 ATAAGGTAATAAAAAATGATACCATTT 349
   :::::|||||:::|||||:::|||||:::|||||:::|||||:::

```

seq_name: gb_estl:AA823163

seq_documentation_block:

LOCUS AA823163 448 bp mRNA linear EST 17-FEB-1998
DEFINITION vw41e03.r1 Soares_mammary_gland_NBMWG Mus musculus cDNA clone
IMAGE:1246396 5' similar to SW:Y079_HUMAN P53992 HYPOTHETICAL
PROTEIN KIAA0079 ;, mRNA sequence.

ACCESSION AA823163

VERSION AA823163.1 GI:2893031

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 448)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Marra M/Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu


```

seq_name: gb_gss:AZ423995

seq_documentation_block:
LOCUS      AZ423995               535 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION  IM0203B13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0203B13 F, DNA sequence.
ACCESSION  AZ423995
VERSION    AZ423995.1 GI:10548008
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 535)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0203 row: B column: 13
            Seq primer: CGTTGTAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 535.
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                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone_lib="UUGC1M0203B13"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /note="vector: pMD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adapted DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pMD42 (gi14732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid RL. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adapted mouse DNA was annealed to
            adapted vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
BASE COUNT 224 a 100 c 86 g 125 t
ORIGIN

alignment_scores:
Quality: 70.50 Length: 39
Ratio: 2.518 Gaps: 2
Percent Similarity: 71.795 Percent Identity: 43.590

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:::||||| ||| ::::: |||:::|||||
77 TATGTTCCGCACCTGGCTCTTCCCTCATGGATGGCTGAGACCAATGCTCT 126
:::||||| ||| ::::: |||:::|||||
19 nThrValThrGlnIleAsnGlySerAsnGluValProLeuAspGlyArg 36
:::||||| ||| ::::: |||:::|||||
127 CTTCTACCTCGGCTCTACCTACTGACAAAGTCTCCCTTGATAGTACCG 176
:::||||| ||| ::::: |||:::|||||
36 yrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetGlnAspGlyAsp 52
:::||||| ||| ::::: |||:::|||||
177 CTGAACCAACGACGAGTTCGAGCTCTCTGAAGAGCGCGCTTAAGCAGTGC 226
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US-09-528-682-3 x AZ423995
Align seg 1/1 to: AZ423995 from: 1 to: 535

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:::||||| ::| |||||:::||||| ||||| ::
163 ACAACCTTCATATATATCAACAATAATAGAAATACCTTGGAGTGACTCT 212
:::||||| ::| |||||:::||||| ||||| ::
80 eSerAlaAsnValLys.....TyrAspMetAsnPheLysLysLeuLeuA 95
:::||||| ||||| ||||| |||||:::||||| |
213 AACTTAGGAGTGAAGATCTGTATGATAAAACCTTCAAGTCTCTGAAGA 262
:::||||| ||||| ||||| |||||:::||||| |

95 rgPheMetGluAspAsp 100
|| :::|||||:::|||||
263 GAGAAATCGAAGAAGAT 279
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seq_name: gb_est2:BG804725
seq_documentation_block:
LOCUS      BG804725               600 bp      mRNA      linear      EST 20-DEC-2001
DEFINITION  0271-56 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
mRNA sequence.
ACCESSION  BG804725
VERSION    BG804725.1 GI:17951649
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 600)
AUTHORS    Mu,X., Zhao,S., Perashad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
            White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
TITLE      Gene expression in the developing mouse retina by EST sequencing
            and microarray analysis
JOURNAL    Nucleic Acids Res. 29 (24), 4983-4993 (2001)
COMMENT    Department of Biochemistry and Molecular Biology
            University of Texas M.D. Anderson Cancer Center
            Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
            Tel: 713 792 3646
            Fax: 713 790 0329.
FEATURES   Location/Qualifiers
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                /db_xref="taxon:10090"
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                /tissue_type="neural retina"
                /dev_stage="embryonic day 14.5 post-fertilization"
BASE COUNT 142 a 143 c 161 g 154 t
ORIGIN

alignment_scores:
Quality: 70.50 Length: 128
Ratio: 1.102 Gaps: 3
Percent Similarity: 50.000 Percent Identity: 21.094

alignment_block:
US-09-528-682-3 x BG804725
Align seg 1/1 to: BG804725 from: 1 to: 600

3 PheThrArgAlaLeuGlnGlnAlaTyrGluProlleGluValAsnThrAs 19
:::||||| ||| ::::: |||:::|||||
77 TATGTTCCGCACCTGGCTCTTCCCTCATGGATGGCTGAGACCAATGCTCT 126
:::||||| ||| ::::: |||:::|||||
19 nThrValThrGlnIleAsnGlySerAsnGluValProLeuAspGlyArg 36
:::||||| ||| ::::: |||:::|||||
127 CTTCTACCTCGGCTCTACCTACTGACAAAGTCTCCCTTGATAGTACCG 176
:::||||| ||| ::::: |||:::|||||
36 yrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetGlnAspGlyAsp 52
:::||||| ||| ::::: |||:::|||||
177 CTGAACCAACGACGAGTTCGAGCTCTCTGAAGAGCGCGCTTAAGCAGTGC 226
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alignment_scores:
  Quality: 70.50      Length: 128
  Ratio: 1.102       Gaps: 3
  Percent Similarity: 50.000   Percent Identity: 21.094

alignment_block:
  US-09-528-682-3 x BG865274 ..
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19 nThrValThrGlnIleAsnGlySerAsnGluValProLeuAspGlyArgT 36
190 CTTCTACCTCGGCTCTACCACTGACAAAGTCTCCCTTGATAGTACCG 239
36 yrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetGlnAspGlyAsp 52
240 CTGACACCACGAGCTGCGACCTCTGAAGAGCGCCTAAGCAGTGGCGAT 289
53 LeuPhe..... 54
290 ATATATTGCTGGAATGGGCTCAACCTCTTTGCTGGTGGGAGCAAG 339
55 .....GlyThrValAsnGlnSerAsnPheProMetSerThrPheG 68
340 CGTCCAAACAAGGTGTGTC...CAGAGCCTTTTCAACGTGTCTCCTTCA 386
68 luGlnVal.....ProAsn 72
387 GTCAGATCACCAGCGGCTTGAGTGTTCGCCAGTCTGGATATCCACTG 436
73 AsnLysGluPheLysGlyValIleSerAlaAsnValLysTyrrAspMetAs 89
437 TCTAAGAAAGTTCGAGGTCTCATCGATAGCTTACGGGCACAGAGAAATGCG 486
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seq_name: gb_est2:BI696195

seq_documentation_block:
LOCUS      BI696195      832 bp      mRNA      linear      EST 18-SEP-2001
DEFINITION 603345846F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5373466 5',
            mRNA sequence.
ACCESSION  BI696195
VERSION    BI696195.1 GI:15658824
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 832)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue procurement: Gilbert Smith, Ph.D.
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLML1950 row: 1 column: 11
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            Location/Qualifiers

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/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT      198 a      199 c      217 g      218 t
ORIGIN

alignment_scores:
  Quality: 70.50      Length: 128
  Ratio: 1.102       Gaps: 3
  Percent Similarity: 50.000   Percent Identity: 21.094

alignment_block:
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  Align seg 1/1 to: BI696195 from: 1 to: 832

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63 TATGTCGGCAGCTGGTTCCTCCATGATGGTGGTGGACCAATGCTT 112
19 nThrValThrGlnIleAsnGlySerAsnGluValProLeuAspGlyArgT 36
113 CTTCTACCTCGGCTCTACCACTGACAAAGTCTCCCTTGATAGTACCG 162
36 yrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetGlnAspGlyAsp 52
163 CTGAACCCACGAGCTGCGAGCCTCTGAAGAGCGCCTAAGCAGTGGCGAT 212
53 LeuPhe..... 54
213 ATATATTGCTGGAATGGGCTCAACCTCTTTGCTGGTGGGAGCAAG 262
55 .....GlyThrValAsnGlnSerAsnPheProMetSerThrPheG 68
263 CGTCCAAACAAGGTGTGTC...CAGAGCCTTTTCAACGTGTCTCCTTCA 309
68 luGlnVal.....ProAsn 72
310 GTCAGATCACCAGCGGCTTGAGTGTTCGCCAGTCTGGATAATCCACTG 359
73 AsnLysGluPheLysGlyValIleSerAlaAsnValLysTyrrAspMetAs 89
360 TCTAAGAAAGTTCGAGGTCTCATCGATAGCTTACGGGCACAGAGAAATGCG 409
89 nPheLysLysLeuLeuArgPheMetGluAspAsp 100
410 GTACATGAAGCTTATCGTGTCAAGCAGGAGAGAC 443

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OM of: US-09-528-682-3 to: Issued_Patents_NA:* out_format : pfs
 Date: Jun 18, 2002 7:41 PM
 About: Results were produced by the GenCore software, version 4.5,
 Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:
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Search information block:

Query: US-09-528-682-3
 Query length: 107
 Database: Issued_Patents_NA:*
 Database sequences: 303533
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 Search time (sec): 143.210000

score list:

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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-216-276A-15 +	68.00	141.55	3.39	1471	
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-998-416-30 -	65.50	146.41	1.82	518	
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-676-974-4 -	65.00	129.39	16.14	2277	
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Sequence	Strd Orig	ZScore	Escore	Len	Documentation
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-326-117B-1 +	60.00	107.33	273.20	5577	
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-385-335A-9 +	60.00	105.95	326.21	6350	
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-557-892-6 +	59.50	134.72	8.15	379	
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-387-858A-6 +	59.50	134.72	8.15	379	
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; Patent No. 5595912
; GENERAL INFORMATION:
; APPLICANT: VAKHARIA, VIKRAM
; APPLICANT: SNYDER, DAVID
; TITLE OF INVENTION: SPECIFIC DNA AND RNA SEQUENCES
; TITLE OF INVENTION: ASSOCIATED WITH US IBDV VARIANTS, VECTOR CARRYING DNA
; TITLE OF INVENTION: SEQUENCES, HOST CARRYING CLONED VECTOR, DEDUCED AMINO ACID
; TITLE OF INVENTION: SEQUENCES, VACCINE AND METHOD OF VACCINATION
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/216,276A
; FILING DATE: 23-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/083,784
; FILING DATE: 28-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/519,202
; FILING DATE: 04-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/227,311
; FILING DATE: 02-AUG-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelber, Steven B.
; REGISTRATION NUMBER: 30,073
; REFERENCE/DOCKET NUMBER: 2747-054-27 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 30:
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; GENERAL INFORMATION:
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; APPLICANT: SNYDER, DAVID
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; TITLE OF INVENTION: ASSOCIATED WITH US IBDV VARIANTS, VECTOR CARRYING DNA
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 08/083,784
; FILING DATE: 28-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/519,202
; FILING DATE: 04-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/227,311
; FILING DATE: 02-AUG-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelber, Steven B.
; REGISTRATION NUMBER: 30,073
; REFERENCE/DOCKET NUMBER: 2747-054-27 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3230 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Infectious bursal disease virus
; STRAIN: GLS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 114..3149
; US-08-216-276A-18

alignment_scores:
  Quality: 77.00 Length: 125
  Ratio: 1.305 Gaps: 6
  Percent Similarity: 47.200 Percent Identity: 21.600

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16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
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999 ATTCCAACCAACGAGATACCCAG.....CCAAAT 1027

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
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1028 CACATCC.....ATCAAACTGGAGATAGTACCTCCAAAGAGTGGTGC 1071

49 InAspGlyAsp.....LeuPheGlyThr 56
   ::::::::::::::::::::
1072 AGGAAGGGGACCATGATGTCATGTCGGCAAGTGGAGCCCTCAGCATGACG 1121

57 ValAsnGlnSerAsnPhePro..... 63
   ::::::::::::::::::::
1122 ATTCATGTGGCAACTATCCAGGGGCCCTCCGTCGCGTCACACTAGTAGC 1171

64 .....MetSerT 66
   ::::::::::::::::::::
1172 CTACGAAAGAGTGGCAACAGGATCTGCTACGGTCGCTGGGTGAGCA 1221

66 hPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
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83 AsnValLysTyrAsp.....MetAsnPheLysLeuLeuArgPh 96
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96 eMetGluAspPheIleGlyVal 104
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; seq_name: /cgn2_6/ptodata/2/lna/5A_COMB.seq:US-08-219-262B-11
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; seq_documentation_block:
; Sequence 11, Application US/08219262B
; Patent No. 5788970
; GENERAL INFORMATION:
; APPLICANT: VAKHARIA, VIKRAM
; APPLICANT: SNYDER, DAVID B
; TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
; TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
; TITLE OF INVENTION: THEREON
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,262B
; FILING DATE: 29-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 2747-047-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3230 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 114..3149
; US-08-219-262B-11

alignment_scores:
  Quality: 77.00 Length: 125
  Ratio: 1.305 Gaps: 6
  Percent Similarity: 47.200 Percent Identity: 21.600

alignment_block:
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Align seg 1/1 to: US-08-219-262B-11 from: 1 to: 3230

16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
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999 ATTCCAACCAACGAGATACCCAG.....CCAAAT 1027

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
   ::::::::::::::::::::
1028 CACATCC.....ATCAAACTGGAGATAGTACCTCCAAAGAGTGGTGC 1071

49 InAspGlyAsp.....LeuPheGlyThr 56
   ::::::::::::::::::::
1072 AGGAAGGGGACCATGATGTCATGTCGGCAAGTGGAGCCCTCAGCATGACG 1121

57 ValAsnGlnSerAsnPhePro..... 63
   ::::::::::::::::::::
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64 .....MetSerT 66
   ::::::::::::::::::::
1172 CTACGAAAGAGTGGCAACAGGATCTGCTACGGTCGCTGGGTGAGCA 1221

66 hPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
   ::::::::::::::::::::
1222 ACTTCGAGCTGATCCCAATCTGTAAGTACGAAAGAACCTGGTTACAGAA 1271

83 AsnValLysTyrAsp.....MetAsnPheLysLeuLeuArgPh 96
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96 eMetGluAspPheIleGlyVal 104
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96 emetGluAspPheIleGlyVal 104
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seq_name: /cgn2_6/ptodata/2/lna/5B_COMB.seq:US-08-708-541A-27

seq_documentation_block:
; Sequence 27, Application US/08708541A
; Patent No. 5871744
; GENERAL INFORMATION:
; APPLICANT: VAKHARIA, Vikram N.
; APPLICANT: MUNDT, Egbert
; TITLE OF INVENTION: A METHOD FOR GENERATING BIRNAVIRUS FROM
; TITLE OF INVENTION: SYNTHETIC RNA TRANSCRIPTS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W.,
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/708.541A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P8172-6002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3261 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..531
US-08-708-541A-27

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  Quality: 73.00      Length: 125
  Ratio: 1.259       Gaps: 6
Percent Similarity: 46.400      Percent Identity: 21.600

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32 uAspGlyArgTy-SerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
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1045 CACATCC.....ATCAAACTGGAGATAGTACCTCCAAAGGTGGTGC 1088

49 lnAspGlyAsp.....LeuPheGlyThr 56
:   |||   |||   |||
1089 AGCAGGGGATCAGATGTCTATGTCGCGCAAGAGGACCTAGCAGTGACG 1138

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57 ValAsnGlnSerAsnPhePro..... 63
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1139 ATCCATGGTGGCAACTATCCAGGGGCCCTCCGTCCTCAGCTAGTAGTGGC 1188

64 .....MetSerT 66
:   :   :   :   :   :   :   :   :   :   :   :   :
1189 CTAGAAAGAGTGGCAACAGGATCCGTCGTGTACGGTCGCTGGGTGAGCA 1238

66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
:   |||   |||   |||   |||   |||   |||   |||   |||   |||
1239 ACTTCGAGCTGATCCCAATCTGAAGTACGAAAGAACCTGGTTACAGAA 1288

83 AsnValIleTyrrAsp.....MetAsnPhelLysLysLeuLeuArgph 96
:   |||   |||   |||   |||   |||   |||   |||   |||   |||
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; Sequence 29, Application US/08708541A
; Patent No. 5871744
; GENERAL INFORMATION:
; APPLICANT: VAKHARIA, Vikram N.
; APPLICANT: MUNDT, Egbert
; TITLE OF INVENTION: A METHOD FOR GENERATING BIRNAVIRUS FROM
; TITLE OF INVENTION: SYNTHETIC RNA TRANSCRIPTS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARMELESTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W.,
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/708.541A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P8172-6002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3261 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 131..3166
US-08-708-541A-29

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alignment_scores:
  Quality: 73.00      Length: 125
  Ratio: 1.259       Gaps: 6
Percent Similarity: 46.400      Percent Identity: 21.600

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1016 ATTCCAACAACAGAGATAACCCAG.....CCAAAT 1044

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
   :: :: ::||| ::|||
1045 CACATCC.....ATCAAACTGGAGATAGTACCTCCAAAAGTGGTGC 1088

49 InAspGlyAsp.....LeuPheGlyThr 56
   || |||||
1089 AGCAGGGGATCAGATCTCATGGTCGGCAAGAGGGAGCCTAGCAGTGACG 1138

57 ValAsnGlnSerAsnPhePro.....MetSert 66
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1139 ATCCATGGTGGCAACTATCCAGGGGCCCTCCGTCCTCAGCTAGTGGC 1188

64 .....MetSert 66
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1189 CTACGAAAGAGTGGCAACAGGATCCGCTTACGGTCGCTGGGTGAGCA 1238

66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
   ::||| ::|||
1239 ACTTCGAGCTGATCCCAATCCTGAACCTAGCAAAAGACCTGGTTACAGAA 1288

83 AsnValLysTyrAsp.....MetAsnPheLysLysLeuLeuArgPh 96
   ::||| ::|||
1289 TAGGCGCGATTGACCCAGGAGCCATGAACACTACACAAAATTGATA...CT 1335

96 eMetGluAspAspPheIleGlyVal 104
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1336 GAGTGAGAGGGACCGCTCTGGCATC 1360

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-940-968-23

seq_documentation_block:
; Sequence 23, Application US/08940968
; Patent No. 6231868
; GENERAL INFORMATION:
; APPLICANT: YAO, Kun
; TITLE OF INVENTION: A METHOD FOR GENERATING NONPATHOGENIC, INFECTIOUS,
; FILE REFERENCE: 8288-7002
; CURRENT APPLICATION NUMBER: US/08/940,968
; CURRENT FILING DATE: 1997-09-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: pUC19FLAD78
; US-08-940-968-23

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Ratio: 1.259 Gaps: 6
Percent Similarity: 46.400 Percent Identity: 21.600

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-663-566A-1

seq_documentation_block:
; Sequence 1, Application US/08663566A
; Patent No. 5853733
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,566A
; FILING DATE: June 13, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:

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NAME/KEY: CDS
LOCATION: 129..2522
US-08-663-566A-1

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Quality: 73.00 Length: 125
Ratio: 1.259 Gaps: 6
Percent Similarity: 46.400 Percent Identity: 21.600

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1011 ATTCCCAACAAACGAGATACCCAG.....CCAAAT 1039

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
1040 CACATCC.....ATCAAACTGGAGATAGTACCTCCAAAAGTGGTGTC 1083

49 InAspGlyAsp.....LeuPheGlyThr 56
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1084 AGGCAGGGGATCAGATGTTATGTGTCGCGCAAGAGGGAGCCTAGCAGTGACG 1133

57 ValAsnGlnSerAsnPhePro.....MetSert 66
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64 .....MetSert 66

1184 CTACGAAAGAGTGGCAACAGGATCCGTCGTACGTCGCTGGGTGAGCA 1233

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1234 ACTTCGAGCTGATCCCAAACTCTGTAAGTACGAAAGAACCTGGTTACAGAA 1283

83 AsnValLysTyrAsp.....MetAsnPheLysLysLeuLeuArgPh 96
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96 eMetGluAspPheIleGlyVal 104
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; Sequence 1, Application US/08023610
; Patent No. 5928648
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkey
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/023,610
; FILING DATE: February 26, 1993
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3350 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 129..2522
US-08-023-610-1

alignment_scores:

Quality: 73.00 Length: 125
Ratio: 1.259 Gaps: 6
Percent Similarity: 46.400 Percent Identity: 21.600

alignment_block:

US-09-528-682-3 x US-08-023-610-1 ..

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1011 ATTCCCAACAAACGAGATACCCAG.....CCAAAT 1039

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
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1040 CACATCC.....ATCAAACTGGAGATAGTACCTCCAAAAGTGGTGTC 1083

49 InAspGlyAsp.....LeuPheGlyThr 56
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66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
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96 eMetGluAspPheIleGlyVal 104
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; Sequence 1, Application US/08288065A
; Patent No. 5961982
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkey S-
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; TITLE OF INVENTION: HVT-050 and Uses Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,065A
; FILING DATE: Aug-09-94
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 129..2522
; US-08-288-065A-1

alignment_scores:
  Quality: 73.00      Length: 125
  Ratio: 1.259       Gaps: 6
  Percent Similarity: 46.400   Percent Identity: 21.600

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32 uAspGlyArgTyrSerAsnPheAlaLeulleSerAlaGluGlyMetG 49
   :::: :::: :::: :::: :::: :::: :::: ::::
1040 CACATCC.....ATCAAACTGGAGATAGTACCTCCAAAAGTGTGTC 1083

49 lAspGlyAsp.....LeupheGlyThr 56
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1084 AGGACGGGGATCAGATGTTATGGTCGACAGGAGCCTAGCAGTGACG 1133

57 ValAsnGlnSerAsnPhePro..... 63
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1134 ATCCATGGTGGCACTACTCCAGGGGCCCTCGTCGCTACCGCTAGTCGC 1183

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56 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
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1234 ACTTCGAGCTGATCCCAATCTCTGAACCTAGCAAGAACCTGGTTACAGAA 1283

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83 AsnValLysTyrAsp.....MetAsnPheLysLysLeuLeuArgPh 96
   :::: |||||
1284 TACGGCGGATTTGACCCAGGAGCATGAACTACACAAATTTGATA...CT 1330

96 eMetGluAspPheIleGlyVal 104
   : ||| ||| ::::
1331 GAGTGAGAGGGAGCGCTCTGGGCATC 1355

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-362-240A-1

seq_documentation_block:
; Sequence 1, Application US/08362240A
; Patent No. 5965138
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Junker, David
; APPLICANT: Wild, Martha A
; TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/362,240A
; FILING DATE: Dec-22-94
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 129..2522
; US-08-362-240A-1

alignment_scores:
  Quality: 73.00      Length: 125
  Ratio: 1.259       Gaps: 6
  Percent Similarity: 46.400   Percent Identity: 21.600

alignment_block:
US-09-528-682-3 x US-08-362-240A-1 ..
Align seg 1/1 to: US-08-362-240A-1 from: 1 to: 3350

16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
   :::: ||||| :::: |||||
1011 ATTCACAAACAGAGATACCCAG.....CCAAAT 1039

32 uAspGlyArgTyrSerAsnPheAlaLeulleSerAlaGluGlyMetG 49
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1040 CACATCC.....ATCAAACTGGAGATAGTGACCTCCAAAGGTGGTGC 1083
49 lnAspGlyAsp.....LeuPheGlyThr 56
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1084 AGCAGGGGATCAGATGTTATGTCGCGAAGAGGGAGCCCTAGCAGTGACG 1133
57 ValAsnGlnSerAsnPhePro..... 63
: : : : :
1134 ATCCATGTTGGCAACTATCCAGGGGCCCTCCGTCGCGTCACGCTAGTGCG 1183
64 .....MetSert 66
: : : : :
1184 CTACGAAAGAGTGGCAACAGGATCCGTCGTCGCTGCGGTGAGCA 1233
66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
: : : : :
1234 ACTTCGAGCTGATCCCAATCTGTAAGTACGAAAGAACCTGTTACAGAA 1283
83 AsnValLysTyrAsp.....MetAsnPheLysLysLeuLeuArgPh 96
: : : : :
1284 TACGGCCGATTGACCCAGGAGCCATGACACACAAATTGATA...CT 1330
96 eMetGluAspAspPheIleGlyVal 104
: ||| ||| : : : : :
1331 GAGTGAGAGGACCGTCTTGGCATC 1355
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq: PCT-US95-10245-1

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seq_documentation_block:
; Sequence 1, Application PC/TUS9510245
; GENERAL INFORMATION:
; APPLICANT: SYNTRO CORPORATION
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10245
; FILING DATE: 09-AUG-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 129..2522
PCT-US95-10245-1

alignment_scores:
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Quality: 73.00 Length: 125
Ratio: 1.259 Gaps: 6
Percent Similarity: 46.400 Percent Identity: 21.600

alignment_block:
US-09-528-682-3 x PCT-US95-10245-1 ..
Align seg 1/1 to: PCT-US95-10245-1 from: 1 to: 3350

16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
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1011 ATTCAACAACAGAGATAACCCAG.....CCAAT 1039
32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetG 49
: : : : : : : : : : : : : : : : : :
1040 CACATC.....ATCAAACTGGAGATAGTGACCTCCAAAGGTGGTGC 1083
49 lnAspGlyAsp.....LeuPheGlyThr 56
|| |||||
1084 AGCAGGGGATCAGATGTTATGTCGCGAAGAGGGAGCCCTAGCAGTGACG 1133
57 ValAsnGlnSerAsnPhePro..... 63
: : : : :
1134 ATCCATGTTGGCAACTATCCAGGGGCCCTCCGTCGCGTCACGCTAGTGCG 1183
64 .....MetSert 66
: : : : :
1184 CTACGAAAGAGTGGCAACAGGATCCGTCGTCGCTGCGGTGAGCA 1233
66 hrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 82
: : ||||| : : |||||
1234 ACTTCGAGCTGATCCCAATCTGTAAGTACGAAAGAACCTGTTACAGAA 1283
83 AsnValLysTyrAsp.....MetAsnPheLysLysLeuLeuArgPh 96
: : : : :
1284 TACGGCCGATTGACCCAGGAGCCATGACACACAAATTGATA...CT 1330
96 eMetGluAspAspPheIleGlyVal 104
: ||| ||| : : : : :
1331 GAGTGAGAGGACCGTCTTGGCATC 1355
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq: US-08-530-492-2

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seq_documentation_block:
; Sequence 2, Application US/08530492
; Patent No. 5689052
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Dean, Duff A.
; APPLICANT: Fromm, Michael E.
; APPLICANT: Sanders, Patricia R.
; TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
; TITLE OF INVENTION: Expression in Monocotyledonous Plants and Method For
; TELECOMMUNICATION INFORMATION: Preparation Thereof
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF
; STREET: 700 Chesterfield Parkway No. 5689052th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,492
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/172,333
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10605)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1931 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-530-492-2

alignment_scores:
    Quality: 71.00      Length: 71
    Ratio: 1.690      Gaps: 4
    Percent Similarity: 59.155      Percent Identity: 33.803

alignment_block:
US-09-528-682-3 x US-08-530-492-2 ..
Align seg 1/1 to: US-08-530-492-2 from: 1 to: 1931
11 TyrGluProIleGluValAsnThrAsnThrValThrGlnIleAsnGly.. 26
||||: ||||:||||:||||: ||| ||| ||| ||| ||| ||| |||
903 TATTCTGTTGTTCCAAAGTCAACTCCAACTAGTGC.....CTCAACGGCTT 946
27 .....SerAsnGluValPro.....LeuAspG 34
||||: ||||:||||:||||: ||| ||| ||| ||| ||| |||
947 CTCGTGTCGCGCTCTCCAAACACCTTCCCAACATTGTTGGCTCCCGC 996
34 lyArgTyrSerAsnThrAlaLeuIleSerAla.....GluGly 46
||||: ||||:||||:||||: ||| ||| ||| ||| ||| |||
997 GCTCCACCAACACATCATGCTCTGCTGCTGCCAGAGTGAACACTCCGGC 1046
47 GlyMetGlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPhePr 63
||||: ||||:||||:||||: ||| ||| ||| ||| ||| |||
1047 GGCATCTCGAGCGCGACATGTTGTCATCGCGCTTCAACCAAGAACTTCAA 1096
63 oMetSerThrPhe 67
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-517-2

seq_documentation_block:
; Sequence 2, Application US/08906517
; Patent No. 6180774
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Dean, Duff A.
; APPLICANT: Fromm, Michael E.
; APPLICANT: Sanders, Patricia R.
; TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
; TITLE OF INVENTION: Expression in Monocotyledonous Plants and Method For
; TITLE OF INVENTION: Preparation Thereof
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,517
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:170
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1931 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-906-517-2

alignment_scores:
    Quality: 71.00      Length: 71
    Ratio: 1.690      Gaps: 4
    Percent Similarity: 59.155      Percent Identity: 33.803

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Align seg 1/1 to: US-08-906-517-2 from: 1 to: 1931
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||||: ||||:||||:||||: ||| ||| ||| ||| ||| ||| |||
903 TATTCTGTTGTTCCAAAGTCAACTCCAACTAGTGC.....CTCAACGGCTT 946
27 .....SerAsnGluValPro.....LeuAspG 34
||||: ||||:||||:||||: ||| ||| ||| ||| ||| |||
947 CTCGTGTCGCGCTCTCCAAACACCTTCCCAACATTGTTGGCTCCCGC 996
34 lyArgTyrSerAsnThrAlaLeuIleSerAla.....GluGly 46
||||: ||||:||||:||||: ||| ||| ||| ||| ||| |||
997 GCTCCACCAACACATCATGCTGCTGCTGCCAGAGTGAACACTCCGGC 1046
47 GlyMetGlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPhePr 63
||||: ||||:||||:||||: ||| ||| ||| ||| ||| |||
1047 GGCATCTCGAGCGCGACATGTTGTCATCGCGCTTCAACCAAGAACTTCAA 1096
63 oMetSerThrPhe 67
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-356-952-11

seq_documentation_block:
; Sequence 11, Application US/09356952
; Patent No. 6117663
; GENERAL INFORMATION:
; APPLICANT: Boriack-Sjodin, Ann
; APPLICANT: Margarit, S. M.
; APPLICANT: Bor-Sogil, Dafna
; APPLICANT: Cole, Philip
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 600-1-228N
; CURRENT APPLICATION NUMBER: US/09/356,952
; CURRENT FILING DATE: 1999-07-19
; EARLIER APPLICATION NUMBER: 60/093,631
; EARLIER FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5398
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;; TYPE: DNA
;; ORGANISM: Saccharomyces cerevisiae
US-09-356-952-11

alignment_scores:

Quality: 70.00 Length: 101
Ratio: 1.250 Gaps: 4
Percent Similarity: 55.446 Percent Identity: 25.743

alignment_block:

US-09-528-682-3 x US-09-356-952-11 ..

Align seg 1/1 to: US-09-356-952-11 from: 1 to: 5398

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36TyrSerAsnPheA 40

2094 TGTAACTACCACTACACCGATACATTGACTCCCAATGAGATCATCATCA 2143

40 laLeuIleSerAlaGluGlyMetGlnAspGlyAspLeuPheGlyThr 56

2144 GTACAGTCAAT...GAGACGATATGAAAAATTTCTCAGTCTTAGGTCCA 2190

57 ValAsnGlnSerAsn.....PheProMetSe 65

2191 AGAAATAGTGTAAATTTCTGCTGTAACCAAGGACTTCAATACAAAAATTC 2240

65 rThrPheGluGlnVal...ProAsnAsnLysGluPheLysGlyValIle 81

2241 TACTTTGGAGATTTTTCACCGTCCACAAAAATTTTAAGTCAGCTAAAT 2290

81 erAlaAsnValIlyTyrAspMetAsnPheLysLysLeuLeuArgPheMet 97

2291 CGATTTACGAAATGGTTGATGTGGAATTTCTCGAAATTTTAAAGGCATGTT 2340

98 Glu 98

2341 CAG 2343

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-103-840A-2

seq_documentation_block:

;; Sequence 2, Application US/09103840A

;; Patent No. 6294328

;; GENERAL INFORMATION:

;; APPLICANT: FLEISCHMAN, Robert D.

;; APPLICANT: WHITE, Owen R.

;; APPLICANT: FRASER, Claire M.

;; APPLICANT: VENTER, John C.

;; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

;; FILE REFERENCE: 24366-20007.00

;; CURRENT APPLICATION NUMBER: US/09/103,840A

;; CURRENT FILING DATE: 1998-06-24

;; NUMBER OF SEQ ID NOS: 2

;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 2

;; LENGTH: 4403765

;; ORGANISM: Mycobacterium tuberculosis

;; FEATURE:

;; OTHER INFORMATION: CDC 1551

;; OTHER INFORMATION: "n" bases at various positions throughout the sequence

;; OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2

alignment_scores:

Quality: 70.00 Length: 75

Ratio: 1.489 Gaps: 4
Percent Similarity: 62.667 Percent Identity: 28.000

alignment_block:

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25 nGlySerAsn.....GluValProLeuAspGlyArgTyrSerAsnPheA 40

4044811CGGCGCAACGCTCAAGAGCCACAGATCGGATCGGAGCAACAGCTGC 4044762

40 laLeuIleSerAlaGluGlyGlyMetGln...AspGly..... 51

4044761GGCTGATCTCTGAAGAGGGTAACAACGAGACCGGTCGAGAGGTC 4044712

52AspLeuPheGlyThrValAs 58

4044711ATCACCAGTACCCACCGGTCAGCGCTGACCTGTTCACGCGCTCAG 4044662

58 nGlnSerAsnPheProMetSerThr 66

4044661CGGCCAAAAACGCAAGGTCAGCACG 4044637

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-103-840A-1

seq_documentation_block:

;; Sequence 1, Application US/09103840A

;; Patent No. 6294328

;; GENERAL INFORMATION:

;; APPLICANT: FLEISCHMAN, Robert D.

;; APPLICANT: WHITE, Owen R.

;; APPLICANT: FRASER, Claire M.

;; APPLICANT: VENTER, John C.

;; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

;; FILE REFERENCE: 24366-20007.00

;; CURRENT APPLICATION NUMBER: US/09/103,840A

;; CURRENT FILING DATE: 1998-06-24

;; NUMBER OF SEQ ID NOS: 2

;; SOFTWARE: PatentIn Ver. 2.1

;; SEQ ID NO 1

;; LENGTH: 4411529

;; TYPE: DNA

;; ORGANISM: Mycobacterium tuberculosis

;; OTHER INFORMATION: H37Rv

US-09-103-840A-1

alignment_scores:

Quality: 70.00 Length: 75

Ratio: 1.489 Gaps: 4

Percent Similarity: 62.667 Percent Identity: 28.000

alignment_block:

US-09-528-682-3 x US-09-103-840A-1/rev ..

Align seg 1/1 to reverse of: US-09-103-840A-1 from: 1 to: 4411529

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25 nGlySerAsn.....GluValProLeuAspGlyArgTyrSerAsnPheA 40

4052743CGGCGCAACGCTCAAGAGCCACAGATCGGATCGGAGCAACAGCTGC 4052694

40 laLeuIleSerAlaGluGlyGlyMetGln...AspGly..... 51

4052693GGCTGATCCTGAAGAAGGGTAACAACGAGACCGAGCGGTCCGAGAAAGGTC 4052644

52AspLeuPheGlyThrValAs 58

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58 GlnSerAsnPheProMetSerThr 66

4052593CGCCCAAAACGCGAAGGTCAGCAGC 4052569

seq_name: /cqn2_6/ptodata/2/1na/5A_COMB.seq:us-07-944-525-1

seq_documentation_block:

; Sequence 1, Application US/07944525
; Patent No. 5632989
; GENERAL INFORMATION:
; APPLICANT: SNYDER, DAVID B.
; APPLICANT: VAKHARIA, VIKRAM
; APPLICANT: LUETTICKEN, HEINRICH D.
; TITLE OF INVENTION: ATTENUATED, LIVE VACCINE FOR DELAWARE
; TITLE OF INVENTION: STRAIN IBDV
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER AND
; STREET: 1755 JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/944,525

FILING DATE: 19920914

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KELBER, STEVEN B.

REGISTRATION NUMBER: 30,073

REFERENCE/DOCKET NUMBER: 2284-028-0 CIP

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3180 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 64..3099

US-07-944-525-1

alignment_scores:

Quality: 69.00 Length: 123

Ratio: 1.190 Gaps: 6

Percent Similarity: 47.154 Percent Identity: 21.951

alignment_block:

US-09-528-682-3 x US-07-944-525-1 ..

Align seg 1/1 to: US-07-944-525-1 from: 1 to: 3180

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...:|||||:|||||

949 ATTCCAACCAATGAGATAACCCAG.....CCAAT 977

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGly.....G 47

978 CACATCCATCATACTGGAGATAGTACCTCCAAAGTGTGGTCAGGCAG 1027

47 lyMetGln.....AspGlyAspLeuPheGlyThrValAsn 58

1028 GGGAAACAGATGTCTATGGTCGGCAAGTGGGAGCCTAGCAGTGCAGATCCAT 1077

59 GlnSerAsnPhePro..... 63

1078 GGTGGCAACTATCCAGGAGCCCTCCGTCACACTAGTGGCCTACGA 1127

64MetSerThrPheG 68

1128 AACAGTGGCAACAGGATCTCTCGTTACGGTCGCTGGGTGAGCAACTCG 1177

68 luGlnValProAsnAsnLysGluPheGlyValIleSerAlaAsnVal 84

1178 AGCTGATCCCAATCCTGAACTAGCAAGAACCTGTTACAGAATACGGC 1227

85 LysTyrAsp.....MetAsnPheLysLysLeuLeuArgPheMetG1 98

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98 uAspAspPheIleGlyVal 104

1275 GAGGAGACCACCTTGGCATC 1293

seq_name: /cqn2_6/ptodata/2/1na/5A_COMB.seq:US-08-219-262B-13

seq_documentation_block:

; Sequence 13, Application US/08219262B

; Patent No. 5788970

; GENERAL INFORMATION:

; APPLICANT: VAKHARIA, VIKRAM

; APPLICANT: SNYDER, DAVID B

; APPLICANT: MENGEL-WHERSAT, STEPHANIE A

; TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS

; TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED

; TITLE OF INVENTION: THEREON

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT

; STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/219,262B

; FILING DATE: 29-MAR-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 2747-047-27

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 413-3000

; TELEFAX: (703) 413-2220

; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3180 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA (genomic)


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;
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 64...3099
;
US-08-219-262B-13

alignment_scores:
  Quality: 69.00      Length: 123
  Ratio: 1.190       Gaps: 6
  Percent Similarity: 47.154      Percent Identity: 21.951

alignment_block:
US-09-528-682-3 x US-08-219-262B-13
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Align seg 1/1 to: US-08-219-262B-13 from: 1 to: 3180

16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
   ::: ||||| ::|||
949 ATTCCAAACCAATGAGATAACCCAG.....CCAAAT 977

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGly.....G 47
   ::: ::|||
978 CACATCCATCATCTAGGAGATAGTACCTCCAAAGTGTAGTGCAGGCAG 1027

47 lyMetGln.....AspGlyAspLeuPheGlyThrValAsn 58
   || |||
1028 GGGAACAGATGTCATGTCGGCAAGTGGGAGCCTAGCAGTGCAGTCCAT 1077

59 GlnSerAsnPhePro..... 63
   :::|||
1078 GGTGGCAACTATCCAGGAGCCCTCCGTCGCTCACACTAGTGGCCTACGA 1127

64 .....MetSerThrPheG 68
   :::|||
1128 AGAGTGGCAACAGGATCTCTGTTACGTCGTCGGGTGAGCAACTTCG 1177

68 luGlnValProAsnAsnLysGluPheLysGlyValIleSerAlaAsnVal 84
   || ::|||
1178 AGCTGATCCCAATCCTGAACTAGCAAGAACCTGTTACAGATACGGC 1227

85 LysTyrAsp.....MetAsnPheLysLysLeuLeuArgPheMetG1 98
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1228 CGATTGACCCAGGAGCCATGAACTACACGAAATTGATA...CTGAGTGA 1274

98 uAspAspPheIleGlyVal 104
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1275 GAGGACCCACTTGGCATC 1293

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-031-655-13

seq_documentation_block:
; Sequence 13, Application US/09031655
; Patent No. 6017759
; GENERAL INFORMATION:
; APPLICANT: VAKHARIA, VIKRAM
; APPLICANT: SNYDER, DAVID B
; APPLICANT: MENGEL-WHERSAT, STEPHANIE A
; TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
; TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
; TITLE OF INVENTION: THEREON
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,655
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/219,262
; FILING DATE: 29-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 2747-047-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3180 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 64...3099
;
US-09-031-655-13

alignment_scores:
  Quality: 69.00      Length: 123
  Ratio: 1.190       Gaps: 6
  Percent Similarity: 47.154      Percent Identity: 21.951

alignment_block:
US-09-528-682-3 x US-09-031-655-13
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Align seg 1/1 to: US-09-031-655-13 from: 1 to: 3180

16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
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949 ATTCCAAACCAATGAGATAACCCAG.....CCAAAT 977

32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGly.....G 47
   ::: ::|||
978 CACATCCATCATCTAGGAGATAGTACCTCCAAAGTGTAGTGCAGGCAG 1027

47 lyMetGln.....AspGlyAspLeuPheGlyThrValAsn 58
   || |||
1028 GGGAACAGATGTCATGTCGGCAAGTGGGAGCCTAGCAGTGCAGTCCAT 1077

59 GlnSerAsnPhePro..... 63
   :::|||
1078 GGTGGCAACTATCCAGGAGCCCTCCGTCGCTCACACTAGTGGCCTACGA 1127

64 .....MetSerThrPheG 68
   :::|||
1128 AGAGTGGCAACAGGATCTCTGTTACGTCGTCGGGTGAGCAACTTCG 1177

68 luGlnValProAsnAsnLysGluPheLysGlyValIleSerAlaAsnVal 84
   || ::|||
1178 AGCTGATCCCAATCCTGAACTAGCAAGAACCTGTTACAGATACGGC 1227

85 LysTyrAsp.....MetAsnPheLysLysLeuLeuArgPheMetG1 98
   :::|||
1228 CGATTGACCCAGGAGCCATGAACTACACGAAATTGATA...CTGAGTGA 1274

98 uAspAspPheIleGlyVal 104
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1275 GAGGACCCACTTGGCATC 1293

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-031-655-13

seq_documentation_block:
; Sequence 13, Application US/09031655
; Patent No. 6017759
; GENERAL INFORMATION:
; APPLICANT: VAKHARIA, VIKRAM
; APPLICANT: SNYDER, DAVID B
; APPLICANT: MENGEL-WHERSAT, STEPHANIE A
; TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
; TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
; TITLE OF INVENTION: THEREON
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,655
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/219,262
; FILING DATE: 29-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 2747-047-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3180 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 64...3099
;
US-09-031-655-13
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1219 T...GTACAGCTTGCAGGGGTGACCAACTTCGAGCTAATCCCAACCTGTG 1265
      74 ysGluPheLysGlyValIleSerAlaAsnValLysTyrAsp..... 87
      :: |||:||||:||||: |||:||||: |||:||||: |||:||||:
1266 AGCTTGCAAGAACACTAGTTCACAGATGTCGCGCTTTGACCCCGGAGCA 1315
      88 MetAsnPheLysGlyValIleSerAlaAsnValLysTyrAsp..... 104
      |||||:||||:||||: |||:||||: |||:||||: |||:||||:
1316 ATGAAGTACACAAACTAATA...CTGAGTGAGAGAGATCGTCTAGGCAT 1362
      104 l 104
      1363 C 1363

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-708-541A-33

seq_documentation_block:
; Sequence 33, Application US/08708541A
; Patent No. 5871744
; GENERAL INFORMATION:
; APPLICANT: VAKHARIA, Vikram N.
; APPLICANT: MUNDT, Egbert
; TITLE OF INVENTION: A METHOD FOR GENERATING BIRNAVIRUS FROM
; TITLE OF INVENTION: SYNTHETIC RNA TRANSCRIPTS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKADO, MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N.W.,
; STREET: Suite 330 - G Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/708,541A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTS, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P8172-6002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3264 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 131..3169
; US-08-708-541A-33

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      Ratio: 1.232      Gaps: 5
      Percent Similarity: 47.863      Percent Identity: 24.786

alignment_block:
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16 ValAsnThrAsnThrValThrGln..... 23

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seq_name: /cqn2_6/ptodata/2/ina/6B_COMB.seq:US-09-398-550-1

FILING DATE: 19910718


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2936 GACATTATGCTGTTATATATAAACACGATTCTGCTTCAAATATATATCCTAT 2985
      87 AspMetAsnPhelysLysLeu 93
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2986 TCTTTAAACATAAAGGATTA 3006

seq_name: /cgn2_6/ptodata/2/1na/6B_COMB.seq:US-08-998-416-30

seq_documentation_block:
; Sequence 30, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebeschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPTII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Melgs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/GCG1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 518 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1007RP
; US-08-998-416-30

alignment_scores:
      Quality: 65.50      Length: 63
      Ratio: 1.489      Gaps: 4
Percent Similarity: 69.841      Percent Identity: 31.746

alignment_block:
US-09-528-682-3 x US-08-998-416-30/rev ..

Align seg 1/1 to reverse of: US-08-998-416-30 from: 1 to: 518

53 LeuPheGlyThrValAsnGlnSerAsnPhePrometSerThrPheGl 69
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222 CTTATCCCAACACCACTGGTTCTCTCCACAGACTAAGGACATTGG 173

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,974
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-676-974-4

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alignment_scores:
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  Ratio: 1.140       Gaps: 4
  Percent Similarity: 49.138   Percent Identity: 24.138

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alignment_block:

US-09-528-682-3 x US-08-676-974-4/rev ..

Align seg 1/1 to reverse of: US-08-676-974-4 from: 1 to: 2277

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18 ThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLeuAspG1 34
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1353 ACCAGCAGGATCAGACCTTCACGAGCCAGGTACAGGTACGGGTACCGG 1304

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34 yArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetGlnAspG 51
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1303 TCGGTTTTTTAACTTT.....GGTGTCTGCAGTTTA 1272

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51 lYAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSerThrPhe 67
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1271 GCAGCTTCACGGGTACACGCCAGGTCACTTTTCAGCTGACGACCGTC 1222

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68 GluGlnValProAsnAsnLysGluPheLys..... 77
:::
1221 CAGTTTCAGACCAACAGCTTCGTTTTCGGGGAAGCAGCAGGCATT 1172

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78 .....GlyV 79
1171 TCTGAGCAGCTTCCTGGGTCACTGAACCTGAGCGAAAGCGCAACCTTTGGAG 1122

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```

79 alileSerAlaAsnValLysTyrAspMetAsn.....PheLysLys 92
|||||
1121 TGTTCGGTGTCCGGGTGACAGCATACAGCATATTTTCAGTTTACCGGAA 1072

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93 LeuLeu...ArgPheMetGluAspAspPheIleGlyValHisGlyGlu 107
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1071 CTGCTGCAGCAGTTTACCCAGTCTCTTCTTCGGAGTGAAGGACAG 1024

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-098-487-4

seq_documentation_block:

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; Sequence 4, Application US/09098487
; Patent No. 5917025
; GENERAL INFORMATION:
; APPLICANT: COLLINS, Kathleen
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 11

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,487
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-098-487-4

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alignment_scores:
  Quality: 65.00      Length: 116
  Ratio: 1.140       Gaps: 4
  Percent Similarity: 49.138   Percent Identity: 24.138

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18 ThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLeuAspG1 34
|||||
1353 ACCAGCAGGATCAGACCTTCACGAGCCAGGTACAGGTACGGGTACCGG 1304

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34 yArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetGlnAspG 51
|||||
1303 TCGGTTTTTTAACTTT.....GGTGTCTGCAGTTTA 1272

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51 lYAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSerThrPhe 67
|||||
1271 GCAGCTTCACGGGTACACGCCAGGTCACTTTTCAGCTGACGACCGTC 1222

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68 GluGlnValProAsnAsnLysGluPheLys..... 77
:::
1221 CAGTTTCAGACCAACAGCTTCGTTTTCGGGGAAGCAGCAGGCATT 1172

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78 .....GlyV 79
1171 TCTGAGCAGCTTCCTGGGTCACTGAACCTGAGCGAAAGCGCAACCTTTGGAG 1122

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79 alileSerAlaAsnValLysTyrAspMetAsn.....PheLysLys 92
|||||
1121 TGTTCGGTGTCCGGGTGACAGCATACAGCATATTTTCAGTTTACCGGAA 1072

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alignment_scores: 64
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Percent Similarity: 51.562 Percent Identity: 32.812

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1021 ATCATTGCAAAATCTGGGATTCACCTGGGGACCTGCTGAAATTCAC
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54  eGlyThrValAsnGlnSerAsnPhProMet.....
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1071 TGGAGGAGCAAAATGTCTCTGGATTTCAGATTGTAGACTACGACGATTV
    ..

65  .....SerThrPheGluGlnValPro.....
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1121 TGGTGTCTAAATTTATAGAAAGTGGTCAACACTGGGAAG.....
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73  AsnLysGluPheLysGlyValIleSerAlaAsnValLysTyr 86

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54 eGlyThrValAsnGlnSerAsnPheProMet..... 64
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65 .....SerThrPheGluGlnValProAsn 72
1121 TGGTGCTCTAAATTTATAGAAAGATGCTCAACACTGGAAGAG..... 1161
73 AsnLysGluPheLysGlyValIleSerAlaAsnValLysTyr 86
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seq_name: /cgn2_6/ptodata/2/1na/5B_COMB.seq:us-08-486-269A-3
seq_documentation_block:
; Sequence 3, Application us/08486269A
; Patent No. 5945509
; GENERAL INFORMATION:
; APPLICANT: Heinemann, Stephen F.
; APPLICANT: Boulter, James R.
; APPLICANT: Hollmann, Michael
; APPLICANT: Bettler, Bernhard
; APPLICANT: Jensen, Jan E.
; TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows DEMONSTRATION Version 2.0D
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,269A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/013,767
; FILING DATE: 04-FEB-1993
; APPLICATION NUMBER: 07/718,575
; FILING DATE: 21-JUN-1991
; APPLICATION NUMBER: PCT/US90/06153
; FILING DATE: 25-OCT-1990
; APPLICATION NUMBER: 07/428,116
; FILING DATE: 27-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9986
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3505 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: Glur2
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 316...2964
; OTHER INFORMATION:
; US-08-486-269A-3
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  Quality: 62.50      Length: 64
  Ratio: 1.894       Gaps: 3
  Percent Similarity: 51.562  Percent Identity: 32.812
alignment_block:
US-09-528-682-3 x US-08-486-269A-3 ..
Align seg 1/1 to: US-08-486-269A-3 from: 1 to: 3505
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1021 ATCATTTGCAAAATCTGGGATTCTACTGATGGGACCTGCTGAAATTCAGTT 1070
54 eGlyThrValAsnGlnSerAsnPheProMet..... 64
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1071 TGGAGGAGCAAAATGCTCTGGATTCTAGACTAGCAGGATTCCC 1120
65 .....SerThrPheGluGlnValProAsn 72
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seq_documentation_block:
; Sequence 8, Application US/08397602A
; Patent No. 5646044
; GENERAL INFORMATION:
; APPLICANT: Wilson, Charles R
; APPLICANT: Tang, Maria R
; APPLICANT: Berger, Harald
; APPLICANT: Christianson, Teresa M
; APPLICANT: Hansen, Dieter
; TITLE OF INVENTION: Expression Systems for the Production
; TITLE OF INVENTION: of Target Proteins in Bacillus
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henkel Corporation Law Department
; STREET: 140 Germantown Pike, Suite 150
; CITY: Plymouth Meeting
; STATE: PA
; COUNTRY: USA
; ZIP: 19462
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,602A
; FILING DATE: 02-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jaeschke, Wayne C
; REGISTRATION NUMBER: 21,062
; REFERENCE/DOCKET NUMBER: D8969/M4828
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 832-2200
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA sequence of the
; DESCRIPTION: alkaline protease gene of strain ATCC 53926 and its controlling
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;
; DESCRIPTION: elements*
; ORIGINAL SOURCE:
; ORGANISM: Bacillus licheniformis
; STRAIN: ATCC 53926
; US-08-397-602A-8

alignment_scores:
  Quality: 62.00      Length: 42
  Ratio: 2.296       Gaps: 0
  Percent Similarity: 64.286   Percent Identity: 35.714

alignment_block:
US-09-528-682-3 x US-08-397-602A-8 ..
Align seg 1/1 to: US-08-397-602A-8 from: 1 to: 1452

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1188 ATTGAACGGAACGTCATATGCTCTCTCATGTAGCGGAGCAGCGTT 1237

30 lProLeuAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyG 47
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1238 TGATCTTGTCAAACATCCGAACCTTTCAGCTTCACAAGTCCGCAACCGT 1287

47 lyMetGlnAspGlyAspLeuPheGly 55
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1288 CTCCTCCAGCAGCGGACATTATTGGG 1313

seq_name: /cgn2_6/ptodata/2/ina/3A_COMB.seq:US-08-685-774-1

seq_documentation_block:
; Sequence 1, Application US/08685774
; Patent No. 5712147
; GENERAL INFORMATION:
; APPLICANT: Shih, Jason C. H.
; APPLICANT: Lin, Xiang
; APPLICANT: Miller, Eric S.
; TITLE OF INVENTION: DNA ENCODING BACILLUS LICHENIFORMIS
; TITLE OF INVENTION: PWD-1 KERATINASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5712147th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,774
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/250,028
; FILING DATE: 27-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5051-260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 420-2200
; TELEFAX: (919) 881-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1457 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus licheniformis
; STRAIN: PWD-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 215..1354
; US-08-685-774-1

alignment_scores:
  Quality: 62.00      Length: 42
  Ratio: 2.296       Gaps: 0
  Percent Similarity: 64.286   Percent Identity: 35.714

alignment_block:
US-09-528-682-3 x US-08-685-774-1 ..
Align seg 1/1 to: US-08-685-774-1 from: 1 to: 1457

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1174 ATTGAACGGAACGTCATATGCTCTCTCATGTAGCGGAGCAGCGTT 1223

30 lProLeuAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyG 47
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1224 TGATCTTGTCAAACATCCGAACCTTTCAGCTTCACAAGTCCGCAACCGT 1273

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1274 CTCCTCCAGCAGCGGACATTATTGGG 1299

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-282-147-36

seq_documentation_block:
; Sequence 36, Application US/09282147
; Patent No. 6274147
; GENERAL INFORMATION:
; APPLICANT: YAKHARIA, Vikram
; APPLICANT: YAO, Kun
; TITLE OF INVENTION: METHOD FOR GENERATING NONPATHOGENIC, INFECTIOUS
; TITLE OF INVENTION: PANCREATIC NECROSIS VIRUS (IPNV) FROM SYNTHETIC RNA
; TITLE OF INVENTION: TRANSCRIPTS
; FILE REFERENCE: 8288-9023
; CURRENT APPLICATION NUMBER: US/09/282,147
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER: US/60/080,278
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: PCT/US97/12955
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 3097
; TYPE: DNA
; ORGANISM: Infectious pancreatic necrosis virus
; US-09-282-147-36

alignment_scores:
  Quality: 61.50      Length: 116
  Ratio: 1.008       Gaps: 4
  Percent Similarity: 52.586   Percent Identity: 18.966

alignment_block:
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Align seg 1/1 to: US-09-282-147-36 from: 1 to: 3097

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; REFERENCE/DOCKET NUMBER: WH194-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 148..4407
; US-08-218-265-13

alignment_scores:
  Quality: 61.50      Length: 100
  Ratio: 1.500       Gaps: 3
  Percent Similarity: 41.000   Percent Identity: 26.000

alignment_block:
  US-09-528-682-3 x US-08-218-265-13  ..

  Align seg 1/1 to: US-08-218-265-13 from: 1 to: 4849

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28 .....AsnGluValProLeuAspGlyA 35
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1488 GACAGGAAGCGTAGACACACTTCATAATAAAGAGGGAACACTGGAACAAC 1537
35 rGtyrSerAsnPheAlaLeuIleSerAlaGlu..... 45
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1538 GAGAACAAGCAAGAAATCTGCCAAGTGTATAAAGTGACTCTATGCTAGAC 1587
46 .....GlyGlyMetGlnAspGlyAspLeuPheGlyThrValAs 58
   ||| ::::| ||| ||| ||| |||
1588 AGGAAATGTTTGGTCAGGATGAGGATGAGGATTTATTGCGGATAGCAA 1637
58 nGlnSerAsn..... 61
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1638 TAAATCGAATCTACAAACGAATCGAACAAAGTATATATCGGACGAAATTA 1687
62 .....PheProMetSerThrPheGluGlnValProAsnAsnLys 74
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1688 CCGAGGATATGTTCTGCAATGCTGTGATGAAGAAGAAATAATAACAATAAA 1737

seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-08-521-872-13

seq_documentation_block:
; Sequence 13, Application US/08521872
; Patent No. 6015682
; GENERAL INFORMATION:
; APPLICANT: Young, Richard A.
; APPLICANT: Koleske, Anthony J.
; APPLICANT: Thompson, Craig M.
; APPLICANT: Chao, David M.
; TITLE OF INVENTION: No. 6015682el Factors Which Modify Gene
; TITLE OF INVENTION: Transcription and Methods of Use Therefor
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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/cgn2_6/ptodata/2/pna/US06020_COMB.seq:US-60-206-026-19 +	68.00	115.00	5.9e+03	1804	/cgn2_6/ptodata/2/pna/US06014_COMB.seq:US-60-147-189-111 +	67.50	127.37	1.2e+03
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/cgn2_6/ptodata/2/pna/US093_COMB.seq:US-60-253-378-3905 +	67.50	153.49	42.44	31	/cgn2_6/ptodata/2/pna/US06012_COMB.seq:US-60-125-817-3369 +	67.00	147.23	94.74
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/cgn2_6/ptodata/2/pna/US098C_COMB.seq:US-09-867-716-18580 +	67.50	151.37	55.66	39	/cgn2_6/ptodata/2/pna/US06025_COMB.seq:US-60-255-592-24328 +	67.00	145.37	120.17
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/cgn2_6/ptodata/2/pna/US100_COMB.seq:US-10-068-800-93 +	67.50	145.49	118.39	714	/cgn2_6/ptodata/2/pna/US096B_COMB.seq:US-09-620-392-66593 +	67.00	129.00	981.29
/cgn2_6/ptodata/2/pna/US098A_COMB.seq:PCT-US01-08631-4236 +	67.50	144.48	134.68	79	/cgn2_6/ptodata/2/pna/US096B_COMB.seq:US-09-620-392-67284 +	67.00	127.47	1.2e+03
/cgn2_6/ptodata/2/pna/US098A_COMB.seq:US-09-815-264-14331 -	67.50	138.20	301.62	1	/cgn2_6/ptodata/2/pna/US086_COMB.seq:US-08-621-425-30 +	67.00	124.31	1.8e+03
/cgn2_6/ptodata/2/pna/US092_COMB.seq:US-09-205-070-15008 +	67.50	138.04	307.96	15	/cgn2_6/ptodata/2/pna/US096B_COMB.seq:US-09-620-392-63594 -	67.00	108.64	1.3e+04
/cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-340-623-15008 +	67.50	138.04	307.96	15	/cgn2_6/ptodata/2/pna/US06014_COMB.seq:US-60-144-351-838 -	67.00	107.36	1.6e+04
/cgn2_6/ptodata/2/pna/US098C_COMB.seq:US-09-898-888A-15008 +	67.50	138.04	307.96	11	/cgn2_6/ptodata/2/pna/US096B_COMB.seq:US-09-620-392-10944 -	67.00	104.21	2.4e+04
/cgn2_6/ptodata/2/pna/US098C_COMB.seq:US-09-898-888A-15008 +	67.50	136.36	381.76	18	/cgn2_6/ptodata/2/pna/US06016_COMB.seq:US-60-161-932-23 +	67.00	103.52	2.6e+04
/cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-359-922-12794 -	67.50	136.36	381.76	18	/cgn2_6/ptodata/2/pna/US06016_COMB.seq:US-60-167-217-12207 +	67.00	102.26	3.0e+04
/cgn2_6/ptodata/2/pna/US096C_COMB.seq:US-09-644-867-7593 +	67.50	135.94	402.85	18	/cgn2_6/ptodata/2/pna/US06016_COMB.seq:US-60-173-464-9904 +	67.00	99.53	4.3e+04
/cgn2_6/ptodata/2/pna/US096C_COMB.seq:US-09-644-868-9899 +	67.50	135.94	402.85	18	/cgn2_6/ptodata/2/pna/US097A_COMB.seq:US-09-702-134-8888 -	67.00	99.53	4.3e+04
/cgn2_6/ptodata/2/pna/US096C_COMB.seq:US-09-649-161-9902 +	67.50	135.94	402.85	18	/cgn2_6/ptodata/2/pna/US097A_COMB.seq:US-09-815-264-81757 -	67.00	99.53	4.3e+04
/cgn2_6/ptodata/2/pna/US097A_COMB.seq:US-09-710-286-3225 +	67.50	135.94	402.85	18	/cgn2_6/ptodata/2/pna/US098A_COMB.seq:US-09-803-736-1345 -	67.00	95.72	7.0e+04
/cgn2_6/ptodata/2/pna/US097A_COMB.seq:US-09-726-174-4918 +	67.50	135.94	402.85	18	/cgn2_6/ptodata/2/pna/US095A_COMB.seq:US-09-528-237A-1415 +	67.00	94.95	7.7e+04
/cgn2_6/ptodata/2/pna/US097B_COMB.seq:US-09-727-382-296 +	67.50	135.94	402.85	188	/cgn2_6/ptodata/2/pna/US090_COMB.seq:US-09-012-031-312 +	67.00	77.17	7.5e+05
/cgn2_6/ptodata/2/pna/US096D_COMB.seq:US-09-867-322A-1 +	67.50	135.89	405.54	1899	/cgn2_6/ptodata/2/pna/US090_COMB.seq:US-09-012-031B-312 +	67.00	77.17	7.5e+05
/cgn2_6/ptodata/2/pna/US097B_COMB.seq:US-09-756-296A-1 +	67.50	135.89	405.54	1899	/cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-335-032-12214 +	67.00	77.17	7.5e+05
/cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-474-436-8327 +	67.50	135.88	405.54	1899	/cgn2_6/ptodata/2/pna/US06022_COMB.seq:US-60-220-535-212 -	66.50	150.56	61.76
/cgn2_6/ptodata/2/pna/US06016_COMB.seq:US-60-167-217-18965 +	67.50	135.24	440.51	2	/cgn2_6/ptodata/2/pna/US06025_COMB.seq:US-60-253-457-44909 -	66.50	143.92	144.70
/cgn2_6/ptodata/2/pna/US098A_COMB.seq:PCT-US01-11797-1 +	67.50	134.78	467.75	2127	/cgn2_6/ptodata/2/pna/US095A_COMB.seq:US-09-514-000-3355 -	66.50	141.04	209.54
/cgn2_6/ptodata/2/pna/US094_COMB.seq:PCT-US01-11797-2 +	67.50	134.40	481.12	2211	/cgn2_6/ptodata/2/pna/US095A_COMB.seq:US-09-514-000-3355 -	66.50	138.83	278.20
/cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-471-275-4954 +	67.50	134.02	515.56	229	/cgn2_6/ptodata/2/pna/US097B_COMB.seq:US-09-739-449-3751 +	66.50	138.83	278.20
/cgn2_6/ptodata/2/pna/US095A_COMB.seq:US-09-526-994-1005 +	67.50	133.89	524.05	23	/cgn2_6/ptodata/2/pna/US098A_COMB.seq:US-09-803-110-3751 +	66.50	138.83	278.20
/cgn2_6/ptodata/2/pna/US096A_COMB.seq:US-09-614-150-40175 +	67.50	133.68	538.54	2	/cgn2_6/ptodata/2/pna/US06036_COMB.seq:US-60-360-207-35888 +	66.50	135.30	437.29
/cgn2_6/ptodata/2/pna/US096A_COMB.seq:US-60-191-681-39810 +	67.50	133.68	538.54	2	/cgn2_6/ptodata/2/pna/US096A_COMB.seq:US-09-614-150-4577 +	66.50	132.57	621.08
/cgn2_6/ptodata/2/pna/US06019_COMB.seq:US-60-191-681-39810 +	67.50	133.68	538.54	2	/cgn2_6/ptodata/2/pna/US06017_COMB.seq:US-60-173-464-3787 +	66.50	132.57	621.08

[illegible]

[illegible]

```

seq_documentation_block:
; Sequence 1769, Application US/09522305
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Donovan, Michael J.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: HUMAN FETAL LIBRARY
; FILE REFERENCE: 1600.1085-001
; CURRENT APPLICATION NUMBER: US/09/522,305
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/123,524
; EARLIER FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 1861
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1769
; LENGTH: 770
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-522-305-1769

```

```

alignment_scores:
  Quality: 80.50      Length: 129
  Ratio: 1.238       Gaps: 5
  Percent Similarity: 50.388      Percent Identity: 27.132

alignment_block:
  US-09-528-682-3 x US-09-522-305-1769
  ..

```

```
Align seg 1/1 to: US-09-522-305-1769 from: 1 to: 770
```

1 AspPhePheThrArgAlaLeuGlnGlnAlatyrGluProIleGluValas 17
|||||
:::
197 GATTTCCTCCTCAATTTCCGTGGAGCATCGCTTTGGGCCCAAGTGACAT 246

17 nThrAsnThrValThr.....GlnIleAsnClySerAsnC 29
::: :::
247 GGCTCTGGCGTCTATACTATTTTGAATAATATCAAGACTCTCCACTCCAACG 296

29 luVal.....ProLeuAspGlyArgTyrSerAsnPhe 39
|||| |
297 AGCTTAGCAGTCAGTCTCTATCCAGCTCTTGATGGAAAGCGGAGTGCAGAA 346

40 AlaLeulle..... 42
::: :::
347 GTGTATGTGCACCACAGAGGACAGACAGTAGCCCCAGCTGCTGAAGGAGATGAC 396

43SerAlaGluGlyGlyMetGlnAspClyAspLeuPheGlyt 56
||| :
397 AAATGCTGCACAGTCAGAACGAGGCGGTACTTAACCATGGAGCAGTTCAACA 446

56 hrValAsnGlnSerAsnPheProMetSerThrPheGluGlnValProAsn 72
|||| |
447 CTGTCCCTCAAGAGTACCTCTCCCTCTCAAGACAGAGAAGCAAAATCCAGGAG 496

73 AsnLysGluPheLysGlyValIleSerAlaAsnVallYstyrAsp...Me 88
||| |||
497 CTGTATGAGGCGAGGCGCTGGCATCCCGACGACGAGCAAGTATGCGAGACTTGCT 546

```

88  tAsnPhleLysLysLeuLeuArgPheMetGluAspAsp 100
   :|||||:|||||:|||||:|||||:|||||:|||||:
547  CAACTACCGCTCACTG.....TTTATGAGGATGAC 577

seq_name: /cgn2_6/ptodata/2/pna/US096B_COMB.seq;seq:US-09-634-306B-203708

seq_documentation_block:
; Sequence 203708, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203708
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-203708

```

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alignment_scores:
  Quality: 78.00      length: 113
  Ratio: 1.300       Gaps: 5
  Percent similarity: 53.097    Percent Identity: 25.664

alignment_block:
  US-09-538-682-3  x US-09-634-306B-203708/rev  ..
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```

Align seg 1/1 to reverse of: US-09-634-306B-203708 from: 1 to: 11934

2  PhePheThrArgAlaLeuGlnAlaTyrGluProIleGluValAsnThr 18
   ||||| ::::||||| ||| ::::|||||
863 TTCTTCAGAGCCAGCATCCAACAGCCACAGAGCTCTGAGTATTTCCTC 814

18 rAsnThrValThrGlnIleAsnGlySerAsnGluVal.....ProL 32
   ::::|||||:|||||: ||| ::::
813 TTCTTCAGTCACCCACATAAATGGCTTCAGGGCCCTCTGGGGGAAGCCCT. 765

32 euAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMet 48
   :|||:|||||:|||||: ||| |||||
764 ..GAAGGAGAGATTACAGCATACACTGTGTGGYCATTTGAAGC..... 723

49 GlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSe 65
   ||| ::::
722 .....TTCACTCTTCC 712

65 rThrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerA 82
   ||| ||| :|||: ||| :|||
711 TCAAGGATCCAATCTCCCTTCAGTCAAGAAGCTCCAGGTATCTGAAC TG 662

82 la.....AsnValLysTyrAspMetAsnPheLysLysLeu.... 93
   :||| ||| :|||: |||: |||
661 GATGCCAGGTCATAAATCCCCCATTTGTTGACTCCATCAGGTCCTCTGTC 612

94 .....LeuArgPheMetGluAspPheIleGlyVal 104

```



```
|||||.....
611 TCAGAACTAGAGCTAGTAAAGATAGACTCATGGGAGTC 573

seq_name: /cgn2_6/ptodata/2/pna/US092_COMB.seq:US-09-234-611-7401

seq_documentation_block:
; Sequence 7401, Application US/09234611
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-757
; CURRENT APPLICATION NUMBER: US/09/234,611
; CURRENT FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 21025
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7401
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(455)
; OTHER INFORMATION: n = A,T,C or G
US-09-234-611-7401

alignment_scores:
  Quality: 77.50      Length: 80
  Ratio: 1.890        Gaps: 2
  Percent Similarity: 51.250  Percent Identity: 27.500

alignment_block:
US-09-528-682-3 x US-09-234-611-7401/rev ..
Align seg 1/1 to reverse of: US-09-234-611-7401 from: 1 to: 455

2 PhePheThrArgAlaLeuGlnGlnAlaTyrGluProIleGluValAsnTh 18
|||||.....
454 TTCTTCAGAGCCAGCATCCACAGCCACAGAGCTGTGAGTATTCCT 405

18 rAsnThrValThrGlnIleAsnGlySerAsnGluVal.....ProLeuA 33
|||||.....
404 TTCTCAGTCAGTCACCATAAATGCTTCAGGGCCTTCTGGGAGGCTTG 355

33 spGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetGln 49
|||||.....
354 AAGGAGATTACAGCATACACTTTGTGGCAGCATTTGAAGGC..... 314

50 AspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSerTh 66
|||||.....
313 .....TTCACCTCTCTCTCA 300

66 rPheGluGlnValProAsnAsnLysGluPheLysGlyVal 79
|||||.....
299 AGGATCCAAATCTCCCTCAGTCAAGAAGCTCCAGGTATC 260

seq_name: /cgn2_6/ptodata/2/pna/US092_COMB.seq:US-09-235-076-11038

seq_documentation_block:
; Sequence 11038, Application US/09235076
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235,076
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11038
; LENGTH: 455
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(455)
; OTHER INFORMATION: n = A,T,C or G
US-09-235-076-11038

alignment_scores:
  Quality: 77.50      Length: 80
  Ratio: 1.890        Gaps: 2
  Percent Similarity: 51.250  Percent Identity: 27.500

alignment_block:
US-09-528-682-3 x US-09-235-076-11038/rev ..
Align seg 1/1 to reverse of: US-09-235-076-11038 from: 1 to: 455

2 PhePheThrArgAlaLeuGlnGlnAlaTyrGluProIleGluValAsnTh 18
|||||.....
454 TTCTTCAGAGCCAGCATCCACAGCCACAGAGCTGTGAGTATTCCT 405

18 rAsnThrValThrGlnIleAsnGlySerAsnGluVal.....ProLeuA 33
|||||.....
404 TTCTCAGTCAGTCACCATAAATGCTTCAGGGCCTTCTGGGAGGCTTG 355

33 spGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetGln 49
|||||.....
354 AAGGAGATTACAGCATACACTTTGTGGCAGCATTTGAAGGC..... 314

50 AspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSerTh 66
|||||.....
313 .....TTCACCTCTCTCTCA 300

66 rPheGluGlnValProAsnAsnLysGluPheLysGlyVal 79
|||||.....
299 AGGATCCAAATCTCCCTCAGTCAAGAAGCTCCAGGTATC 260

seq_name: /cgn2_6/ptodata/2/pna/US092_COMB.seq:US-09-248-797-32436

seq_documentation_block:
; Sequence 32436, Application US/09248797
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-764
; CURRENT APPLICATION NUMBER: US/09/248,797
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 48909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32436
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(455)
; OTHER INFORMATION: n = A,T,C or G
US-09-248-797-32436

alignment_scores:
  Quality: 77.50      Length: 80
  Ratio: 1.890        Gaps: 2
  Percent Similarity: 51.250  Percent Identity: 27.500

alignment_block:
US-09-528-682-3 x US-09-248-797-32436/rev ..
Align seg 1/1 to reverse of: US-09-248-797-32436 from: 1 to: 455

2 PhePheThrArgAlaLeuGlnGlnAlaTyrGluProIleGluValAsnTh 18
```



```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(455)
; OTHER INFORMATION: n = A,T,C or G
US-09-904-809-7401

alignment_scores:
  Quality: 77.50      Length: 80
  Ratio: 1.890        Gaps: 2
  Percent Similarity: 51.250  Percent Identity: 27.500

alignment_block:
US-09-528-682-3 x US-09-904-809-7401/rev ..

Align seg 1/1 to reverse of: US-09-904-809-7401 from: 1 to: 455

2 PhePheThrArgAlaLeuGlnGlnAlaTyrrGluProIleGluValAsnTh 18
||||| : : : : : ||||| ||| : : : : :
454 TTCCTCAGCAGCCATCCACAAAGCCACAGAGCTGTGAGTATTCCT 405
: : : : : ||||| : : : : :
18 rAsnThrValThrGlnIleAsnGlySerAsnGluVal.....ProLeuA 33
: : : : : ||||| : : : : :
404 TTCCTCAGTCAACCCACATAAATGGCTTCAGGCGCTTCTGGGAAGGCTTG 355
: : : : : ||||| : : : : :
33 spGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetGln 49
: : : : : ||||| : : : : :
354 AAGGAAGATTTACAGCATACACTTGTGGCAGCATTTGAAGGC..... 314
: : : : : ||||| : : : : :
50 AspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSerTh 66
||||| : : : : :
313 .....TTCACCTCTTCCTCA 300

66 rPheGluGlnValProAsnAsnLysGluPheLysGlyVal 79
||||| : : : : : |||||
299 AGGGATCCAATCTCCCTCAGTCAGTCAAGAGCTCCAGGTATC 260

seq_name: /cgn2_6/ptodata/2/pna/US099A_COMB.seq:US-09-477-574A-1

seq_documentation_block:
; Sequence 1, Application US/09477574A
; GENERAL INFORMATION:
; APPLICANT: Stram, Yehuda
; APPLICANT: Rogel, Arle
; APPLICANT: Sela, Ilan
; APPLICANT: Edelbaum, Orit
; APPLICANT: Shachar, Yehoshua
; APPLICANT: Zenberg, Yehuda
; APPLICANT: Gontmakher, Tanya
; APPLICANT: Khayat, Eli
; TITLE OF INVENTION: RECOMBINANT VACCINES AGAINST IBDV
; FILE REFERENCE: 0231.00013
; CURRENT APPLICATION NUMBER: US/09/477,574A
; CURRENT FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 60/114,634
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3054
; TYPE: DNA
; ORGANISM: Infectious bursal disease virus
US-09-477-574A-1

alignment_scores:
  Quality: 77.00      Length: 127
  Ratio: 1.283        Gaps: 6
  Percent Similarity: 47.244  Percent Identity: 22.047

alignment_block:
US-09-528-682-3 x US-09-477-574A-1 ..

Align seg 1/1 to: US-09-477-574A-1 from: 1 to: 3054

14 IleGluValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluVa 30
||||| : : : : : |||||
892 ATTGAGATTCACACCCAGCCAGAGATAACCCAG..... 921
: : : : : ||||| : : : : :
30 lProLeuAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGly 47
||||| : : : : :
922 .CCAATCACATCC.....ATCAAACTGGAGATAGTGACCTCCAAAAGTG 964
: : : : : ||||| : : : : :
47 lYMetGlnAspGlyAsp.....LeuPhe 54
||| ||| |||||
965 GTGGCCAGCGGGGGATCATGTCTCATGTGTCAGCAAGTGGGAGCCTAGCA 1014
||| ||| |||||
55 GlyThrValAsnGlnSerAsnPhePro..... 63

```



```

56 hrValasGlnSerAsnPhetPrometSerThrpheGluGlnValProAsn 72
582 CTGTCTCAAGAGTAGCTTCCCTCTCAAGACAGACAGCAAAATCCAGGAG 533
73 AsnLysGluPhelYsGlyValIleSerAlaAsnValLysTyAsp...Me 88
532 CTGATGGAGGAGGGGCTGGCATCCACGACGACGAATCCAGACTTGCT 483
88 tAsnPhelYsLysLeuLeuArgPheMetGluAspAsp 100
482 CAACCTACCGCTCACTG.....TTTATGAGGAGTAGAT 552
seq_name: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:US-09-698-010-14876

seq_documentation_block:
; Sequence 14876, Application US/09698010
; GENERAL INFORMATION:
; APPLICANT: Williamson, Mark
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2029-001
; CURRENT APPLICATION NUMBER: US/09/698,010
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 60/162,358
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 15684
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14876
; LENGTH: 1029
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-698-010-14876

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alignment_scores:
  Quality: 76.50      Length: 129
  Ratio: 1.177      Gaps: 5
  Percent Similarity: 50.388      Percent Identity: 26.357

alignment_block:
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alignment_block:
US-09-528-682-3 x US-09-698-010-14876/rev ..
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Align seq 1/1 to reverse of: US-09-698-010-14876 from: 1 to: 1029

[illegible]

17 nThrAsnThrValThr.....GlnIleAsnGlySerAsnG 29
 ::: ||| ::: ||| |||||
 ::: ::: ::: ::: :::

29 luval.....ProLeuAspGlyArgTyrSerAsnPhe 39
||||| ||| |||::: |||:::

732 AGGTTATGAGTCAGTTCTATGCGAGTCTTGATGGGAAAGCGGAGIGAGAAI 88
40 AlaLeuIle..... 42

682 GTGTATGTCACCCAGAAGGAGACAGTAGCCCCAGCTGCTGAAGGAGATGAC 633

43SerAlaGluGlyGlyMetGlnAspGlyAspLeuPheGlyT 56

632 AAATGCTGACAGTCAGAACGAGGGGCTACTAACTCATGGAGCAGTTCAACA 583
56 hrValAsnGlnSerAsnPheProMetSerThrPheGluGlnValProAsn 72

582 CTGTCTCAAGAGTACCTTCCCTCTCAAGACAGAGAGCAAAATCCAGGAG 533

532 CTGATGGAGGCAGGGGGCTGGCATCCAGCAGCAATGCAGACTTGCT 483

alignment_scores:

alignment_scores:	
Quality:	76.50
Ratio:	1.177
Percent Similarity:	50.388
Percent Identity:	26.357
Gaps:	5
Length:	129

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alignment_block:
US-09-528-682-3 x US-09-606-680-3338/rev ..
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Align seg 1/1 to reverse of: US-09-606-680-3338 from: 1 to: 1029

1 AspPhePheThrArgAlaLeuGlnGlnAlaTyrGluProIleGluValAs 17
||||| : : ||| : : ||| : : : : :
832 GATTTCTTCTCAATTCCTGGAGCATCGCTTTGGCCCCAGTGATGCCAT 783

17 nThrAsnThrValThr.....GlnIleAsnGlySerAsnG 29
::: :: ||| :::: | | | |
282 GCGCTGGCGCTTATACATTATTTTCAGAAATATCAAGATCTCCACTCCAACG 713

29 luVal.....ProLeuAspGlyArgTyrSerAsnSph 39
||||| ||| ||||| |||||

40	AlaLeuIle.....	42
	::: :::	

6882 GTGTATGTTCACCCAGAAAGGAGACAGTAGCCACAGTCGTGAAGGAGATGAC
43SerAlaGluGlyGlyMetGlnAspGlyAspLeuPheGlyT 56

632 AAATGCTGACAGTCAGAACGAGGGGCTACTAACCATGGAGCAGTTCAACA 58

seq_name: /cgn2_6/ptodata/2/pna/US6018_COMB.seq:US-60-185-215-956

```

88 tAsnPheLysLysLeuLeuArgPheMetGluAsp 100
   :|||:::|||||
1065 CAACACCGCTCACTGTTTATGGAGGATGAG 1095

```

```

88 tAsnPheLysLysLeuLeuArgPheMetGluAsp 100
   :|||:::|||||
1065 CAACACCGCTCACTGTTTATGGAGGATGAG 1095

```


; SEQ ID NO 753

; NUMBER OF SEQ ID NOS: 91742

; SEQ ID NO 79236
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Glycine max noir
; FEATURE:
; OTHER INFORMATION: Clone ID: uc-gmflLIB3275P095d05b1
US-09-874-708A-79236

alignment_scores:
Quality: 76.00 Length: 99
Ratio: 1.357 Gaps: 6
Percent Similarity: 56.566 Percent Identity: 29.293

alignment_block:

US-09-528-682-3 x US-09-874-708A-79236/rev ..
Align seg 1/1 to reverse of: US-09-874-708A-79236 from: 1 to: 600

14 IleGluValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluVa 30
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
551 CTGGAAGCCAACTAGAACACATCAACACGACCAACAAAGACGTTGAGTG 502
30 lProLeuAspGlyArgTyrSerAsnPheAlaLeuIle..... 42
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
501 CACGTTGCTTGGACGATATTCTACTTTTGTGGCGATCATAAGCCCTTGAT 452
43 ..SerAlaGluGlyGlyMetGlnAspGlyAspLeuPheGlyThrValAsn 58
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
451 ATAGTTTTCGGCGAGGG.....GGAACCAATTTGGAATGGCAAC 411
59 GlnSer...AsnPhePro.....MetSerTh 66
::: |||||:::|||||
410 ACTGCATTCATATATCCGTTCTTCATGTATATCTCCACACTATCAGG 361
66 rPheGluGlnValProAsnAsn.....LysGluPheLysGlyValI 80
:::|||||:::|||||
360 GTATGAAGAACTCGATCTAAATCGAGTCCAGAAAGAGCATTCGGGT.... 315
80 leSerAlaAsnValLysTyrAspMetAsnPhelLysLysLeuLeuArg 95
:::|||||:::|||||
314GAAACTCGATGTGATCTGCAGCTGAGCGGCGGATTCGA 276

seq_name: /cgn2_6/ptodata/2/pna/US6021_COMB.seq:US-60-211-750-78103

seq_documentation_block:
; Sequence 78103, Application US/60211750
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-211(51933)A
; CURRENT APPLICATION NUMBER: US/60/211.750
; CURRENT FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 90609
; SEQ ID NO 78103
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Glycine max noir
; OTHER INFORMATION: Clone ID: uc-gmflLIB3275P095d05b1
US-60-211-750-78103

alignment_scores:
Quality: 76.00 Length: 99
Ratio: 1.357 Gaps: 6
Percent Similarity: 56.566 Percent Identity: 29.293

alignment_block:

US-09-528-682-3 x US-60-211-750-78103/rev ..

Align seg 1/1 to reverse of: US-60-211-750-78103 from: 1 to: 600

14 IleGluValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluVa 30
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
551 CTGGAAGCCAACTAGAACACATCAACACGACCAACAAAGACGTTGAGTG 502
30 lProLeuAspGlyArgTyrSerAsnPheAlaLeuIle..... 42
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
501 CACGTTGCTTGGACGATATTCTACTTTTGTGGCGATCATAAGCCCTTGAT 452
43 ..SerAlaGluGlyGlyMetGlnAspGlyAspLeuPheGlyThrValAsn 58
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
451 ATAGTTTTCGGCGAGGG.....GGAACCAATTTGGAATGGCAAC 411
59 GlnSer...AsnPhePro.....MetSerTh 66
::: |||||:::|||||
410 ACTGCATTCATATATCCGTTCTTCATGTATATCTCCACACTATCAGG 361
66 rPheGluGlnValProAsnAsn.....LysGluPheLysGlyValI 80
:::|||||:::|||||
360 GTATGAAGAACTCGATCTAAATCGAGTCCAGAAAGAGCATTCGGGT.... 315
80 leSerAlaAsnValLysTyrAspMetAsnPhelLysLysLeuLeuArg 95
:::|||||:::|||||
314GAAACTCGATGTGATCTGCAGCTGAGCGGCGGATTCGA 276

seq_name: /cgn2_6/ptodata/2/pna/US084_COMB.seq:US-08-484-688-2

seq_documentation_block:
; Sequence 2, Application US/08484688
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; APPLICANT: Baruch, Dror I.
; APPLICANT: Howard, Russell J.
; TITLE OF INVENTION: Malaria Vaccines
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; STREET: Affymax Technologies, N.V.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,688
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,285
; FILING DATE: 01-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaster, Kevin R.
; REGISTRATION NUMBER: 32,704
; REFERENCE/DOCKET NUMBER: 1051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1922 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-484-688-2

alignment_scores:
Quality: 76.00 Length: 93


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Ratio: 1.462                                     Gaps: 3
Percent Similarity: 55.914      Percent Identity: 24.731

alignment_block:
US-09-528-682-3 x US-08-484-688-2      ..

Align seg 1/1 to: US-08-484-688-2 from: 1 to: 1922

      8  GlnGlnAlaTyrGluProIleGluValasnThrAsnThrValThrGlnIle 24
      |||::: ||||| |||::: ::::: |||::: |||::: |||:::
1055  CAGTCAAAATATGAAAAAATAAAGGAAAGACGTGCTAGCGAAATGAATG 1104

      24  easnGlySerAsnGluVal...ProLeuAspGlyArgTyrSerAsnPheA 40
      ||| |||::: |||::: |||::: |||::: |||::: |||:::
1105  TAACCAAAATAAATGACATTCGTCTTATGAAAAAAAATTAATAAAGCTACT 1154

      40  laLeuIleSerAlaGluGlyMetGlnAspGlyAspLeuPheGlyThr 56
      ::||| ::: ::: ||| |||
1155  CATTAGATGATATACAAAGAAAGTGTGAC..... 1186

      57  ValAsnGlnSerAsnPheProMetSerThrPheGluGlnValProAsnAs 73
      :|||: |||::: |||::: |||::: |||::: |||:::
1187  .....ATACCAGAAATATTATTTAAAAAATTAACCATGA 1221

      73  nLysGluPheLysGlyValIleSerAlahsnValLysTyrAspMetAsnP 90
      |::: |||::: |||::: |||::: |||::: |||:::
1222  TATAAATGAGATAACATAATTAATGAATCATAT.....AAAAATA 1259

      90  heLysLysLeuLeuArgPheMetGluAsp 99
      ::|||::|||::|||::|||::|||::|||::|||::
1260  ATAACAAATATTATAAATTTATGGAAGAT 1288

seq_name: /cgn2_6/ptodata/2/pna/US084_COMB.seq:US-08-484-688A-2
seq_documentation_block:
; Sequence 2, Application US/08484688A
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; APPLICANT: Baruch, Dror I.
; APPLICANT: Howard, Russell J.
; TITLE OF INVENTION: Malaria Vaccines
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484.688A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,285
; FILING DATE: 01-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1922 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: linear

```

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; MOLECULE TYPE: CDNA
US-08-484-688A-2

alignment_scores:
  Quality: 76.00 Length: 93
  Ratio: 1.462 Gaps: 3
  Percent Similarity: 55.914 Percent Identity: 24.731

alignment_block:
US-09-528-682-3 x US-08-484-688A-2
..
Align seg 1/1 to: US-08-484-688A-2 from: 1 to: 1922

      8  GlnGlnAlaTyrGluProIleGluValAsnThrAsnThrValThrGlnI1 24
          ||||| ||||| ||||| : : : : : : : : : : : : : : : :
1055  CAGTCAAAATATGAAAAATAAAGGAAGAAGTCGTAGCGAAATGAATG 1104
          ||| : : : : : : : : : : : : : : : : : : : : : :
1105  TAACCAATAAATGACATTCGTCCTTATGAAAAAAATTTAAAAAGCTACT 1154
          ||| : : : : : : : : : : : : : : : : : : : : : :
40  laLeuIleSerIaGluGlyMetGlnAsnGlyAsnGlyPheGlyThr 56
          ||||| : : : : : : |||
1155  CATTAGATGATACATAAGAAAGAAAGTTGAC..... 1186
          ||||| : : : : : : |||
57  ValAsnGlnSerAsnGlnPheProMetSerThrPheGluGlnValProAsnAs 73
          : : : : : : : : : : ||||| : : : : : : : : : : ||
1187  .....ATACCAGAAATTTATTTTAAAAAATTTACCCATGAA 1221
          : : : : : : : : : : |||
73  nLysGluPheLysGlyValIleSerAlaAsnValLysTyrAsnMetAsn 90
          ||| : : : : : : : : : : |||
1222  TATAAATGCAGATAACATAATTGAATCATAT.....AAAAATA 1259
          ||| : : : : : : : : : : |||
90  heLysLysLeuLeuArgPheMetGluAsp 99
          : : : : : : : : : : |||||
1260  ATAACAAATTTATTTAAAAATTTATGGAAGAT 1288

seq_name: /cgn2_6/ptodata/2/pna/US6021_COMB.seq:US-60-212-664-145

seq_documentation_block:
; Sequence 145, Application US/60212664
; GENERAL INFORMATION:
; APPLICANT: Ladunga, Steve
; APPLICANT: Spier, Gene
; APPLICANT: Greenberg, Simon
; APPLICANT: Rabkin, Steven
; APPLICANT: Wang, Yu
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SEQ
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000687
; CURRENT APPLICATION NUMBER: US/60/212,664
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 636
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 181488
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(181488)
; OTHER INFORMATION: n = A,T,C or G
;
US-60-212-664-145

alignment_scores:
  Quality: 76.00 Length: 82
  Ratio: 1.583 Gaps: 4
  Percent Similarity: 58.537 Percent Identity: 35.366

alignment_block:

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US-09-528-682-3 x US-60-212-664-145
Align seg 1/1 to: US-60-212-664-145 from: 1 to: 181488
16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
94387 ATTAACACAAATTTGGTTTTCACAAATAAAGGGAACAATATTTTCCTCT 94436
32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetG 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
94437 GGAT.....TTTCTGTAGCCCAAGCACCACCAATTTGAAGAC 94471
49 lAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSe 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
94472 TCGGTGAGACATC.....ACTTCAGATGATAGCATGCTCCCAAGCAA 94515
65 rThrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerA 82
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
94516 GACAAATGAAGG.....GAAATGAAGCAAGGAGAGTGGGGAG 94556
82 laAsnValLysTyrAspMetAsnPheLysLysLeuLeuArgPhe 96
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
94557 CTACAATAAAACCGAGCTATTCTTCCCAAGGCGCTGCTATT 94600
seq_name: /cgn2_6/ptodata/2/pna/US6024_COMB.seq:US-60-245-201-69
seq_documentation_block:
; Sequence 69, Application US/60245201
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHASE II
; TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: HUMAN DRUG-METABOLIZING PHASE II PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000879
; CURRENT APPLICATION NUMBER: US/60/245,201
; CURRENT FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 449058
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)---(449058)
; OTHER INFORMATION: n = A,T,C or G
US-60-245-201-69
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alignment_scores:
  Quality: 76.00      Length: 82
  Ratio: 1.583       Gaps: 4
  Percent Similarity: 58.537   Percent Identity: 35.366
alignment_block:
US-09-528-682-3 x US-60-245-201-69
Align seg 1/1 to: US-60-245-201-69 from: 1 to: 449058
16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProLe 32
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67582 ATTAACACAAATTTGGTTTTCACAAATAAAGGGAACAATATTTTCCTCT 67631
32 uAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetG 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67632 GGAT.....TTTCTGTAGCCCAAGCACCACCAATTTGAAGAC 67666
49 lAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSe 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67667 TCGGTGAGACATC.....ACTTCAGATGATAGCATGCTCCCAAGCAA 67710
65 rThrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerA 82
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
67711 GACAAATGAAGG.....GAAATGAAGCAAGGAGAGTGGGGAG 67751
82 laAsnValLysTyrAspMetAsnPheLysLysLeuLeuArgPhe 96
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67752 CTACAATAAAACCGAGCTATTCTTCCCAAGGCGCTGCTATT 67795
seq_name: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:US-60-127-461-2280
seq_documentation_block:
; Sequence 2280, Application US/60127461
; GENERAL INFORMATION:
; APPLICANT: Chapman, Rowan
; APPLICANT: Thornton, Michael
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF CANDIDA ALBICANS
; FILE REFERENCE: PM-0007-2 P
; CURRENT APPLICATION NUMBER: US/60/127,461
; CURRENT FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 8247
; SOFTWARE: PERL Program
; SEQ ID NO 2280
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SKB807853286
US-60-127-461-2280
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alignment_scores:
  Quality: 75.00      Length: 88
  Ratio: 1.562       Gaps: 2
  Percent Similarity: 54.545   Percent Identity: 25.000
alignment_block:
US-09-528-682-3 x US-60-127-461-2280
Align seg 1/1 to: US-60-127-461-2280 from: 1 to: 636
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```
14 IleGluValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluVa 30
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
292 TTGAATGTTGCTAAACCGCCGTCACAGAAA...TCTGGTCGAGACGATG 338
30 lProLeuAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyG 47
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
339 TATTATGCTGGGCTCTATTGGACCTTATGCTACTTTCCTGCCAACGGAT 388
47 lYMetGlnAspGlyAsp.....
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
389 CAGATATATACGGTGATTATCAAGGTGTTACTGACGAAGAGTTGATTGAA 438
53 .....LeuPheGlyThrValAsnGlnSerAsnPheProMetSe 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
439 TACCACACTCCGTTGTTGAAATTTACGAGAAATTCGACGCTTGACATAT 488
65 rThrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerA 82
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
489 ATGCATTGAGACTATTCACAGCTTCCAAAGCTTCCAGAGATTGAGGGTATAT 538
82 laAsnValLysTyr 86
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
539 TGGCAAAAAGATAC 552
```

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seq_name: /cgn2_6/ptodata/2/pna/US096A_COMB.seq:US-09-614-150-42389
seq_documentation_block:
; Sequence 42389, Application US/09614150
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
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seq_name: /cgn/v/fgdata/w/fga/000010_comp.seq:00 00 107 324
seq_documentation_block:
; Sequence 1740, Application US/60167324
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90 PheLysLysLeuLeuArgPheMetGluAspPheIleGlyValHisG1 106
::: ::::: |||| ::::: |||| ::::: |||| ::::: |||| :::
3020 GTTCGCTTTGTGATCAGTTTCGCACCTGGAGAAATTGAGCGCATTCATGC 3069
106 yGlu 107
:::
3070 AGAA 3073

seq_name: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:US-60-167-324-1739

seq_documentation_block:
; Sequence 1739, Application US/60167324
; GENERAL INFORMATION:
; APPLICANT: Li, Peter W.D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000155
; CURRENT APPLICATION NUMBER: US/60/167,324
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 2272
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1739
; LENGTH: 7767
; TYPE: DNA
; ORGANISM: Drosophila
US-60-167-324-1739

alignment_scores:
Quality: 75.00 Length: 118
Ratio: 1.230 Gaps: 5
Percent Similarity: 51.695 Percent Identity: 25.424

alignment_block:
US-09-528-682-3 x US-60-167-324-1739 ..

Align seg 1/1 to: US-60-167-324-1739 from: 1 to: 7767

11 TyrGluProIleGluValAsnThrAsnThrValThrGlnIleAsnGlySe 27
||||:|||| ||||:|||| ||||:|||| ||||:|||| ||||:||||
4881 TACAATCCTCGTGAGATTATGAAAAATCTAAGGAAGATGATAAACGGACA 4930
27 rAsn.....G 29
:::
4931 AGAGCCAAAGTGTGATGCATCCGTGGTACAGAACTTTTAGGACGATGG 4980
29 luValProLeuAspGlyArgTyr.....SerAsnPheAlaLeuIle 42
|| ||||:|||| ||||:|||| ||||:|||| ||||:|||| ||||:||||
4981 AGTATGTTTCGGATGTCGTTATATTCAGACTGGTAACATTCAAATTTTG 5030
43 SerAlaGluGlyMetGlnAspGlyAspLeuPheGlyThrValAsnG1 59
||||:|||| ||||:|||| ||||:|||| ||||:|||| ||||:||||
5031 TCCGGA...AACCGTTTAGAAATCAGTGAACCTCCCTGTGGCGCATTCGAC 5077
59 nSerAsnPheProMetSerThrPheGluGlnValProAsnAsnLysGlu. 75
::|||::: ||||:|||| ||||:|||| ||||:|||| ||||:||||
5078 GCNAACTACAGGAAATGTCCTGGAGCCTTTATCAACGGCACCGAAA 5127
76 ..PheLysGlyValIleSerAlaAsnValLysTyr.....AspMetAsn 89
|||||:|||| ||||:|||| ||||:|||| ||||:|||| ||||:||||
5128 AGGTTAAGGCTATTATTTCCGAGTACAGGAGTATCATACAGACACCCACC 5177
90 PheLysLysLeuLeuArgPheMetGluAspPheIleGlyValHisG1 106
::: ::::: |||| ::::: |||| ::::: |||| ::::: |||| :::
5178 GTTCGCTTTGTGATCAGTTTCGCACCTGGAGAAATTGAGCGCATTCATGC 5227
106 yGlu 107
:::
5228 AGAA 5231

seq_name: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:US-60-173-386-1619

seq_documentation_block:
; Sequence 1619, Application US/60173386
; GENERAL INFORMATION:
; APPLICANT: Le, Peter W.D.
; TITLE OF INVENTION: Isolated Drosophila proteins, nucleic
; TITLE OF INVENTION: acid molecules encoding drosophila proteins and uses thereof
; FILE REFERENCE: CL000174
; CURRENT APPLICATION NUMBER: US/60/173,386
; CURRENT FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 2023
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1619
; LENGTH: 7767
; TYPE: DNA
; ORGANISM: Drosophila
US-60-173-386-1619

alignment_scores:
Quality: 75.00 Length: 118
Ratio: 1.230 Gaps: 5
Percent Similarity: 51.695 Percent Identity: 25.424

alignment_block:
US-09-528-682-3 x US-60-173-386-1619 ..

Align seg 1/1 to: US-60-173-386-1619 from: 1 to: 7767

11 TyrGluProIleGluValAsnThrAsnThrValThrGlnIleAsnGlySe 27
||||:|||| ||||:|||| ||||:|||| ||||:|||| ||||:||||
4881 TACAATCCTCGTGAGATTATGAAAAATCTAAGGAAGATGATAAACGGACA 4930
27 rAsn.....G 29
:::
4931 AGAGCCAAAGTGTGATGCATCCGTGGTACAGAACTTTTAGGACGATGG 4980
29 luValProLeuAspGlyArgTyr.....SerAsnPheAlaLeuIle 42
|| ||||:|||| ||||:|||| ||||:|||| ||||:|||| ||||:||||
4981 AGTATGTTTCGGATGTCGTTATATTCAGACTGGTAACATTCAAATTTTG 5030
43 SerAlaGluGlyMetGlnAspGlyAspLeuPheGlyThrValAsnG1 59
||||:|||| ||||:|||| ||||:|||| ||||:|||| ||||:||||
5031 TCCGGA...AACCGTTTAGAAATCAGTGAACCTCCCTGTGGCGCATTCGAC 5077
59 nSerAsnPheProMetSerThrPheGluGlnValProAsnAsnLysGlu. 75
::|||::: ||||:|||| ||||:|||| ||||:|||| ||||:||||
5078 GCNAACTACAGGAAATGTCCTGGAGCCTTTATCAACGGCACCGAAA 5127
76 ..PheLysGlyValIleSerAlaAsnValLysTyr.....AspMetAsn 89
|||||:|||| ||||:|||| ||||:|||| ||||:|||| ||||:||||
5128 AGGTTAAGGCTATTATTTCCGAGTACAGGAGTATCATACAGACACCCACC 5177
90 PheLysLysLeuLeuArgPheMetGluAspPheIleGlyValHisG1 106
::: ::::: |||| ::::: |||| ::::: |||| ::::: |||| :::
5178 GTTCGCTTTGTGATCAGTTTCGCACCTGGAGAAATTGAGCGCATTCATGC 5227
106 yGlu 107
:::
5228 AGAA 5231

seq_name: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:US-60-175-871-1811

seq_documentation_block:
; Sequence 1811, Application US/60175871
; GENERAL INFORMATION:
; APPLICANT: Li, Peter, W.D.
; TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000191
; CURRENT APPLICATION NUMBER: US/60/175,871
; CURRENT FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 2269


```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1811
; LENGTH: 7767
; TYPE: DNA
; ORGANISM: Drosophila
US-60-175-871-1811

```

```

alignment_scores:
  Quality: 75.00      Length: 118
  Ratio: 1.230       Gaps: 5
  Percent Similarity: 51.695      Percent Identity: 25.424

alignment_block:
  US-09-528-682-3 x US-60-175-871-1811

```

```

Align seg 1/1 to: US-60-175-871-1811 from: 1 to: 7767

11 TyrGluProIleGluValAsnThrValThrGlnIleAsnGlyse 27
   |||::||| |||:: ||| ::||| |||::
4881 TACAATCCTCGTGAGATTATGAAAAATCTAAGGAAGATGATAACGGACA 4930

27 rAsn.....G 29
   :::: |
4931 AGAGCCAAAGTGTGATGCATCCGTGGTACAAGAATTTTTPAGSACCATGG 4980

29 LuValProLeuAspGlyArgTyr.....SerAsnPheAlaLeuile 42
   |||::||| |||:: ||| ::||| |||::
4981 AGTAGTTTCGGTAGTGCCTTATATTCAGACTGGTAACATTCCAAATTTTG 5030

43 SerAlaGluGlycylMetGlnAspGlyAspLeuPheGlyThrValasnGI 59
   |||::||| |||:: ||| ::||| |||::
5031 TTCGGA...AACCGTTTATAGAAATCACTGAACCTCCCTGTGGCGCGTAGGC 5077

59 nSerAsnPheProMetSerThrPheGluGlnValProAsnAsnLysglu. 75
   |||::||| |||:: ||| ::||| |||::
5078 GCAAAACACTACAGGAAAATGTCTCGAGCCTTTATCAACGGCACCGAAA 5127

76 ..PhELysGlyValIleSerAlaAsnValYstYr.....AspMetAsn 89
   |||::||| |||:: ||| ::||| |||::
5128 AGGTTTAAGGGTATTATTTCCTCGAGTACAGGAGGTATCATACAGACACC 5177

90 PheLysLysLeuArgPheMetGluAspPheIleGlyValHISGL 106
   |||::||| |||:: ||| ::||| |||::
5178 GTTCGGTTGTGATCATAGTTTCGCCACCTGGAGAAATTTTGAGCGCATTCATGC 5227

106 yGlu 107
   :|||
5228 AGAA 5231

```

```

seq_name: /cgn2_6/ptodata/2/pna/us6018_COMB.seq:US-60-184-775-1653
seq_documentation_block:
: Sequence 1653, Application US/60184775
: GENERAL INFORMATION:
: APPLICANT: Lj. Peter W.D.
: TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS. NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES ENCODING DROSOPHILA PROTEINS
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: CL000282
: CURRENT APPLICATION NUMBER: US/60/184,775
: CURRENT FILING DATE: 2000-02-24
: NUMBER OF SEQ ID NOS: 2083
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1653
: LENGTH: 7767
: TYPE: DNA
: ORGANISM: DROSOPHILA
US-60-184-775-1653

```

alignment_scores:	
Quality:	75.00
Length:	118

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Ratio: 1.230          Gaps: 5
Percent Similarity: 51.695      Percent Identity: 25.424

alignment_block:
US-09-528-682-3 x US-60-184-775-1653      ..

Align seg 1/1 to: US-60-184-775-1653 from: 1 to: 7767

11 TyrGluProIleGluValAsnThrAsnThrValThrGlnIleAsnGlySe 27
   |||:||||| |||:: |||   ::||| |||::
4881 TACAATCCTCGTGAGATTATGAAAAATCTAAGGAAGATGATAAACGGACA 4930

27 rAsn.....G 29
   ::::
4931 AGAGCCAAAGTGTGATCGATCCGTGTACAAAGACTTTTATAGGACGCATGG 4980

29 LuValProLeuAspGlyArgTyr.....SerAsnPheAlaLeuIle 42
   || ||||| ||||| |||:: |||:: |||:: |||::
4981 AGTATGTTTCGGATGGTCGCTTATATTCACACGTGGTAACATTCAAATTTCG 5030

43 SerAlaGluGlyGlyMetGlnAspGlyAspLeuPheGlyThrValAsnG1 59
   ||||: :: :|||:: :|||:: |||
5031 TCCGGA..AACCGGTTTACAAATCAGTGAATCCCTGTGGCGGTATGGAC 5077

59 nSerAsnPheProMetSerThrPheGluGlnValProAsnAsnLysGlu. 75
   |||::|||:: |||::|||:: |||:: |||:: |||:: |||::
5078 GCAAAACATACAAGGAAAATGTCTCTGGAGCCTTTATCAAAACGGACCCGAA 5127

76 ..PheLysGlyValIleSerAlaAsnValLysTyr.....AspMetAsn 89
   |||||::||| ||||| ::||| |||:: |||::
5128 AGGTTAAGGGTATTATTCCGAGTACAGGAGTATCATACAGACACACCACC 5177

90 PheLysLysLeuArgPheMetGluAspAspPheIleGlyValHisG1 106
   :: :|||:: ||| ::||| |||:: |||:: |||::
5178 GTTCGCTTTGTGATCAGTTTCGCACCTCGAGAATTTTGGCGCATTCATCGC 5227

106 yGlu 107
   :|||
5228 AGAA 5231

seq name: /cgm2_6/ptodata/2/pna/US096A_COMB.seq:US-09-614-150-42

```

seq name: /cqn2 6/ptodata/2/pna/US096A COMB.seq:US-09-614-150-42388

```

seq_documentation_block:
; Sequence 42388, Application US/09614150
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/09/614,150
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42388
; LENGTH: 7769

```



```

2837 AGAGCCAAAGTGTGATCGTCATCGGTACAGAACTTTTAGGAGCGCATGG 2788
29 luValProLeuAspGlyArgTyr.....SerAsnPheAlaLeuIle 42
2787 AGTATGTTCCGATGGTGGTGTATATTCAGACTGTTAACAATTCAAATTTG 2738
43 SerAlaGluGlyGlyMetGlnAspGlyAspLeuPheGlyThrValAsnG1 59
2737 TCCGGA...AACCGTTTAGAAATCAGTGAACCTCCCTGTGGCGGTATGGAC 2691
59 nSerAsnPheProMetSerThrPheGluGlnValProAsnAsnLysGlu. 75
2690 GCAAAACTACAGGAAATGCTCGGAGCCTTTATCAACGGCACCGGAAA 2641
76 ..PheLysGlyValIleSerAlaAsnValLysTyr.....AspMetAsn 89
2640 AGGTTAAGGGTATTATTTCCGAGTACAGGAGTATCATACAGACACCACC 2591
90 PheLysLysLeuLeuArgPheMetGluAspPheIleGlyValHisG1 106
2590 GTTCGCTTTGTCATCAGTTTCGCACCTGGAGAATTTGAGCGCATTCATGC 2541
106 yGlu 107
2540 AGAA 2537
seq_name: /cqn2_6/ptodata/2/pna/US6015_COMB.seq:US-60-150-584-497

```

```

seq_documentation_block:
; Sequence 497, Application US/60150584
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
; FILE REFERENCE: CL000087
; CURRENT APPLICATION NUMBER: US/60/150,584
; CURRENT FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 1072
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 497
; LENGTH: 13844
; TYPE: DNA
; ORGANISM: Drosophila
US-60-150-584-497

```

```

alignment_scores:
  Quality: 75.00      Length: 118
  Ratio: 1.230       Gaps: 5
  Percent Similarity: 51.695   Percent Identity: 25.424

alignment_block:
US-09-528-682-3 x US-60-150-584-497

Align seg 1/1 to: US-60-150-584-497 from: 1 to: 13844

11 TyrGluProIleGluValAsnThrAsnThrValThrGlnIleAsnGlySe 27
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5151 TACAATCCTCGTGAGATTGAAAAATCTAAGGAAGATGATAACGGACA 5200
27 rAsn.....G 29
5201 AGAGCCAAAGTGTGATCGTCATCGGTACAGAACTTTTAGGAGCGCATGG 5250
29 luValProLeuAspGlyArgTyr.....SerAsnPheAlaLeuIle 42
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5251 AGTATGTTCCGATGGTGGTGTATATTCAGACTGTTAACAATTCAAATTTG 5300
43 SerAlaGluGlyGlyMetGlnAspGlyAspLeuPheGlyThrValAsnG1 59
5301 TCCGGA...AACCGTTTAGAAATCAGTGAACCTCCCTGTGGCGGTATGGAC 5347
59 nSerAsnPheProMetSerThrPheGluGlnValProAsnAsnLysGlu. 75
5348 GCAAACTACAGGAAATGCTCGGAGCCTTTATCAACGGCACCGGAAA 5397
76 ..PheLysGlyValIleSerAlaAsnValLysTyr.....AspMetAsn 89
5398 AGGTTAAGGGTATTATTTCCGAGTACAGGAGTATCATACAGACACCACC 5447
90 PheLysLysLeuLeuArgPheMetGluAspPheIleGlyValHisG1 106
5448 GTTCGCTTTGTCATCAGTTTCGCACCTGGAGAATTTGAGCGCATTCATGC 5497

```

```

59 nSerAsnPheProMetSerThrPheGluGlnValProAsnAsnLysGlu. 75
5348 GCAAACTACAGGAAATGCTCGGAGCCTTTATCAACGGCACCGGAAA 5397
76 ..PheLysGlyValIleSerAlaAsnValLysTyr.....AspMetAsn 89
5398 AGGTTAAGGGTATTATTTCCGAGTACAGGAGTATCATACAGACACCACC 5447
90 PheLysLysLeuLeuArgPheMetGluAspPheIleGlyValHisG1 106
5448 GTTCGCTTTGTCATCAGTTTCGCACCTGGAGAATTTGAGCGCATTCATGC 5497
106 yGlu 107
5498 AGAA 5501
seq_name: /cqn2_6/ptodata/2/pna/US6015_COMB.seq:US-60-150-584-508

```

```

seq_documentation_block:
; Sequence 508, Application US/60150584
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
; FILE REFERENCE: CL000087
; CURRENT APPLICATION NUMBER: US/60/150,584
; CURRENT FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 1072
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 508
; LENGTH: 13844
; TYPE: DNA
; ORGANISM: Drosophila
US-60-150-584-508

```

```

alignment_scores:
  Quality: 75.00      Length: 118
  Ratio: 1.230       Gaps: 5
  Percent Similarity: 51.695   Percent Identity: 25.424

alignment_block:
US-09-528-682-3 x US-60-150-584-508

Align seg 1/1 to: US-60-150-584-508 from: 1 to: 13844

11 TyrGluProIleGluValAsnThrAsnThrValThrGlnIleAsnGlySe 27
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5151 TACAATCCTCGTGAGATTGAAAAATCTAAGGAAGATGATAACGGACA 5200
27 rAsn.....G 29
5201 AGAGCCAAAGTGTGATCGTCATCGGTACAGAACTTTTAGGAGCGCATGG 5250
29 luValProLeuAspGlyArgTyr.....SerAsnPheAlaLeuIle 42
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5251 AGTATGTTCCGATGGTGGTGTATATTCAGACTGTTAACAATTCAAATTTG 5300
43 SerAlaGluGlyGlyMetGlnAspGlyAspLeuPheGlyThrValAsnG1 59
5301 TCCGGA...AACCGTTTAGAAATCAGTGAACCTCCCTGTGGCGGTATGGAC 5347
59 nSerAsnPheProMetSerThrPheGluGlnValProAsnAsnLysGlu. 75
5348 GCAAACTACAGGAAATGCTCGGAGCCTTTATCAACGGCACCGGAAA 5397
76 ..PheLysGlyValIleSerAlaAsnValLysTyr.....AspMetAsn 89
5398 AGGTTAAGGGTATTATTTCCGAGTACAGGAGTATCATACAGACACCACC 5447
90 PheLysLysLeuLeuArgPheMetGluAspPheIleGlyValHisG1 106
5448 GTTCGCTTTGTCATCAGTTTCGCACCTGGAGAATTTGAGCGCATTCATGC 5497

```



```
106 yGlu 107
:||||
5498 AGAA 5501

seq_name: /cgn2_6/ptodata/2/pna/US095A_COMB.seq:US-09-528-237A-1013
seq_documentation_block:
; Sequence 1013, Application US/09528237A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid
; FILE REFERENCE: CL000284
; CURRENT APPLICATION NUMBER: US/09/528,237A
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1013
; LENGTH: 240931
; TYPE: DNA
; ORGANISM: Drosophila
US-09-528-237A-1013

alignment_scores:
Quality: 75.00 Length: 118
Ratio: 1.230 Gaps: 5
Percent Similarity: 51.695 Percent Identity: 25.424

alignment_block:
US-09-528-682-3 x US-09-528-237A-1013/rev ..
Align seg 1/1 to reverse of: US-09-528-237A-1013 from: 1 to: 240931

11 TyrGluProIleGluValAsnThrAsnThrValThrGlnIleAsnGlySer 27
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
37644 TACAATCCCGTGGAGATTATGAAAATCTAAGGAAGATGATAACGGACA 37595
27 rAsn.....AACCCTTTAGAAATCAGTGAACCTCCCTGTGGCGTATGGAC 37448
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
37594 AGAGCCAAAGTGTGATGTCATCCGTGTGACAAAGAACTTTTATGACGCGATGG 37545
29 luValProLeuAspGlyArgTyr.....SerAsnPheAlaLeuIle 42
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
37544 AGTATGTTTCGGATGTCCTTATATTCACACTGGTAACATTCAAATTTTG 37495
43 SerAlaGluGlyGlyMetGlnAspGlyAspLeuPheGlyThrValAsnG1 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
37494 TCCGGA...AACCCTTTAGAAATCAGTGAACCTCCCTGTGGCGTATGGAC 37448
59 nSerAsnPhePrometSerThrPheGluGlnValProAsnAsnLysGlu. 75
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
37477 GCAAAACTCAAGGAAATGTCCTGGAGCCTTTATCAAAACGCGACCGAAA 37398
76 ..PheLysGlyValIleSerAlaAsnValLysTyr.....AspMetAsn 89
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
37397 AGTTAAGGGTATTATTCCGAGTACAGGAGTATCATACAGACACCCACC 37348
90 PheLysLysLeuLeuArgPheMetGluAspAspPheIleGlyValHisG1 106
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
37347 GTTCGGCTTTGTGATCATGTTTCGACCTCGGAGAAATTGGACGCGATTCATGC 37298
106 yGlu 107
:||||
37297 AGAA 37294

seq_name: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:US-09-620-392-53223
seq_documentation_block:
; Sequence 53223, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 24990
; LENGTH: 795
; TYPE: DNA
US-09-620-392-53223

alignment_scores:
Quality: 74.50 Length: 102
Ratio: 1.307 Gaps: 3
Percent Similarity: 55.882 Percent Identity: 24.510

alignment_block:
US-09-528-682-3 x US-09-620-392-53223 ..
Align seg 1/1 to: US-09-620-392-53223 from: 1 to: 795

13 ProIleGluValAsnThrAsnThrValThrGlnIleAsnGlySerAsnG1 29
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
388 CCAATTTGTTTCACACACATCTCAATTCGAGGTCAATTCGACCCAGAA 437
29 uValProLeuAspGlyArgTyrSerAsnPheAlaLeuIle.....42
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
438 AGAGGCGATGGATTTCAAAAGTCGCTTCCTTCTCTACTCTCTCTTAATCG 487
43 .....SerAlaGluGlyGlyMetGlnAspGlyAspLeuPheGly 55
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
488 TCACCTGCGGAGCTGCTCAAGGT.....CAAGCAATGATTTTGGT 528
56 ThrValAsnGlnSerAsnPhePrometSerThrPheGluGlnValProAs 72
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
529 AGCCCTTAATCAACACCTTCCTTCCTCCCTACCTATGCTCCTCCT.. 576
72 nAsnLysGluPheLysGlyValIleSerAlaAsnValLysTyrAspMetA 89
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
577 .....GGCTCCTGCATGCAGTTTGGAAACCA 601
89 snPheLysLysLeuLeuArgPheMetGluAspAspPheIleGlyValHis 105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
602 ACATGTCAAAACATTCCTCAAGGAGGAAATTCGACAAAGTTTTTTTATGTCGCT 651
106 GlyGlu 107
:||||
652 AGTAAA 657

seq_name: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:US-09-702-134-24990
seq_documentation_block:
; Sequence 24990, Application US/09702134
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 24990
; LENGTH: 795
; TYPE: DNA
US-09-702-134-24990
```


; ORGANISM: Oryza sativa
US-09-702-134-24990

alignment_scores:
Quality: 74.50 Length: 102
Ratio: 1.307 Gaps: 3
Percent Similarity: 55.882 Percent Identity: 24.510

alignment_block:
US-09-528-682-3 x US-09-702-134-24990 ..

Align seg 1/1 to: US-09-702-134-24990 from: 1 to: 795

```
13 ProfileGluValAlaSerThrValThrGlnIleAsnGlySerAsnG1 29
||||| : : : : : ||| : : : : : ||| : : : : :
388 CCAATTGTTCTTCACACACATCAATTGCGAGTCAATTGCCAGCCAGAA 437
: : : : : : : : : : : : : : : : : : : : :
29 uValProLeuAspGlyArgTyrSerAsnPheAlaLeuIle..... 42
: : : : : : : : : : : : : : : : : : : : :
438 AGAGGCGATGGATTTCAAAGTCGCTTCCTTCTCTACTCTCTGTTAATCG 487
43 .....SerAlaGluGlyMetGlnAspGlyAspLeuPheGly 55
: : : : : : : : : : : : : : : : : : : : :
488 TCACCTCGGAGCTGCTCAAGGT.....CAAGGCAATGATTTGGT 528
56 ThrValAlaSerAsnPheProMetSerThrPheGluGlnValProAs 72
||| : : : : : ||| : : : : : |||
529 AGCCCTTAATCCACACCTTCCTCTCCCTTACCTATGCTCCTCT... 576
72 nAsnLysGluPheLysGlyValIleSerAlaAsnValLysTyrAspMe 89
: : : : : : : : : : : : : : : : : : : : :
577 .....GGCTCTGCATGCAGTTTGGAAACCA 601
89 snPheLysLysLeuLeuArgPheMetGluAspPheIleGlyValHis 105
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602 ACATGTCAAACATTCTCAAGGGAATAATTGGACAAGTTTTTTATTGTGCGT 651
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seq_documentation_block:
; Sequence 92808, Application US/09815264
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Koshi, Jeffrey M.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51237)G
; CURRENT APPLICATION NUMBER: US/09/815,264
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/702,134
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 109669
; SEQ ID NO 92808
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-815-264-92808
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alignment_scores:
Quality: 74.50 Length: 102

OM of: US-09-528-682-3 to: Pending_Patents_NA_New: * out_format : pfs

Date: Jun 18, 2002 9:49 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-O=/cgn2_1/USPTO_spool/US09528682/runat_18062002_082444_7900/app_query.fasta_1.689
-DB=Pending_Patents_NA_New -QFMT=fastcap -SUFFIX=p2n.rnpn
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOCPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=1000 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09528682@cgn1_1_572 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT_THREADS=1

Search information block:

Query: US-09-528-682-3

Query length: 107

Database: Pending_Patents_NA_New: *

Database sequences: 1014543

Database length: 72792371

Search time (sec): 403.930000

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/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-360-039-25331 + 52.00 96.92 2.8e+0
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-360-039-24908 + 52.00 96.71 2.8e+0
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-540-209B-2309 - 52.00 96.66 2.9e+0
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-919-002-4433 + 52.00 96.66 2.9e+03
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-909-567B-5 + 52.00 95.87 3.2e+03
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-919-002-1839 - 52.00 95.30 3.4e+03
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-548-409B-10 + 52.00 94.84 3.6e+03
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-103-299-12551 - 52.00 94.51 3.8e+0
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-103-310-20 + 52.00 94.41 3.8e+03
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-105-299-11253 + 52.00 94.41 3.8e+03
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-505-477A-17 + 52.00 93.32 3.9e+0
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-916-963-39 + 52.00 90.75 6.1e+03
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-919-002-3489 + 52.00 90.62 6.2e+03
/cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:PCT-US01-13240-8 + 52.00 88.03 8.6e+03
/cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:US-10-105-299-12084 - 52.00 86.71 1.0e+0
/cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:US-10-103-310-18 - 52.00 86.71 1.0e+0
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-109-551-1 + 52.00 76.12 3.9e+04
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-345-882-1 - 52.00 67.74 1.1e+05
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-345-882-1 - 52.00 60.59 2.7e+05
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-345-882-1 - 52.00 60.59 2.7e+05
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-939-964A-1 - 52.00 48.96 9.6e+05
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-811-352B-1 - 52.00 41.18 1.7e+06
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-140-924-1 - 52.00 41.18 1.7e+06
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-067-514-1 - 52.00 37.77 1.9e+06
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-539-800C-11160 - 51.50 121.44 118.8

```



```

: FILE REFERENCE: 108827_129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 203708
: LENGTH: 1194
: TYPE: DNA
: ORGANISM: Human
: US-10-027-632-203708

alignment_scores:
      Quality: 78.00      Length: 113
      Ratio: 1.300      Gaps: 5
Percent Similarity: 53.097      Percent Identity: 25.664

alignment_block:
US-09-528-682-3 x US-10-027-632-203708/rev  ..

Align seg 1/1 to reverse of: US-10-027-632-203708 from: 1 to: 1194

2 PhePheThrArgAlaLeuGlnGlnAlaTyrGluProIleGluValAsnTh 18
863 TTTTTCAGCCGACCATCCAAAGCCACAGAAAGCTCTGAGTATTTCCCT 814
18 rAsnThrValThrGlnIleAsnGlySerAsnGluVal.....ProL 32
813 TTTTTCAGTCCACCATAAATGGCTTCAGGGCCCTCTGGGGAAGGCT. 765
32 euAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMet 48
764 ..GAAGGAAGATTACAGCATACACTTGTGGYAGCATTTGAAGGC..... 723
49 GlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSe 65
722 .....TTCACTCTTCC 712
65 rThrPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerA 82
711 TCAGGATCCATCTCCCTCAGTCAGAAGCTCCAGGTATCTGAAGCTG 662
82 la.....AsnValLysTyrAspMetAsnPheLysLeu... 93
661 GATGCCAGGTCATAAATTCACATATGTTGACTCCATCAGGTCTCTGTCC 612
94 .....LeuArgPheMetGluAspPheIleGlyVal 104
611 TCAGAACTAGAGTAGTAAAGAGTAGACTCATGGGAGTC 573

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-663-870A-5

seq_documentation_block:
: Sequence 5, Application US/09663870A
: GENERAL INFORMATION:
: APPLICANT: Tang, Y Tom
: APPLICANT: Liu, Chenghua
: APPLICANT: Zhou, Ping
: APPLICANT: Asundi Vinod

```



```
3 PheThrArgAlaLeuGlnGlnAlaTyrGluProIleGluValAsnThrAs 19
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
928 TTCAACGATCTCTAGACAACGGCTCAAGAGATTT...GTGAACCGGAA 974

19 nThrValThrGlnIleAsnGlySerAsnGluValPro...LeuAspGlyA 35
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
975 CGAGGCTCGAAA...TCGGGCTCCAAACAGTCACCGGAACGTCTGGCCA 1021

35 rGtyrSerAsnPheAlaLeuIleSerAlaGluGlyMetGlnAspGly 51
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1022 AGTACACGGACGTCTCTCCGCAAGACGACGACCGAGTGAGGAGCG 1071

52 AspLeuPheGlyThrValAsnGlnSerAsnPheProMetSerThrPheG 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1072 GAGCTCGAACAACGCTGACGCAGATT.....ATGACTGTGTCAA 1112

68 uGlnValProAsnAsnLysGluPheLys 77
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1113 GTACATCCAGGACGAAGACGTGTTCAA 1140

seq_name: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-25440

seq_documentation_block:
; Sequence 25440, Application US/603600039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 25440
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-60-360-039-25440

alignment_scores:
Quality: 71.50 Length: 63
Ratio: 1.663 Gaps: 4
Percent Similarity: 68.254 Percent Identity: 36.508

alignment_block:
US-09-528-682-3 x US-60-360-039-25440 ..
Align seg 1/1 to: US-60-360-039-25440 from: 1 to: 2304

53 LeuPheGlyThrValAsnGlnSerAsnPheProMetSerThrPheGlu 69
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1312 TTGTTCCCAACAACAATATTGGTTCCTCCCTCAAAACCAAGGACATCAG 1361

69 nValProAsnAsnLysGluPheLysGlyValIleSerAlaAsnValLys 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1362 AATTAACAAGAAACAANAATTCAACAAGGACCATCTCTGCTGAA...GAAT 1408

86 yrAsp.....MetAsnPheLysLysLeuLeuArgPheMetGlu 98
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1409 ATGAAAAATTCATCAATCTCAAAATGAAAGGTCATCAGATTCCAAGAA 1458

99 AspAspPheIleGly.....ValHisGlyGlu 107
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1459 GAA.....ATTGGTTGGATGCTCTTAGTCCACGGTGAA 1491

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-284619

seq_documentation_block:
; Sequence 284619, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```

```
GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284619
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-284619

alignment_scores:
Quality: 70.50 Length: 81
Ratio: 1.720 Gaps: 3
Percent Similarity: 50.617 Percent Identity: 27.160

alignment_block:
US-09-528-682-3 x US-10-027-632-284619 ..
Align seg 1/1 to: US-10-027-632-284619 from: 1 to: 581

2 PhePheThrArgAlaLeuGlnGlnAlaTyrGluProIleGluValAsnTh 18
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
46 TTCTTCAGAGCCAGCATCCCAACAGCCACAGCAAGCTCTGAGTATTTCCT 95

18 rAsnThrValThrGlnIleAsnGlySerAsnGluVal.....ProL 32
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
96 TTCYTCAGTCACCCACATAAATGGCTTCAGGGCCCTTCTGGGGAAGGCCT. 144

32 euAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMet 48
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
145 ..GAAGGAAGATTTACAGCATACACTTGTGGCAGCATTTGAAGGC..... 186

49 GlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSe 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
187 .....TTCACTCTTCC 197

65 rThrPheGluGlnValProAsnAsnLysGluPheLysGlyVal 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
198 TCAAGGATCCCAATCTCCCTCAGTCAGTCAAGAAGCTCCAGGATC 240

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-284619

seq_documentation_block:
; Sequence 284619, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
```



```
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286485
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-286485
```

```
alignment_scores:
  Quality: 70.50      Length: 81
  Ratio: 1.720       Gaps: 3
  Percent Similarity: 50.617  Percent Identity: 27.160
```

```
alignment_block:
US-09-528-682-3 x US-10-027-632-286485 ..
```

Align seg 1/1 to: US-10-027-632-286485 from: 1 to: 589

```
2 PhePheThrArgAlaLeuGlnAlaTyrGluProIleGluValAsnTh 18
||||| : : : : : ||||| ||| : : : : :
46 TTCTTCAGAGCCAGCATCCACAGAGCCACAGAGCTCTGAGTATTCCCT 95
18 rAsnThrValThrGlnIleAsnGlySerAsnGluVal.....ProL 32
: : : : : ||||| : : : : :
96 TTCTTCAGTCACCCACATAAATGGCTTCAGGGCCTTCTGGGAAGGCCT. 144
32 euAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMet 48
: : : : : ||||| : : : : :
145 ..GAAGGAGATTTCAGCATACACTTGTGGCAGCATTTGAAGGC..... 186
```

```
49 GlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSe 65
||| : : :
187 .....TTCACCTCTTCC 197
```

```
65 rThrPheGluGlnValProAsnAsnLysGluPheLysGlyVal 79
||| ||| : : : : : ||| : : :
198 TCAAGGGATCCCAATCTCCCTCAGTCAGTCAAGAAGCTCCAGGTATC 240
```

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-203709

```
seq_documentation_block:
; Sequence 286486, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
```

```
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203709
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-203709
```

```
alignment_scores:
  Quality: 70.50      Length: 81
  Ratio: 1.720       Gaps: 3
  Percent Similarity: 50.617  Percent Identity: 27.160
```

```
alignment_block:
US-09-528-682-3 x US-10-027-632-203709/rev ..
```

Align seg 1/1 to reverse of: US-10-027-632-203709 from: 1 to: 597

```
2 PhePheThrArgAlaLeuGlnAlaTyrGluProIleGluValAsnTh 18
||||| : : : : : ||||| ||| : : : : :
266 TTCTTCAGAGCCAGCATCCACAGAGCCACAGAGCTCTGAGTATTCCCT 217
18 rAsnThrValThrGlnIleAsnGlySerAsnGluVal.....ProL 32
: : : : : ||||| : : : : :
216 TTCTTCAGTCACCCACATAAATGGCTTCAGGGCCTTCTGGGAAGGCCT. 168
32 euAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMet 48
: : : : : ||||| : : : : :
167 ..GAAGGAGATTTCAGCATACACTTGTGGYAGCATTTGAAGGC..... 126
```

```
49 GlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSe 65
||| : : :
125 .....TTCACCTCTTCC 115
```

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-286486

```
seq_documentation_block:
; Sequence 286486, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286486
; LENGTH: 680
; TYPE: DNA
; ORGANISM: Human
```



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; PRIOR FILING DATE: July 30, 1997
; PRIOR APPLICATION NUMBER: 60/025,478
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/903,556
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/025,217
; PRIOR FILING DATE: August 22, 1996
; PRIOR APPLICATION NUMBER: 08/937,142
; PRIOR FILING DATE: September 23, 1997
; PRIOR APPLICATION NUMBER: 60/026,598
; PRIOR FILING DATE: September 24, 1996
; PRIOR APPLICATION NUMBER: 08/960,746
; PRIOR FILING DATE: October 29, 1997
; PRIOR APPLICATION NUMBER: 60/030,144
; PRIOR FILING DATE: October 30, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/755,524
; PRIOR FILING DATE: November 22, 1996
; PRIOR APPLICATION NUMBER: 60/007,495
; PRIOR FILING DATE: November 22, 1995
; PRIOR APPLICATION NUMBER: 09/021,031
; PRIOR FILING DATE: February 10, 1998
; PRIOR APPLICATION NUMBER: 60/039,325
; PRIOR FILING DATE: February 13, 1997
; PRIOR APPLICATION NUMBER: 09/035,172
; PRIOR FILING DATE: March 4, 1998
; PRIOR APPLICATION NUMBER: 60/040,431
; PRIOR FILING DATE: March 5, 1997
; PRIOR APPLICATION NUMBER: 09/041,894
; PRIOR FILING DATE: March 12, 1998
; PRIOR APPLICATION NUMBER: 60/040,199
; PRIOR FILING DATE: March 14, 1997
; PRIOR APPLICATION NUMBER: 09/050,817
; PRIOR FILING DATE: March 30, 1998
; PRIOR APPLICATION NUMBER: 60/043,792
; PRIOR FILING DATE: April 11, 1997
; PRIOR APPLICATION NUMBER: 09/074,999
; PRIOR FILING DATE: May 8, 1998
; PRIOR APPLICATION NUMBER: 60/048,431
; PRIOR FILING DATE: May 29, 1997
; PRIOR APPLICATION NUMBER: 09/107,592
; PRIOR FILING DATE: June 30, 1998
; PRIOR APPLICATION NUMBER: 60/052,751
; PRIOR FILING DATE: July 1, 1997
; PRIOR APPLICATION NUMBER: 09/094,079
; PRIOR FILING DATE: June 9, 1998
; PRIOR APPLICATION NUMBER: 60/049,975
; PRIOR FILING DATE: June 13, 1997
; NUMBER OF SEQ ID NOS: 35654
; SOFTWARE: PERL Program
; SEQ ID NO 6689
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00285954
; NAME/KEY: unsure
; LOCATION: 228, 243
; OTHER INFORMATION: a, t, c, g, or other
US-09-540-210B-6689

alignment_scores:
    Quality: 69.00      Length: 48
    Ratio: 2.156       Gaps: 2
    Percent Similarity: 66.667      Percent Identity: 35.417

alignment_block:
US-09-528-682-3 x US-09-540-210B-6689/rev ..
```

```
Align seg 1/1 to reverse of: US-09-540-210B-6689 from: 1 to: 261

2 PhePheThrArgAlaLeuGlnAlaTyrGluProIleGluValAsnTh 18
||||| : : : : : ||||| ||| : : : : :
156 TTCTTCAGAGCCAGCATCCCAAGCCACAGAGCTCTGAGTATTTCCT 107
      : : : : : : : : : : : : : : : : : : : :
18 rAsnThrValThrGlnIleAsnGlySerAsnGluVal.....ProL 32
      : : : : : : : : : : : : : : : : : : : :
106 TTCTTCAGTACCCACACATAATGGCTTCAGGGCCTTCTGGGAAGGCT. 58
      : : : : : : : : : : : : : : : : : : : :
32 euAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGly 46
      : : : : : : : : : : : : : : : : : : : :
57 ..GAAGGAGAGATTACAGCATACACTTGTGGCAGCATTTGAAGGC 16

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-34079

seq_documentation_block:
; Sequence 34079, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34079
; LENGTH: 781
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-34079

alignment_scores:
    Quality: 69.00      Length: 48
    Ratio: 2.156       Gaps: 2
    Percent Similarity: 66.667      Percent Identity: 35.417

alignment_block:
US-09-528-682-3 x US-10-027-632-34079/rev ..

Align seg 1/1 to reverse of: US-10-027-632-34079 from: 1 to: 781

2 PhePheThrArgAlaLeuGlnAlaTyrGluProIleGluValAsnTh 18
||||| : : : : : ||||| ||| : : : : :
157 TTCTTCAGAGCCAGCATCCCAAGCCACAGAGCTCTGAGTATTTCCT 108
      : : : : : : : : : : : : : : : : : : : :
18 rAsnThrValThrGlnIleAsnGlySerAsnGluVal.....ProL 32
      : : : : : : : : : : : : : : : : : : : :
107 TTCYTTCAGTACCCACACATAAATGGCTTCAGGGCCTTCTGGGAAGGCT. 59
      : : : : : : : : : : : : : : : : : : : :
32 euAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGly 46
      : : : : : : : : : : : : : : : : : : : :
58 ..GAAGGAGAGATTACAGCATACACTTGTGGCAGCATTTGAAGGC 17

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-34080
```



```
seq_documentation_block:
; Sequence 34080, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34080
; LENGTH: 781
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-34080
```

```
alignment_scores:
Quality: 69.00 Length: 48
Ratio: 2.156 Gaps: 2
Percent Similarity: 66.667 Percent Identity: 35.417
```

```
alignment_block:
US-09-528-682-3 x US-10-027-632-34080/rev ..
Align seg 1/1 to reverse of: US-10-027-632-34080 from: 1 to: 781
2 PhePheThrArgAlaLeuGlnGlnAlaTyrGluProIleGluValAsnTh 18
||||| :|||||:||||| ||| :|||:|||||:
157 TTCCTCAGCAGCAGCATCCACAAAGCCACAGAGCTCTGAGTATTCCCT 108
18 rAsnThrValThrGlnIleAsnGlySerAsnGluVal.....ProL 32
:|||||:|||||:|||||:|||||:
107 TTCYTCACTACCCACATATAATGGCTTCAGGGCCTTCGGGGAAGGCCT. 59
32 euAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGly 46
58 ..GAAGGAAGATTACACATACACTTGTGGCAGCATTTGAAGGC 17
```

seq_name: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:PCT-US02-10421-2010

```
seq_documentation_block:
; Sequence 2010, Application PC/TUS0210421
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Siquing
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Gaiger, Alexander
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.565PC
; CURRENT APPLICATION NUMBER: PCT/US02/10421
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2959
; SEQ ID NO 2010
; LENGTH: 394
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
PCT-US02-10421-2010
alignment_scores:
Quality: 68.50 Length: 59
Ratio: 1.803 Gaps: 2
Percent Similarity: 64.407 Percent Identity: 33.898
alignment_block:
US-09-528-682-3 x PCT-US02-10421-2010 ..
Align seg 1/1 to: PCT-US02-10421-2010 from: 1 to: 394
43 SerAlaGluGlyGlyMetGlnAspGlyAspLeupheGlyThrValAsnGl 59
||| :|||:|||||: ||| :|||:|||||:
28 AGTCAGAACGAGGGGCTACTAACCATGGAGCAGTTCACACACTGTCTCAA 77
59 nSerAsnPheProMetSerThrPheGluGlnValProAsnAsnLysGluP 76
:|||||:|||||:|||||:|||||:
78 GAGTACCTTCCCTCTCAAGACAGAACAGCAATCCAGGAGCTGATGGAGG 127
||| :|||:|||||: ||| :|||:|||||:
76 heLysGlyValIleSerAlaAsnValLysTyrAsp...MetAsnPhelys 91
||| :|||:|||||: ||| :|||:|||||:
128 CAGGGGCTGGCATCCACGACGAGCAGCATGTCAGACTTGTCTCAACTACCGC 177
92 LysLeuLeuArgPheMetGluAspAsp 100
:|||||:|||||:|||||:
178 TCACTG.....TTTATGGAGGATGAG 198
seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-112-699-2010
```

```
seq_documentation_block:
; Sequence 2010, Application US/10112699
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Siquing
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Gaiger, Alexander
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.565
; CURRENT APPLICATION NUMBER: US/10/112,699
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2959
; SEQ ID NO 2010
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-112-699-2010
```

```
alignment_scores:
Quality: 68.50 Length: 59
Ratio: 1.803 Gaps: 2
Percent Similarity: 64.407 Percent Identity: 33.898
alignment_block:
US-09-528-682-3 x US-10-112-699-2010 ..
Align seg 1/1 to: US-10-112-699-2010 from: 1 to: 394
43 SerAlaGluGlyGlyMetGlnAspGlyAspLeupheGlyThrValAsnGl 59
||| :|||:|||||: ||| :|||:|||||:
28 AGTCAGAACGAGGGGCTACTAACCATGGAGCAGTTCACACACTGTCTCAA 77
59 nSerAsnPheProMetSerThrPheGluGlnValProAsnAsnLysGluP 76
:|||||:|||||:|||||:|||||:
78 GAGTACCTTCCCTCTCAAGACAGAACAGCAATCCAGGAGCTGATGGAGG 127
||| :|||:|||||: ||| :|||:|||||:
76 heLysGlyValIleSerAlaAsnValLysTyrAsp...MetAsnPhelys 91
||| :|||:|||||: ||| :|||:|||||:
128 CAGGGGCTGGCATCCACGACGAGCAGCAATGTCAGACTTGTCTCAACTACCGC 177
```


92 LysLeuLeuArgPheMetGluAspAsp 100
:::|||||
178 TCACATG.....TTTATGAGGATGAG 198

seq_name: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-32947

seq_documentation_block:

; Sequence 32947, Application US/60360039

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)A

; CURRENT APPLICATION NUMBER: US/60/360,039

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 32947

; LENGTH: 828

; TYPE: DNA

; ORGANISM: Xylella fastidiosa

US-60-360-039-32947

alignment_scores:

Quality: 67.50 Length: 59

Ratio: 2.045 Gaps: 2

Percent Similarity: 55.932 Percent Identity: 32.203

alignment_block:

US-09-528-682-3 x US-60-360-039-32947 ..

Align seg 1/1 to: US-60-360-039-32947 from: 1 to: 828

2 PhePheThrArgAlaLeuGlnGlnAlaTyrGluProIleGluValAsnTh 18
|||||
187 TTTTTCACCGATGACTTAACCGCGGTACGCCCTGATCCGAATCC 236
:::|||||

18 rAsnThrValThrGlnIleAsnGlySerAsnGluValProLeuAspGlyA 35
:::|||||

237 GCACACATTGCTC.....ATGCCAGCCGACGGAC 265
:::|||||

35 rGtyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetGlnAspGly 51
|||
266 GC.....ATCAGCCAACTCGGCCCAATCGCGAAGG 297
:::|||||

52 AspLeuPheGlyThrValAsnGlnSer 60
:::|||||

298 CCATCTTTCAAGCCAAGGCCAGTCC 324
:::|||||

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-919-002-12794

seq_documentation_block:

; Sequence 12794, Application US/09919002

; GENERAL INFORMATION:

; APPLICANT: Leshkowitz, Dana

; APPLICANT: Liu, Jin

; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA

; FILE REFERENCE: 20411-752CON1

; CURRENT APPLICATION NUMBER: US/09/919,002

; CURRENT FILING DATE: 2001-07-30

; PRIOR FILING DATE: FILING DATE: 1999-07-22

; PRIOR FILING DATE: FILING DATE: 1999-07-22

; PRIOR FILING DATE: FILING DATE: 1998-02-13

; NUMBER OF SEQ ID NOS: 13203

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 12794

; LENGTH: 1810
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-002-12794

alignment_scores:

Quality: 67.50 Length: 105

Ratio: 1.089 Gaps: 6

Percent Similarity: 59.048 Percent Identity: 27.619

alignment_block:

US-09-528-682-3 x US-09-919-002-12794/rev ..

Align seg 1/1 to reverse of: US-09-919-002-12794 from: 1 to: 1810

11 TyrGluProIleGluValAsnThrValThrGlnIleAsnGlySe 27
|||||

1229 TATGAAGCATCAGTCTCACCATGAATCC...AAACTCCTGAATGGTTC 1183
:::|||||

27 rAsnGluValProLeuAspGly..... 34
|:::|||||

1182 CCAGCGGGTGGTGGAGCGGCTAATCTCTGACCAGGAGTGTGAGGAC 1133
|||

35ArgTyrSerAsnPheAlaLeuIleSerAlaGluGly.....Gly 47
|||

1132 TGCAGAGACTGACCAATGTGGCAGCAACCTCAGGAGATGCTACCGGGT 1083
|||

48 MetGlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheProMe 64
::: |||

1082 CAGACCTCCACAT.....ACTCCCAATGAAAAGTTCTATGGTGT 1042
|||

64 tSerThrPheGluGlnValProAsnAsnLysGluPheLysGlyValIle. 80
::: |||

1041 CACTGTCTTCAAGCCCTCAAGCTGGGCAAGCAAGCAAGTCTCTCTGC 992
|||

81 ..SerAlaAsnValLysTyrAspMetAsnPheLysLysLeuLeuArgPhe 96
|||

991 AGAGTGGCCACCTGTACTACACGTGACG...GAGAAGTGGCGGCATC 945
|||

97 MetGluAspPhe 101
|||

944 ATGGAGTCTCTACTTC 930
|||

seq_name: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-25839

seq_documentation_block:

; Sequence 25839, Application US/60360039

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Chen, Xianfeng

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)A

; CURRENT APPLICATION NUMBER: US/60/360,039

; CURRENT FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 25839

; LENGTH: 2292

; TYPE: DNA

; ORGANISM: Schizosaccharomyces pombe

US-60-360-039-25839

alignment_scores:

Quality: 66.50 Length: 104

Ratio: 1.108 Gaps: 5

Percent Similarity: 57.692 Percent Identity: 25.962

alignment_block:

US-09-528-682-3 x US-60-360-039-25839 ..
Align seg 1/1 to: US-60-360-039-25839 from: 1 to: 2292

12 GluProIleGluValAsnThrAsnThrValThrGluIleAsnGlySerAs 28
||| : : : : : ||||| : : : : :
1201 GAGGCGGTTCGTGAAGCTCAAGCAAGGTTACTCCCAAAATGCATGAACG 1250

28 nGluValProLeuAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaG 45
: : : : : ||||| : : : : :
1251 TAGAGTCCCTTTGAGACCGCTTATGCCAAG.....C 1282

45 luGlyGlyMetGlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsn 61
: : : : : ||||| : : : : :
1283 ACAAGCTTCCCTTAAGCTTCCTCTTTCCCTACCACCACTATTGGCTCT 1332

62 PheProMetSerThrPheGluGlnValProAsnAsnLysGluPheLysG 78
||| : : : : : ||||| : : : : :
1333 TTTCCCTCAACCAAGGAATTCGTGTGAACAGAAACAGATTCCGTAAGGG 1382

78 yValIleSerAlaAsnValLysTyrAspMetAsnPheLysLys..... 92
: : : : : ||||| : : : : :
1383 TCCATTTTCACAGAG...GAATATGATGCTTCATCCGTAAGGAGATT 1429

93LeuLeuArgPheMetGluAspPheIleGly..... 103
: : : : : ||||| : : : : :
1430 CTGATGTTGTCAAAATCCAAAGAGAA.....GTTGTCTTGACGTTCTG 1473

104 ValHisGlyGlu 107
||| : : : : : ||||| : : : : :
1474 GTTCACGGTGAA 1485

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-104-580-1
seq_documentation_block:
; Sequence 1, Application US/10104580
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; TITLE OF INVENTION: poplar and other plant species.
; FILE REFERENCE: 62486
; CURRENT APPLICATION NUMBER: US/10/104,580
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/410,464
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/287,700
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,851
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4285
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-10-104-580-1

alignment_scores:
Quality: 66.00 Length: 49
Ratio: 1.833 Gaps: 0
Percent Similarity: 73.469 Percent Identity: 26.531
alignment_block:
US-09-528-682-3 x US-10-104-580-1 ..
Align seg 1/1 to: US-10-104-580-1 from: 1 to: 4285

54 PheGlyThrValAsnGlnSerAsnPheProMetSerThrPheGluGlnVa 70
||| : : : : : ||||| : : : : :
2832 TTCGGTCGGTGTATCAAGCAGGTTAATCTAGATCTAGTTTTCCTT 2881
70 lProAsnAsnLysGluPheLysGlyValIleSerAlaAsnValLysTyrA 87

: ||||| : : : : : ||||| : : : : :
2882 ACCAATCAAGTCATTTTGAGGATTTTATAAAAAATATTGAATTT 2931
87 spMetAsnPheLysLeuLeuArgPheMetGluAspPheIle 102
: : : : : ||||| : : : : :
2932 GAATCAACTATACAATCATCATCTACAACCTGAATCTTACATT 2978

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-103464
seq_documentation_block:
; Sequence 103464, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103464
; LENGTH: 707
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-103464

alignment_scores:
Quality: 65.50 Length: 86
Ratio: 1.260 Gaps: 3
Percent Similarity: 60.465 Percent Identity: 31.395
alignment_block:
US-09-528-682-3 x US-10-027-632-103464 ..
Align seg 1/1 to: US-10-027-632-103464 from: 1 to: 707
4 ThrArgAlaLeuGlnGlnAlaTyrGluProIle.....GluValAs 17
||| : : : : : ||||| : : : : :
305 ACAAGAGCTCTGGAAGCCATGCTAGAGCCTATCTAAATGCAGGAGTAAA 354
17 nThrAsnThrValThrGlnIleAsnGlySerAsnGlu...ValProLeuA 33
| : : : : : ||||| : : : : :
355 CAGGCACCTCGTATCCATCTGCTCGCTCWTCTCATCTACAATGCCACATC 404
33 spGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMetGln 49
||| : : : : : ||||| : : : : :
405 CTGGTAATGAAGTGTCTCAAGGTGATCCCAACACATTTTAAAGAGAAG 454
50 AspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSerth 66
: : : : : ||||| : : : : :
455 TCCCTTTAGATACCATTTGGTTGTAGGATGCCT...TTCTTGTCTCAGT 501
66 rPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAlaA 83
||| : : : : : ||||| : : : : :
502 ATCAATCACATGCCCTCGGAAGCAAGCAACTCTTGGGTTTCATTTCATCA 551
83 snValLys 85
: : : : : |||||

552 CTTTAAAA 559

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-540-209B-4162

seq_documentation_block:

```
; Sequence 4162, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540, 209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 4162
; LENGTH: 747
; TYPE: DNA
; ORGANISM: B.fragilis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (593)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
US-09-540-209B-4162
```

```
alignment_scores:
  Quality: 65.50      Length: 119
  Ratio: 1.023       Gaps: 5
  Percent Similarity: 53.782   Percent Identity: 21.849
```

alignment_block:

US-09-528-682-3 x US-09-540-209B-4162 ..

Align seg 1/1 to: US-09-540-209B-4162 from: 1 to: 747

```
12 GluProleGluValAsnThrAsnThrValThrGlnIleAsnGlySerAs 28
   ::::::::::::::::::::
211 GATGAAGTGGATGGAATACCTATAAGGTGGAGATTGTTGATTAATGCCAC 260
   ::::::::::::::::::::
```

```
28 nGlu.....V 30
   ::::
```

```
261 TGAAGCGGTGGTCCGTCATTTGCCAGCTATGCAAAAGTTGAAAGAGCTT 310
   ::::
```

```
30 alProLeuAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGly 46
   ::::::::::::::::::::
311 TGGCGTGGTGGTCCGGTAGGAACCTATAAGATTGGCTAAAGCGGT 360
   ::::::::::::::::::::
```

```
47 GlyMetGlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPhePr 63
   ::::::::::::::::::::
361 GTTTTGAAGATGCTTCG.....CGTACTCCCTATTTTGA 395
   ::::
```

```
63 oMetSerThrPheGluGlnValProAsnAsnLysGluPheLysGlyValI 80
   :::::
396 AGGAAGTTCTTCTATCCAGTGAAGCAAGCAAGTGGAGTCTAAGCGCAGAAG 445
   ::::
```

```
80 le.....SerAlaAsnValLysTyrAspMetAsnPhe...LysLys 92
   ::::::::::::::::::::
446 TTCTTGTAAATCGGCNACTGTGAAGTTAGTTGAATATATCAGAAGAG 495
   ::::
```

```
93 LeuLeuArgPheMetGluAspAspPheIle.....GlyVa 104
   ::::::::::::::::::::
496 TTCTCAATATGTTGGCGGATGATTAGCTGTTCACTGTTTCAACGCGAAT 545
   ::::
```

```
104 lHisGly 106
   ::::
546 CGGCGGA 552
```

seq_name: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-25694

seq_documentation_block:

```
; Sequence 25694, Application US/603600039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
```

```
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 25694
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-60-360-039-25694
```

```
alignment_scores:
  Quality: 65.50      Length: 69
  Ratio: 1.456       Gaps: 2
  Percent Similarity: 65.217   Percent Identity: 23.188
```

alignment_block:

US-09-528-682-3 x US-60-360-039-25694 ..

Align seg 1/1 to: US-60-360-039-25694 from: 1 to: 1770

```
32 LeuAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMe 48
   ::::::::::::::::::::
1108 ATTTCTGTAAGTTGTTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1157
   ::::::::::::::::::::
```

```
48 t.....GlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPhe 63
   ::::::::::::::::::::
1158 ATATGTGTACCAAGCAGCAAGCAAGTGGTGAATCAATTTCAAGAACCTGC 1207
   ::::::::::::::::::::
```

```
63 roMetSerThrPheGluGlnValProAsnAsnLysGluPheLysGlyVal 79
   ::::::::::::::::::::
1208 CTATCGAAAAATACGAGGATGTCGAAGTTAGAAATAACTATGATGCGGATC 1257
   ::::::::::::::::::::
```

```
80 lIleSerAlaAsnValLysTyrAspMetAsnPheLysLysLeuLeuArgPh 96
   :::::
1258 .....AAGGAAGAGCATGGAGAAACTCGAAGGAGAGATGAAGAGGTT 1298
   ::::
```

```
96 eMetGlu 98
   ::::
```

```
1299 TTGGAA 1305
```

seq_name: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-45758

seq_documentation_block:

```
; Sequence 45758, Application US/603600039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 45758
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-60-360-039-45758
```

```
alignment_scores:
  Quality: 65.50      Length: 69
  Ratio: 1.456       Gaps: 2
```



```
Percent Similarity: 65.217   Percent Identity: 23.188

alignment_block:
US-09-528-682-3 x US-60-360-039-45758   ..

Align seg 1/1 to: US-60-360-039-45758 from: 1 to: 1770

32 LeuAspGlyArgTyrSerAsnPhelaLeuIleSerAlaGluClyGlyMe 48
:::||||| :: |::||| ::|||::| ::|||::|
1108 ATTTCTGGTAAGTGTTGTCTGTGTGTGGTGTCACTGACCGGTACTCT 1157
:::||||| :: ||||| ::|||::| ::|||::|

48 t.....GlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPhep 63
: ::|||:: ::|||::| ::|||::| ::|||::|
1158 ATATCTGTTACCAGACAGGAAGCTGGTGAATCAATTTCAGAAGCTGGC 1207

63 roMetSerThrPheGluGlnValProAsnAsnLysGlupheLysGlyVal 79
||::|::| ::|||::| ::|||::| ::|||::|
1208 CPTATCGAAAATAACGAGGATGTGGAAGTTAGAAATAACTATGATGCATC 1257
:::||||| :: ||||| ::|||::| ::|||::|

80 IleSerAlaAsnValLystyrAspMetAsnPhelLysLysLeuLeuArgph 96
:::||||| :: ||||| ::|||::| ::|||::|
1258 .....AAGCAAGAGCATGCAGAAAACTCGAAGGAGATGAAGAGTTT 1298
:::||||| :: ||||| ::|||::| ::|||::|

96 eMetGlu 98
I::|||
1299 TTTGGAA 1305
```

```

seq_name: /cgn2_5/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-45811
seq_documentation_block:
; Sequence 45811, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkie, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 45811
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-60-360-039-45811

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```

alignment_scores:
  Quality: 65.50      Length: 69
  Ratio: 1.456       Gaps: 2
  Percent Similarity: 65.217  Percent Identity: 23.188

alignment_block:
  US-09-528-682-3 x US-60-360-039-45811  ..

Align seg 1/1  to: US-60-360-039-45811  from: 1  to: 1770

32  LeuAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMet 48
    :::::||||:  ::  |||::|::|  ::|||  ::  ::|||  ::
1108  ATTTCGTGTAACCTGTGTCTGTGTGTGGTCTCACTGAGCGGTACTCT 1157

48  t.....GlnAspGlyAspLeupheGlyThrValAsnGlnSerAsnPheP 63
    :::::||||:  ::  |||::|::|  ::|||  ::  ::|||  ::
1158  ATATGTGTACCAAGACAGGAACTGGTCAATCAATTTCAAGAACTGGC 1207

63  roMetSerThrPheGluGlnValProAsnAsnLysGluPheLysGlyVal 79
    ||:::||||:  ::  |||::|::|  ::|||  ::  ::|||  ::
1208  CTATCGAAATAATCCAGGATGTGCGAAGTTAGAAATAAATCATGATCGATC 1257

80  lleSerAlaAsnValLysTyrAspMetAsnPheLysLysLeuLeuArqPh 96

```

```

::: ::::: ||| ||||:::::: |||||
1258 .....AAGGAAGACGATGGAGAAAACTCGAAGGAGATGAAGAGTT 1298
          96 eMetGlu 98
          I::|||I
1299 TTTGGAA 1305

seq_name: /cgn2_6/ptodata/1/pna/us09_NEW_COMB.seq:US-09-540-209B-3205S

seq_documentation_block:
; Sequence 3205, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; TO THE INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709, 1001-001
; CURRENT APPLICATION NUMBER: US/09/540, 209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 3205
; LENGTH: 2223
; TYPE: DNA
; ORGANISM: B.fragilis
; US-09-540-209B-3205

alignment_scores:
      Quality:    65.50      Length:   110
      Ratio:     1.056      Gaps:       7
Percent Similarity: 56.364 Percent Identity: 28.182

alignment_block:
US-09-528-682-3 x US-09-540-209B-3205 ..

Align seg 1/1 to: US-09-540-209B-3205 from: 1 to: 2223

3 PheThrArgAlaLeuLeuGlnAla.TyrGluProIleGluValAsnThra 19
|||||::: :::: |||||::: |||||
1620 TTACTAAATGTCTTACTCAGGTTTTATAACCA.....ACAA 1657

19 snThrValThrGlnIleAsnGlySerAsnGluValProLeuAspGly... 34
|| :::::::::::::: |||
1658 ATGCTGAAATTGAAGTCGGAGA.....GTGCCATTAGATAATATC 1698

35 .....ArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyme 48
|||||::: |||||
1699 GATTTATATCGTTGGCGTAAT.....AGTTCGGTGCCGTATT 1736

48 tclnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPhePromets 65
:|||||::: |||||::: :::: |||||:::
1737 ACAAGATGTTAACTTTTAAATGACACTATCTTATAATATCATCTGG 1786

65 eThrPheGluGlnValProAsnAsnLysGluPhe...LysGlyValIle 80
:: |||::: ||::: |||||::: |||||:::
1787 AAGATGAAGAAATCAAGCTAAATCAAACAACACTAGTGAAGGCGATCAA 1836

81 SerAlaAsnValLysTyrAspMetAsnPheLysLysLeuLeuArgPheMe 97
|||||::: ||::: |||||
1837 CTGGCAACGCAGAAAAATTCATTAAATGCTCGCCCTTTAAAGCTATACAC 1886

97 tcluAspAspPheIleGlyValHisGly 106
:::|||::: |||||
1887 TCCA.....CTTGGAACTAATGTT 1905

seq_name: /cgn2_6/ptodata/1/pna/us10_NEW_COMB.seq:US-10-104-047-464

seq_documentation_block:
; Sequence 464, Application US/10104047
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
```



```
67 .PheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAla 83
: : : : : : : : : : : : : : : : : : : : : : : : : :
253 CCTCAAGACACACCGCAATTAAGGCGTGAAGAGGTACAAATAGCCTAA 204
: : : : : : : : : : : : : : : : : : : : : : : : : :
83 snValLysTyrAspMetAsnPhe 90
: : : : : : : : : : : : : : : : : : : : : : : : : :
203 AGTATAAATCTGATTAAACTTT 181
: : : : : : : : : : : : : : : : : : : : : : : : : :

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-930-213-248

seq_documentation_block:
; Sequence 248, Application US/09930213
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHAFER, REINHARD
; APPLICANT: ZUBER, JOHANNES
; APPLICANT: TCHE-NITSE, OLEG
; APPLICANT: GRIPS, MARTIN
; APPLICANT: HELLMER, MARTIN
; APPLICANT: SCHMITZ, ANNE-CHANTAL
; APPLICANT: SERS, CHRISTINE
; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
; FILE REFERENCE: ALBRE-14
; CURRENT APPLICATION NUMBER: US/09/930,213
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: DE 10004102.7
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 885
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 248
; LENGTH: 5298
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-930-213-248

alignment_scores:
Quality: 64.00 Length: 71
Ratio: 1.488 Gaps: 2
Percent Similarity: 60.563 Percent Identity: 26.761

alignment_block:
US-09-528-682-3 x US-09-930-213-248 ..
Align seg 1/1 to: US-09-930-213-248 from: 1 to: 5298

33 AspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetol 49
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3101 GATGGCGGCTCTGTAATAGTACGACTACTCTCAGCTGTCTTCAACAA 3150

49 nAspGlyAsp.....LeuPheGlyThrValAsnGlnSerAsnP 62
: ||| : : : : : : : : : : : : : : : : : : : :
3151 GGATGATGACCGCAGATCCCTTTCATTAGAAAGAAATGATGTAGACAATA 3200

62 heProMetSerThrPheGluGlnValProAsnAsn.....Lys 74
: : : : : : : : : : : : : : : : : : : : : : : :
3201 TGCCCAACCAATATAAGAGTACGACCATCAATGGAAGTGAAGAAAT 3250

75 GluPheLysGlyValIleSerAlaAsnValLysTyrAspMetAsnPhe 91
: : : : : : : : : : : : : : : : : : : : : : : :
3251 GACTCTAAAGGAGTCTGACACAGACCTTAGAGATGAGAGAGAACTTCA 3300

91 sLysLeuLeuArg 95
: ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3301 GAAGCAGTTACAG 3313

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-151-129-15

seq_documentation_block:
; Sequence 15, Application US/10151129
; GENERAL INFORMATION:
```

```
; APPLICANT: Essential Therapeutics, Inc.
; TITLE OF INVENTION: Staphylococcus Aureus in Vivo Survival Genes
; FILE REFERENCE: 273/209
; CURRENT APPLICATION NUMBER: US/10/151,129
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-151-129-15

alignment_scores:
Quality: 63.50 Length: 105
Ratio: 1.323 Gaps: 2
Percent Similarity: 45.714 Percent Identity: 27.619

alignment_block:
US-09-528-682-3 x US-10-151-129-15 ..
Align seg 1/1 to: US-10-151-129-15 from: 1 to: 1062

13 ProIleGluValAsnThrAsnThrValThrGlnIleAsnGlySerAsnG1 29
||| : : : : : ||| : : : : :
193 CCAGCTGGTGAAAGACGCAAAACATTTGAGCAATATCAAGAAACATTAGA 242

29 uValProLeuAspGlyArgTyrSerAsnPheAlaLeuIleSerAlaGluG 46
| ||| : : : : : : : : : : : : : : : : : :
243 GTATATTTATCCCATCATGTAACCTGTAATACAGCAATATTGCTGTTG 292

46 LyGlyMetGlnAspGlyAspLeuPheGlyThrValAsnGlnSerAsnPhe 62
|||| | ||| : : : : : ||| : : : : :
293 GTGGTGGTCAACTGGTATTGCTGGGTTATTGCGCGGACACTTTTA 342

63 ProMetSerThrPheGluGlnValPro..... 71
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

343 CGAGCGGTGCACCTTTATACAAAGTGCCACGACTACTAGCGCATGATTC 392

72 .....AsnAsnLysGluPheLysGlyValI 80
||| : : : : : ||| : : : : :
393 TAGTGTTCGCGGTAAAGTGGGTATTAACTCAAGCAAGTAAACCTTA 442

80 LeSerAla.....AsnValLysTyrAspMetAsnPheLys 91
||| : : : : : ||| : : : : :
443 TCGGTGCATTTATCGTCCCAACTGCTGTGATTATGATTTAGTCTTTTA 492

92 LysLeuLeuArgPhe 96
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
493 AAGACGTTACCATTT 507

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-540-209B-1978

seq_documentation_block:
; Sequence 1978, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES
; FILE REFERENCE: 2709,1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 1978
; LENGTH: 2091
; TYPE: DNA
; ORGANISM: B.fragilis
US-09-540-209B-1978

alignment_scores:
Quality: 63.50 Length: 104
```



```
Ratio: 1.198          Gaps: 6
Percent Similarity: 50.962  Percent Identity: 27.885

alignment_block:
US-09-528-682-3 x US-09-540-209B-1978  ..

Align seg 1/1 to: US-09-540-209B-1978 from: 1 to: 2091

5 ArgAlaLeuGlnGlnAlaTyrGluProIleGluValAsnThrAsnThrVa 21
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
646 AGTTGCACGACGAAGGAAGTATCCGAGGCTGAATCGGATTTAAATCACCC 695

21 lThrGlnIleAsnGlySerAsnGluValProLeuAspGlyArgTyrSera 38
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
696 GACACATTTGAATGCTAANAATGCC.....GGAAACTATATTA 733

38 snPheAlaLeuIle.....SerAlaGluGlyGlyMetGln 49
   || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
734 ACCGTGCTTTGGACGCTTCCACCAACAATCTGCGCGTGTATGAGT 783

50 AspGlyAspLeuPheGlyThrValAsnGlnSerAsnPheProMetSerTh 66
   ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
784 GACTATGACCTGGCTCCTCATATGATCGAACACTTT...ATCGGACA 830

66 rPheGluGlnValProAsnAsnLysGluPheLysGlyValIleSerAlaa 83
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
831 CTATAAC.....CGGGCTTGCTCCGGGCGC 856

83 snValLysTyrAspMetAsnPheLysLeuLeuArgPheMetGluAsp 99
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
857 AGGTAGGGGACGACAAAC.....CGTGTATCGAGGAC 888

100 ...AspPheile 102
   |||||:|||||:
889 TTTGATTTTGTA 900

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-947-953-1

seq_documentation_block:
; Sequence 1, Application US/09947953
; GENERAL INFORMATION:
; APPLICANT: DONAHUE, J. KEVIN
; APPLICANT: MARBAN, EDUARDO
; TITLE OF INVENTION: CARDIAC ARRHYTHMIA TREATMENT METHODS
; FILE REFERENCE: 71699/56415
; CURRENT APPLICATION NUMBER: US/09/947,953
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/230,311
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/295,889
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2985
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-947-953-1
```

```
alignment_scores:
Quality: 63.50          Length: 50
Ratio: 2.352           Gaps: 1
Percent Similarity: 54.000  Percent Identity: 34.000

alignment_block:
US-09-528-682-3 x US-09-947-953-1  ..

Align seg 1/1 to: US-09-947-953-1 from: 1 to: 2985
```

```
34 GlyArgTyrSerAsnPheAlaLeuIleSerAlaGluGly..... 46
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
1462 GGGCGTCACAGCCATCATCTTCTGCGTAGCCTTGAGCGCCTATGACTTGG 1511
```

```
47 .....GlyMetGlnAspGlyAspLeuPheGlyThrValAsnGlns 60
   ||| |||||:|||||:|||||:|||||:|||||:|||||:
1512 TGCTAGCTGAGGACGAGGATGTTGAGATATTTACCCCCAGAACCGCA 1561

60 erAsnPheProMetSerThrPheGluGlnValProAsnAsnLysGluPhe 76
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:
1562 TGCATGAGAGCATGAAGCTATTCTGATAGCATCTGCAACAACAAGTGGTTC 1611

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-105-299-1227

seq_documentation_block:
; Sequence 1227, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: ROSEN, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1227
; LENGTH: 3371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-1227
```

```
alignment_scores:
Quality: 63.50          Length: 121
Ratio: 1.114           Gaps: 5
Percent Similarity: 47.107  Percent Identity: 23.967
```

```
alignment_block:
US-09-528-682-3 x US-10-105-299-1227  ..

Align seg 1/1 to: US-10-105-299-1227 from: 1 to: 3371

2 PhePheThrArgAlaLeuGlnGlnAlaTyrGluProIleGluValAsnTh 18
   |||||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1824 TTCTACCTCGGCTCTTACCTTTTGACAAAGTCTCCCGTTGAG...AGTAC 1870

18 rAsnThrValThrGlnIleAsnGlySerAsnGluValProLeuAspGlyA 35
   ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1871 TACCGAACCCACGACGATTCGAGCCTCTGAAGAG.....C 1905

35 rgTyrSerAsnPheAlaLeuIleSerAlaGluGlyGlyMet..... 48
   || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1906 GTCTAAGCAATGGGATATATATTTACTGGAGAATGGGCTCAACCTCTTC 1955

49 .....GlnAspGlyAspLeuPheGlyThrValas 58
   || ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1956 CTCTGGGTGGGACGAAGCGTCCCAACAGGGT.....GTTGT 1990

58 nGlnSerAsnPheProMetSerThrPheGluGlnVal..... 70
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1991 CCAGAGCCTTTTCAGCGCTCTCTCTTCAGTCAGATCACCAGTGGTTTGA 2040

71 .....ProAsnAsnLysGluPheLysGlyVal 79
   ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2041 GTGTTCTGCCAGTTCTGGATAATCCACTGTGCCAAGAAGTTCGAGGCGTC 2090

80 IleSerAlaAsnValLysTyrAspMetAsnPheLysLysLeuLeuArgPh 96
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
2091 ATTGATAGCTTACGGGCACAGAGATCCCGGTACATGAAGCTTACCGTGGT 2140

96 eMetGluAspAsp 100
   :|||:|||||:
2141 GAAACAGGAAGAC 2153

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-634-754C-766
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```
seq_documentation_block:
; Sequence 766, Application US/09634754C
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DETECTING EXPRESSION OF GENES ENCODING SECRETED PROTEINS
; FILE REFERENCE: PA-0017 US
; CURRENT APPLICATION NUMBER: US/09/634,754C
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 809
; SOFTWARE: PERL Program
; SEQ ID NO 766
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 2121260CT1
; PUBLICATION INFORMATION:
US-09-634-754C-766

alignment_scores:
Quality: 63.00 Length: 35
Ratio: 2.739 Gaps: 0
Percent Similarity: 65.714 Percent Identity: 40.000

alignment_block:
US-09-528-682-3 x US-09-634-754C-766/rev ..
Align seg 1/1 to reverse of: US-09-634-754C-766 from: 1 to: 524

45 GluGlyMetGlnAspGlyAspLeuPheGlyThrValAsnGlnSerAs 61
|||||:||||| ||| ||| |||:|||||:|||||
185 GAAGGTTCCCTCGATGATCCATTAAATGGAAGAGTAACCCCAAGAAA 136

61 nPhePrometSerThrPheGluGlnValProAsnAsnLysGluPheLysG 78
||||| ||| |||:||||| ||| |||
135 CATCATGAATCCAAGAATCAGTGGATCCAGCACACAAAGAGCAAGG 86

78 lyVal 79
|||||
85 GAAT 81

seq_name: /cgn2_5/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-168431

seq_documentation_block:
; Sequence 168431, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 168431
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-168431

alignment_scores:
Quality: 63.00 Length: 26
Ratio: 3.500 Gaps: 0
Percent Similarity: 69.231 Percent Identity: 46.154

alignment_block:
US-09-528-682-3 x US-10-027-632-168431/rev ..
Align seg 1/1 to reverse of: US-10-027-632-168431 from: 1 to: 832

26 GlySerAsnGluValProLeuAspGlyArgTyrSerAsnPheAlaLeuI 42
|||||:||||| |||:|||||:||||| |||:
269 GGCTCAAAACGGCTGCTCTATTGATGGTCCCATGCTGCCCTTCCAACATGT 220

42 eSerAlaGluGlyGlyMetGlnAspGly 51
||||| |||:|||||
219 AAAGGATGAAGGACACACAGGATGGA 192

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-935-625-121

seq_documentation_block:
; Sequence 121, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
; FILE REFERENCE: MODULATING VARIOUS RESPONSES
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 121
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: Misc.feature
; LOCATION: 1..1588
; OTHER INFORMATION: Ceres seq. ID no. 1028963
US-09-935-625-121

alignment_scores:
Quality: 63.00 Length: 47
Ratio: 2.032 Gaps: 0
Percent Similarity: 65.957 Percent Identity: 38.298

alignment_block:
US-09-528-682-3 x US-09-935-625-121/rev ..
Align seg 1/1 to reverse of: US-09-935-625-121 from: 1 to: 1588

56 ThrValAsnGlnSerAsnPhePrometSerThrPheGluGlnValProAs 72
|||||:|||||:||||| |||:|||||:||||| |||:
1110 ACAAGAGCTCAAAGCCGCTCAAGAGTCTCCTCTTTCACAAGTAATATA 1061

72 nAsnLysGluPheLysGlyValIleSerAlaAsnValLysTyrAspMetA 89
||||| |||:||||| |||:
1060 TGAGAGTGAAGTAACACTCACTATCAGGCTTACATCCTCTGTTCCACCAT 1011

89 snPheLysLysLeuLeuArgPheMetGluAspPhePhe 102
|||||:|||||:||||| |||:
1010 ACCTTAAACAACCTTCTCGCTTCTCGAAATCATCTTCATT 970

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-540-209B-330
```



```
seq_documentation_block:
; Sequence 330, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 330
; LENGTH: 1809
; TYPE: DNA
; ORGANISM: B. fragilis
US-09-540-209B-330

alignment_scores:
  Quality: 63.00      Length: 122
  Ratio: 1.000       Gaps: 5
Percent Similarity: 51.639 Percent Identity: 24.590

alignment_block:
US-09-528-682-3 x US-09-540-209B-330 ..
Align seg 1/1 to: US-09-540-209B-330 from: 1 to: 1809

2 PhepethrargAlaLeuGlnGlnAlaTyrcIuProIleGluValAsnTh 18
::: ::::: ::::: ::::: ::::: ::::: :::::
1324 TACATTTCGGCGTGAAGGTAATCCATACATCAACCTTTCGATGAAACGG 1373
::: ::::: ::::: ::::: ::::: ::::: :::::

18 rAsnThrValGlnIleAsnGlySerAsnGluValProLeuAspGlyA 35
::: ::::: ::::: ::::: ::::: ::::: :::::
1374 AAATTATGATATGATTCGATGTTTCAGACAAATTCGATCGGATTTAG 1423
::: ::::: ::::: ::::: ::::: ::::: :::::

35 rGlyTy.....SerAsnPheAlaLeuIle 42
::: ::::: ::::: ::::: ::::: ::::: :::::
1424 GGTTTAATATTTTGAAGAGCGTAAATAATCTCGAATGAGGAACGATT 1473
::: ::::: ::::: ::::: ::::: ::::: :::::

43 SerAlaGluGlyGlyMetGlnAspGlyAspLeu..... 53
::: ::::: ::::: ::::: ::::: ::::: :::::
1474 AATGCACCTTCGTCTATTTTTCGATGAGAGTTACGTTTTTAATGATAAACT 1523
::: ::::: ::::: ::::: ::::: ::::: :::::

54 ....PheGlyThrValAsnGlnSerAsnPheProMetSerThrPheGluG 69
::: ::::: ::::: ::::: ::::: ::::: :::::
1524 GAAGTTTACAACTCAACTGTTTGCATTTGGATTAAGCATCGAAAGAAC 1573
::: ::::: ::::: ::::: ::::: ::::: :::::

69 lnValProAsnAsnLysGluPheLys...GlyValIleSerAlaAsnVal 84
::: ::::: ::::: ::::: ::::: ::::: :::::
1574 AGATTGCGGATAAGAGAGATTTTTCATGCGTATATAATTTCGCAAAACAGT 1623
::: ::::: ::::: ::::: ::::: ::::: :::::

85 LysTy.....AspMetAsnPheLysLysLeuLeuArgPheMetGluAspAs 100
::: ::::: ::::: ::::: ::::: ::::: :::::
1624 AAATATTGGGATCTCGCTCCCAAGCAATAAATACTATTATTCGCGACGG 1673
::: ::::: ::::: ::::: ::::: ::::: :::::

100 pPheileGlyValHis 105
::: ::::: ::::: ::::: ::::: ::::: :::::
1674 A.....GGAGTGCAT 1683
::: ::::: ::::: ::::: ::::: ::::: :::::

seq_name: /cgn2_6/ptodata/1/pna/us09_NEW_COMB.seq:us-09-053-375B-832

seq_documentation_block:
; Sequence 832, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 832
```

```
; LENGTH: 8877
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-053-375B-832

alignment_scores:
  Quality: 63.00      Length: 89
  Ratio: 1.167       Gaps: 5
Percent Similarity: 60.674 Percent Identity: 24.719

alignment_block:
US-09-528-682-3 x US-09-053-375B-832 ..
Align seg 1/1 to: US-09-053-375B-832 from: 1 to: 8877

16 ValAsnThrAsnThrValThrGlnIleAsnGlySerAsnGluValProIle 32
::: ::::: ::::: ::::: ::::: ::::: :::::
6487 GTGAGGCTCAGAGAGTGACCATGTTGTAACGGAACGCTTCACCAACCTGT 6536
::: ::::: ::::: ::::: ::::: ::::: :::::

32 uAspGlyArgTySerAsn.....PheAlaLeuIleSerA 44
::: ::::: ::::: ::::: ::::: ::::: :::::
6537 GACCGCAAGAGCTTCAGCTCGCGGAGATTTATTTAAGCTCTTCACGG 6586
::: ::::: ::::: ::::: ::::: ::::: :::::

44 laGluGlyGlyMetGln...AspGlyAspLeuPhe..... 54
::: ::::: ::::: ::::: ::::: ::::: :::::
6587 CCTCTGGAGACATGAGGACCAATGGGACAACTACCTGTATGAAATCCAG 6636
::: ::::: ::::: ::::: ::::: ::::: :::::

55 ...GlyThrValAsnGlnSerAsnPheProMetSerThrPheGluGlnVa 70
::: ::::: ::::: ::::: ::::: ::::: :::::
6637 CTCCTCTCCATCAGCAGCTCTTCTTACCTGCATGCGCTGCTGCAACAT 6686
::: ::::: ::::: ::::: ::::: ::::: :::::

70 l.....ProAsnAsnLysGluPheLysGlyValIleSerAlaA 83
::: ::::: ::::: ::::: ::::: ::::: :::::
6687 CTGCCAGGTGAAGCCCAATACCAGCATTTCCAGCAGGAAGTAGGCACCT 6736
::: ::::: ::::: ::::: ::::: ::::: :::::

83 sn.....VallysTy 86
::: ::::: ::::: ::::: ::::: ::::: :::::
6737 CTGACATGACCAAGTAC 6753
::: ::::: ::::: ::::: ::::: ::::: :::::

seq_name: /cgn2_6/ptodata/1/pna/us09_NEW_COMB.seq:us-09-539-800C-13583

seq_documentation_block:
; Sequence 13583, Application US/09539800C
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahey, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
; FILE REFERENCE: PD-1023 CIP
; CURRENT APPLICATION NUMBER: US/09/539,800C
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 08/521,383
; PRIOR FILING DATE: August 16, 1995
; PRIOR APPLICATION NUMBER: 08/271,217
; PRIOR FILING DATE: June 27, 1994
; PRIOR APPLICATION NUMBER: 08/334,881
; PRIOR FILING DATE: November 4, 1994
; PRIOR APPLICATION NUMBER: 08/943,978
; PRIOR FILING DATE: October 4, 1997
; PRIOR APPLICATION NUMBER: 60/027,782
; PRIOR FILING DATE: October 4, 1996
; PRIOR APPLICATION NUMBER: 60/028,732
; PRIOR FILING DATE: October 4, 1996
; PRIOR APPLICATION NUMBER: 08/943,979
; PRIOR FILING DATE: October 4, 1997
; PRIOR APPLICATION NUMBER: 60/027,782
; PRIOR FILING DATE: October 4, 1996
; PRIOR APPLICATION NUMBER: 08/993,774
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/034,975
; PRIOR FILING DATE: December 20, 1996
```



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; PRIOR APPLICATION NUMBER: 09/250,003
; PRIOR FILING DATE: February 10, 1999
; PRIOR APPLICATION NUMBER: 60/074,364
; PRIOR FILING DATE: February 12, 1998
; PRIOR APPLICATION NUMBER: 09/452,747
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: 60/111,910
; PRIOR FILING DATE: December 10, 1998
; NUMBER OF SEQ ID NOS: 19698
; SOFTWARE: PERL Program
; SEQ ID NO 13583
; LENGTH: 299
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01060356
US-09-539-800C-13583

alignment_scores:
  Quality: 62.50      Length: 63
  Ratio: 1.603       Gaps: 2
  Percent Similarity: 61.905      Percent Identity: 30.159

alignment_block:
US-09-528-682-3 x US-09-539-800C-13583 ..
Align seg 1/1 to: US-09-539-800C-13583 from: 1 to: 299

35 ArgTyrSerAsnPheAlaLeuIleSerAlaGluGlyMetClnAsp... 50
||||| ||| |||||:|||||:|||||:|||||:|||||
112 CGATACAGT...GCTGCTCGATCTTCGTCGATTCAATATGACGATAT 158
51 .....GlyAspLeuPheGlyThrValA 58
|||||:|||||:|||||:|||||:|||||:|||||:
159 TTGTAAGCTGCTTCGAAGTACAGGTATTCTAGCCAAACGAGTGCACAAA 208
58 snGlnSerAsnPheProMetSerThrPheGluGlnValProAsnAsnLys 74
:: |||||:||||| ||| |||||:|||||:|||||:|||||:|||||
209 GACCATCCAACTATCCCGAGAGCTATTCCAGAGAGTGCCTATCAACGAA 258
75 GluPheLysGlyValIleSerAlaAsnValLysTyrAsp 87
|||||:|||||:|||||:|||||:|||||:|||||:
259 TCCTTCATCATGATGTCATTGTCGACGATGATCTGAT 297

seq_name: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-34787

seq_documentation_block:
; Sequence 34787, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 34787
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Ferroplasma acidarmanus
US-60-360-039-34787

alignment_scores:
  Quality: 62.50      Length: 93
  Ratio: 1.179       Gaps: 4
  Percent Similarity: 56.989      Percent Identity: 26.882

```

```

alignment_block:
US-09-528-682-3 x US-60-360-039-34787 ..
Align seg 1/1 to: US-60-360-039-34787 from: 1 to: 960

23 GlnIleAsnGlySerAsnGluValProLeuAspGlyArgTyrSer..... 37
|||||:|||||:|||||:|||||:|||||:|||||
15 CAGGTCAACGGGAAAAATAAACACAGAAAGGCTGGAGCAGGCAACACC 64
38 .....Asn.PheAlaLeuIleSerAlaGluGlyMetClnAsp... 50
|||: |||: |||||:|||||:|||||:|||||:
65 TTAATAAATAATATGAATCCATAGTGGAGAAGCTGTTGAGGAGGACAGG 114
51 .....GlyAspLeuPheGlyThrValAsn.....GlnSerAs 61
|||||:|||||:|||||:|||||:|||||:|||||
115 ATTTCGTAGGGGAAAAAGATATCTGGGACATTGAATATAGAGCCACCTGA 164
61 nPheProMetSerThrPheGluGlnValProAsnAsnLysGluPheLysG 78
||||| |||||:|||||:|||||:|||||:|||||
165 GATTCCAAAAGTTACATTTTCAGGATGTTGCTGGATTAGAAAATGTAAAAA 214
78 lyValIleSerAlaAsnValLysTyrAspMetAsnPheLysLeuLeu 94
|||: |||: |||||:|||||:|||||:|||||:
215 CAGAGATTATGTCAAAGATAATATACCTATCGGTATATAAAGAGCTATCA 264
95 ArgPheMetGluAspPheIleGly 103
::: |||: ||||| |||
265 CAGGAATATATATTGAATTGAGCGC 291

seq_name: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-46330

seq_documentation_block:
; Sequence 46330, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 46330
; LENGTH: 1396
; TYPE: DNA
; ORGANISM: Schizosaccharomyces pombe
US-60-360-039-46330

alignment_scores:
  Quality: 62.50      Length: 114
  Ratio: 1.250       Gaps: 5
  Percent Similarity: 43.860      Percent Identity: 27.193

alignment_block:
US-09-528-682-3 x US-60-360-039-46330/rev ..
Align seg 1/1 to reverse of: US-60-360-039-46330 from: 1 to: 1396

1 AspPhePheThrArgAla.....LeuGlnG1 9
|||||:|||||:|||||:|||||:|||||:
1319 GATTTTACAGGGAGACATGCATACCCGATCGATGAAGTAGATTCGTGA 1270
9 nAlaTyrGluProIleGluValAsnThrAsnThrValThrGlnIleAsnG 26
|||: |||: |||||:|||||:|||||:|||||
1269 AACGGTGAACCGCGCGCTTCGGAAAAGGTAAGTACACAGCA..... 1227
26 lySerAsnGluValProLeuAspGlyArgTyrSerAsnPheAlaLeuIle 42
||||| ||||| ||| |||||:|||||:

```



```
1226 ..AGCAATGAGTGACATTGGATTTCGGACCAAGGAATTT ..... 1188
43 SerAlaGluGlyGlyMetGlnAspGlyAspLeuPheGlyThrValAsnG1 59
1187 .....CG 1186
59 nSerAsnPheProMetSerThrPheGluGlnValProAsnAsnLysGluP 76
:|||||:|||||:|||||:|||||:|||||:|||||:
1185 CTCAGTTTTCATGGAACAATGATGATAAGATCGAGCAAGATGCT 1136
76 heLysGlyValIleSerAlaAsn.....ValLysTyr 86
:|||||:|||||:|||||:|||||:|||||:|||||:
1135 TGAAGGATTGACACGAGACAACACTAGGGCATTCGATCGGTAAAGTAC 1086
87 AspMetAsnPheLysLysLeuLeuArgPheMetGluAspAsp 100
:|||||:|||||:|||||:|||||:|||||:|||||:
1085 .....AACTTTTCCTTTACACGAGGACAAT 1059
seq_name: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-33321
seq_documentation_block:
; Sequence 33321, Application US/603600039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 33321
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Desulfitobacterium hafniese
US-60-360-039-33321
```

```
alignment_scores:
  Quality: 62.50      Length: 117
  Ratio: 1.179       Gaps: 5
  Percent Similarity: 45.299   Percent Identity: 24.786
alignment_block:
US-09-528-682-3 x US-60-360-039-33321 ..
Align seg 1/1 to: US-60-360-039-33321 from: 1 to: 1581
4 ThrArgAlaLeuGlnGlnAlaTyrGluProIleGluValAsnThrAsnTh 20
:|||||:|||||:|||||:|||||:|||||:|||||:
748 AGCAATGCTGCTACGCCATTTTCGAAGTCTTGGAGTAGAGAACCAAGCT 797
20 rValThrGlnIleAsnGlySerAsnGluValProLeuAspGlyArgTyr 37
:|||||:|||||:|||||:|||||:|||||:|||||:
798 GGAATCTGAGTTGAATGGG.....GTGGAATTGGCGGA..... 831
37 erAsnPheAlaLeuIleSerAlaGluGlyMetGlnAspGlyAspLeu 53
:|||||:|||||:|||||:|||||:|||||:|||||:
832 .....GGGCGGAGGAGCGCGGTCAATTG 855
54 PheGlyThrValAsnGlnSerAsnPheProMetSerThrPheGluGlnVa 70
:|||||:|||||:|||||:|||||:|||||:|||||:
856 TTCAGG.....GGAGAGCAAGCGCCCTTGGCTTACATTAAACAGGT 899
70 lProAsnAsnLysGluPheLysGlyValIleSerAlaAsnValLysTyr 87
:|||||:|||||:|||||:|||||:|||||:|||||:
900 GGACCTATGCTATGAGCAAGGGA.....GAAAGAGTTTAAAGG 940
87 spMetAsnPhe..... 90
|||||:|||||
```

```
941 ATATTAACTTTTACCCTCCGCTTGGTGAACGGTGGCTTTGATTGGACCC 990
91 .....LysLysLeuLeuArgPheMetG1 98
:|||||:|||||:|||||:|||||:|||||:|||||:
991 AGTGGCGGGGAAAAAGCTCCCTTCTGCGAGATTCTGCTTAGGTTGTAGA 1040
98 u 98
1041 A 1041
seq_name: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-36604
seq_documentation_block:
; Sequence 36604, Application US/603600039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 36604
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-60-360-039-36604
```

```
alignment_scores:
  Quality: 62.50      Length: 109
  Ratio: 1.042       Gaps: 7
  Percent Similarity: 55.046   Percent Identity: 28.440
alignment_block:
US-09-528-682-3 x US-60-360-039-36604 ..
Align seg 1/1 to: US-60-360-039-36604 from: 1 to: 1890
1 AspPhePheThrArgAlaLeuGlnGlnAlaTyrGluProIleGluValas 17
:|||||:|||||:|||||:|||||:|||||:|||||:
556 GACTTTTTCAGAAAAGTGAGTAATCTGGCTGCTGCACCTGAATCGGTGG 605
17 nThrAsnThrValThrGlnIleAsnGlySerAsn..... 28
:|||||:|||||:|||||:|||||:|||||:|||||:
606 G.....CACGGTAATAACTAACCTCTACTAGTGG 634
29 .....GluValProLeuAspGlyArgTyrSerAsnPheAlaLeu 41
:|||||:|||||:|||||:|||||:|||||:|||||:
635 TTGTGGATGCGGTTCTCTCGCTCGACCAAGACGATCTGAATGAGAAGTTG 684
42 IleSerAlaGlu.....GlyGlyMetGlnAspGlyAspLeuPh 54
:|||||:|||||:|||||:|||||:|||||:|||||:
685 ATTGGGTTAAAAAGGTCACCTGGCGGGTCTGCAGGAC...TCTCTCTT 731
54 e.....GlyThrValAsnGlnSerAsnPheProMetSerThrPheGluG 69
:|||||:|||||:|||||:|||||:|||||:|||||:
732 CGTCAATGGAGTGGCATTCAAAAAGACATTCTCTACGCCGCTTTTGAAC 781
69 lnValProAsnAsnLysGluPheLysGly.....ValIleSerAlaAsn 83
:|||||:|||||:|||||:|||||:|||||:|||||:
782 AACAGCCCC.....AAGTCTTTTAAAGAACCCGCAAGATCGTGTGTTGAAT 825
84 ValLysTyrAspMetAsnPheLysLys 92
:|||||:|||||:|||||:|||||:|||||:|||||:
826 GTGGAGTTGGAACTGAAGAGTGAAGAG 852
seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-045-815-5
```


OM of: US-09-528-682-4 to: GenEmbl:* out_format : pfs

Date: Jun 18, 2002 7:35 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODE=frame+ p2n.spool -DEV=xlp
-Q=cgnt2.1/USPTO.spool/US09528682/runat_18062002_082443_7808/app_query.fasta_1.689
-DB=GenEmbl -QFM=fastap -SUFFIX=p2n.rge -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-XGAPOP=4.500 -XGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40 cdi -LIST=1000 -DOALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09528682_@CGN1_1.8225 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-528-682-4

Query length: 110

Database: GenEmbl.*

Database sequences: 1797656

Database length: 187333701

Search time (sec): 3690.420000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
gb_ba:ECOE0XHL	+ 181.00	369.18	3.4e-12	1262	M28523 Escherichia coli (strain
gb_ba:AE000850	- 83.50	142.08	14.99	11069	AE000850 Methanobacterium the
gb_in:PFSC04095	- 81.50	146.20	8.84	4300	AL010267 Plasmodium falciparum
gb_pat:AX067456	+ 81.00	120.95	225.27	65792	AX067456 Sequence 31 from pat
gb_in:PFU05963	+ 80.50	145.95	9.12	3474	U85963 Plasmodium falciparum a
gb_in:PFMAL4P2	+ 80.50	108.63	1.1e+03	234112	AL035475 Plasmodium falcipar
gb_in:CELM4	+ 80.00	132.72	4.76	13705	AF100670 Caenorhabditis eleg
gb_hgt:AC006890	+ 80.00	105.42	1.7e+03	238195	AC006890 Caenorhabditis eleg
gb_hgt:AC017108	- 79.00	120.80	229.64	41363	AC107108 Rattus norvegicus cl
gb_pat:AX067440	+ 78.00	121.93	198.63	28626	AX067440 Sequence 15 from pat
gb_hgt:CMS07EFS	- 77.00	104.82	1.8e+03	155031	AL513402 Oryza sativa chromo
gb_in:TAV15795	+ 76.50	148.86	6.29	957	V15795 theileria annulata spm2
gb_ba:AF160726	+ 76.50	134.25	40.93	4374	AF160726 Peanut witches'-broom
gb_hgt:AC097767	+ 76.50	110.47	864.05	72729	AC097767 Rattus norvegicus cl
gb_in:AF410153	- 76.50	104.26	1.9e+03	146454	AF410153 Swinepox virus isol
gb_ro:MMU52925	+ 76.00	130.69	64.56	6585	U52925 Mus musculus coagulatio
gb_ba:AF279106	+ 76.00	105.73	1.5e+03	105184	AF279106 Uncultured proteoba
gb_hgt:PFMAL13P2_0	+ 76.00	106.13	1.6e+03	110000	AL049125 Plasmodium falcipar
gb_pat:150034	+ 74.50	144.96	10.36	918	I90034 Sequence 3 from patent
gb_pat:190033	+ 74.50	142.42	14.34	1222	I90033 Sequence 1 from patent
gb_pat:190036	+ 74.50	135.25	35.98	2745	I90036 Sequence 6 from patent
gb_ba:PPB276891	+ 74.50	134.37	40.29	3032	AJ276891 Pedicoccus pentosace
gb_pl:SCYKR021W	+ 74.50	133.52	44.94	3338	Z28246 S.cerevisiae chromoso
gb_pat:150035	+ 74.50	133.10	47.43	3500	I90035 Sequence 4 from patent
gb_in:LL14324	- 74.50	111.90	719.45	38269	LL14324 Caenorhabditis elegans
gb_pl:PF37058	- 74.50	99.03	3.7e+03	163390	AL137058 Human DNA sequence
gb_ba:AP003581	+ 74.50	92.33	8.9e+03	348050	AF003581 Nostoc sp. PCC 7120
gb_ba:AE000809	+ 74.00	122.32	189.05	10473	AE000809 Agrobacterium tumefa
gb_ba:AE009125	+ 74.00	122.20	191.78	10606	AE009125 Agrobacterium tumefa
gb_hgt:AC094854	- 74.00	104.77	1.8e+03	75818	AC094854 Rattus norvegicus cl
gb_pl:AP002867	+ 74.00	99.06	3.7e+03	144322	AF002867 Oryza sativa genom
gb_pl:AP002747	+ 74.00	98.85	3.8e+03	147857	AF002747 Oryza sativa genom
gb_hgt:AC027163	- 74.00	98.33	4.1e+03	156690	AC027163 Homo sapiens chromo
gb_ba:AP003600	+ 74.00	91.42	9.9e+03	341950	AF003600 Nostoc sp. PCC 7120
gb_pl:AP0148XYL	+ 73.50	137.78	26.02	1623	Z68891 A.pisi endo-1,4-beta
gb_hgt:AC103259	+ 73.50	100.21	3.2e+03	12484	AC103259 Rattus norvegicus c
gb_vl:AF325155	+ 73.50	98.31	4.1e+03	193342	AF325155 Spodoptera litura n
gb_hgt:AC095438	- 73.50	95.67	5.8e+03	187586	AC095438 Rattus norvegicus c
gb_pl:AL353732	+ 73.00	95.31	6.0e+03	173211	AL353732 Human DNA sequence
gb_ba:MMU75887	+ 72.50	121.56	208.41	7955	U75887 Methanococcus maripalud

gb_hgt:AC095031	- 72.50	95.63	5.8e+03	148238	AC095031 Homo sapiens chr
gb_hgt:AC099184	- 72.50	94.58	6.6e+03	166852	AC099184 Rattus norvegicu
gb_hgt:AC099452	- 72.50	94.30	6.9e+03	172199	AC099452 Rattus norvegicu
gb_hgt:AC094036	+ 72.50	93.78	7.3e+03	182583	AC094036 Rattus norvegicu
gb_hgt:AC104308	+ 72.50	93.34	7.8e+03	191971	AC104308 Homo sapiens chr
gb_pl:TAVDAC1	- 72.00	137.56	26.74	1159	TT7733 T.aestivum VDAC 1 mR
gb_ba:AE006005	- 72.00	118.18	321.50	10328	AE006005 Caulobacter cresc
gb_ba:AE009725	- 72.00	116.24	411.93	12844	U39725 Mycoplasma genitali
gb_hgt:AC103288	+ 72.00	112.37	677.41	13894	AC103288 Rattus norvegicus
gb_pl:SPAC458	- 72.00	106.92	1.4e+03	36776	Z56276 S.pombe chromosome
gb_in:CEC06H5	- 72.00	105.89	1.6e+03	41299	Z92775 Caenorhabditis eleg
gb_hgt:AC106600	- 72.00	93.91	7.2e+03	159630	AC106600 Rattus norvegicu
gb_hgt:CEY59A8	- 72.00	88.52	1.4e+04	293024	Z98870 Caenorhabditis ele
gb_ba:AF226440	+ 71.50	134.56	39.34	1443	AF226440 Neisseria mening
gb_pat:AR003712	+ 71.50	119.95	255.93	7493	AR003712 Sequence 5 from pa
gb_pat:AR029067	+ 71.50	119.95	255.93	7493	AR029067 Sequence 5 from pa
gb_pat:ARI26886	+ 71.50	119.95	255.93	7493	ARI26886 Sequence 7 from pa
gb_ro:MUSCCVII1	- 71.50	119.95	255.93	7493	L05573 Mus domesticus coagu
gb_hgt:AC094529	- 71.50	97.40	4.6e+03	95426	AC094529 Rattus norvegicu
gb_pr:AC092326	+ 71.50	94.41	6.8e+03	133709	AC092326 Homo sapiens chr
gb_pl:AC079736	+ 71.50	94.26	6.9e+03	135932	AC079736 Oryza sativa chr
gb_hgt:AC011432	+ 71.50	93.33	7.8e+03	131044	AC011432 Homo sapiens chr
gb_hgt:AC010373	+ 71.50	93.18	7.9e+03	153693	AC010373 Homo sapiens chr
gb_hgt:AC093526	+ 71.50	91.53	9.8e+03	185074	AC093526 Homo sapiens chr
gb_hgt:AC087558	- 71.50	90.04	1.2e+04	218939	AC087558 Mus musculus clo
gb_ba:AP003009	- 71.50	86.15	2.0e+04	339681	AP003009 Mesorhizobium lo
em_hgt:inv.AC032918	+ 71.00	136.38	31.15	1042	AC032918 Giardia intestinal
gb_pat:AR083442	+ 71.00	126.16	115.51	3300	AR083442 Sequence 6 from pa
gb_pat:ARI44911	+ 71.00	126.16	115.51	3300	ARI44911 Sequence 6 from pa
gb_pat:AX006403	+ 71.00	126.16	115.51	3300	AX006403 Sequence 4 from pa
gb_pat:118647	+ 71.00	126.16	115.51	3300	118647 Sequence 6 from pate
gb_vl:AF291685	+ 71.00	124.73	138.77	3878	AF291685 Trichoplusia ni cy
gb_ba:AF193063	+ 71.00	123.90	154.21	4255	AF193063 Caulobacter cresc
gb_ba:AE005779	- 71.00	118.89	293.42	7493	AE005779 Caulobacter cresc
gb_hgt:AC109071	- 71.00	113.50	585.52	13759	AC109071 Rattus norvegicu
gb_ba:AF062345	- 71.00	110.24	889.86	19883	AF062345 Caulobacter cresc
gb_pr:HS04488	+ 71.00	92.25	8.9e+03	151236	AL023883 Human DNA sequen
gb_hgt:AC097684	+ 71.00	91.22	1.0e+04	159907	AC097684 Rattus norvegicu
gb_pr:AC006039	- 71.00	90.90	1.1e+04	176257	AC006039 Homo sapiens BAC
gb_hgt:AC0094782	- 71.00	90.70	1.1e+04	180106	AC094782 Rattus norvegicu
gb_ba:AF079317	- 71.00	90.49	1.1e+04	184457	AF079317 Spingomonas bac
gb_pr:AC018710	- 71.00	89.90	1.2e+04	197236	AC018710 Homo sapiens BAC
gb_hgt:AC091335	- 71.00	88.29	1.5e+04	236389	AC091335 Rattus norvegicu
gb_in:PFMAL3P7	+ 71.00	87.68	1.6e+04	253303	AL034559 Plasmodium falci
gb_pl:CCUXJANAS	+ 70.50	131.29	59.81	1640	L13596 Cochliobus carbonum
gb_pat:HTU238895	+ 70.50	129.57	74.56	1991	AJ238895 Helminthosporium t
gb_pat:I28324	+ 70.50	125.15	131.52	3280	IA01449 Recombinant DNA comp
gb_ba:STAFNBP	+ 70.50	125.15	131.52	3280	I28324 Sequence 4 from pate
gb_ba:WSU131242	+ 70.50	124.98	134.35	3342	J04151 S.aureus fibronectin
gb_ba:RTI1467	+ 70.50	121.04	222.80	5215	AJ131242 Wolinella succinog
gb_ba:ID90917	+ 70.50	120.64	253.20	2836	II1467 T.thermophilus yqjy
gb_ba:AE008771	- 70.50	108.63	1.1e+03	21131	AE008771 Salmonella typhim
gb_hgt:AC099206	- 70.50	90.98	1.1e+04	154619	D90917 Synecocystis sp.
em_hgt:inv.AC032900	+ 70.00	137.04	28.60	760	AC032900 Giardia intestinali
gb_sts:CN506HV7	- 70.00	134.93	37.48	964	AL399497 T3 end of clone AS0
em_hgt:inv.AC072546	+ 70.00	134.06	41.93	1084	AC072546 Giardia intestinal
gb_ba:AF237557	+ 70.00	128.98	80.42	1887	AF004832 Vibrio mimicus ATC
gb_ba:AF237557	+ 70.00	126.13	115.98	2604	AF237557 Porphyromonas ging
gb_pat:AX250677	- 70.00	124.26	147.29	3213	AX250677 Sequence 4 from pa
gb_pl:AC071188	- 70.00	94.57	6.6e+03	91589	AC007188 Arabidopsis thali
gb_in:AC084459	- 70.00	94.45	6.7e+03	92783	AC084459 Caenorhabditis br
gb_pl:CPU30821	- 70.00	92.94	8.2e+03	110000	AL034557 Plasmodium falci
gb_pr:AL512644	- 70.00	91.09	1.0e+04	135599	U30821 Cyanophora paradoxi
gb_hgt:AC073919	+ 70.00	90.56	1.1e+04	143919	AL512644 Human DNA sequen
gb_hgt:AC087100	+ 70.00	88.98	1.4e+04	172116	AC087100 Mus musculus clo
gb_pl:AF083031	- 70.00	88.87	1.4e+04	174133	AF083031 Guillardia theta
gb_hgt:AC005505	- 70.00	87.96	1.5e+04	192929	AC005505 Plasmodium falci
gb_hgt:AC106130	+ 70.00	87.67	1.6e+04	193342	AC106130 Rattus norvegicu
gb_hgt:AC105137	- 70.00	87.18	1.7e+04	210651	AC105137 Homo sapiens chr

gb_btg.AC005139	AC005139	Plasmodium falciparum	256172	70.00	85.45	2.1e+04	gb_in.AC023708	AC023708	Drosophila melanogaster	175353	69.00	86.68	1.8e+04	175353
gb_pl.AC003583	AC003583	Nostoc sp. PCC 7120	339650	70.50	82.95	2.9e+04	gb_in.AC009725	AC009725	Drosophila melanogaster	176509	69.00	86.62	1.8e+04	176509
gb_pl.HVLP60	X15691	Barley mRNA for chlorophyll a	764	69.50	135.93	32.99	gb_in.AC010211	AC010211	Drosophila melanogaster	177857	69.00	86.55	1.9e+04	177857
gb_pat.AC086020	AC086020	Sequence 17 from Patent	904	69.50	134.44	39.94	gb_in.AC007825	AC007825	Drosophila melanogaster	179171	69.00	86.49	1.9e+04	179171
gb_pr.AC057012	AC057012	Homo sapiens cDNA FLJ	1107	69.50	132.64	50.28	gb_in.AC009357	AC009357	Drosophila melanogaster	179375	69.00	86.48	1.9e+04	179375
gb_ba.AF005686	AF005686	Shewanella alga DNA	1257	69.50	131.52	58.10	gb_in.AC008224	AC008224	Drosophila melanogaster	181636	69.00	86.37	1.9e+04	181636
gb_pl.AC052086	AF052086	Mucor circinelloides	1546	69.50	129.68	73.51	gb_in.AC008224	AC008224	Drosophila melanogaster	181636	69.00	86.37	1.9e+04	181636
gb_ba.AF290090	AF290090	Staphylococcus epidermidis	2869	69.50	124.20	148.46	gb_in.AC008211	AC008211	Drosophila melanogaster	181905	69.00	86.35	1.9e+04	181905
gb_pl.AF258809	AF258809	Lycopersicon esculentum	4631	69.50	119.96	255.87	gb_in.AC010051	AC010051	Drosophila melanogaster	184416	69.00	86.23	1.9e+04	184416
gb_ba.AF054600	AF054600	Lactococcus lactis	7853	69.50	115.27	466.42	gb_in.AC009090	AC009090	Drosophila melanogaster	186285	69.00	86.14	2.0e+04	186285
gb_pl.AF258813	AF258813	Lycopersicon esculentum	9775	69.50	113.33	598.23	gb_pr.AL353734	AL353734	Human DNA sequence	186608	69.00	86.13	2.0e+04	186608
gb_ba.AE004032	AE004032	Xylella fastidiosa	18959	69.50	107.46	1.4e+03	gb_in.AC007418	AC007418	Drosophila melanogaster	186690	69.00	86.12	2.0e+04	186690
gb_ba.AE004082	AE004082	Xylella fastidiosa	20956	69.50	106.57	1.4e+03	gb_in.AC010414	AC010414	Drosophila melanogaster	186753	69.00	86.12	2.0e+04	186753
gb_pl.Y5C8H167	AC095872	Rattus norvegicus	38868	69.50	101.10	2.8e+03	gb_in.AC008331	AC008331	Drosophila melanogaster	186938	69.00	86.11	2.0e+04	186938
gb_btg.AC083754	AC083754	Saccharomyces cerevisiae	61577	69.50	97.02	4.8e+03	gb_in.AC009848	AC009848	Drosophila melanogaster	189694	69.00	85.98	2.0e+04	189694
gb_btg.PFWAL13B	AL109814	Plasmodium falciparum	83110	69.50	94.36	6.8e+03	gb_in.AC010032	AC010032	Drosophila melanogaster	192393	69.00	85.86	2.0e+04	192393
gb_pl.AC006841	AC006841	Arabidopsis thaliana	123183	69.50	90.87	1.1e+04	gb_in.AC010419	AC010419	Drosophila melanogaster	193714	69.00	85.80	2.0e+04	193714
gb_pr.AL355878	AL355878	Human DNA sequence	166718	69.50	88.19	1.5e+04	gb_in.AC008308	AC008308	Drosophila melanogaster	195868	69.00	85.70	2.1e+04	195868
gb_btg.AC016094	AC016094	Homo sapiens clone	169312	69.50	88.05	1.5e+04	gb_btg.AC106532	AC106532	Rattus norvegicus	214765	69.00	84.88	2.3e+04	214765
gb_btg.AC095872	AC095872	Rattus norvegicus	171378	69.50	87.95	1.6e+04	gb_htg.AC097423	AC097423	Rattus norvegicus	236247	69.00	84.04	2.6e+04	236247
gb_btg.AC097529	AC097529	Mus musculus clone	209301	69.50	86.18	1.9e+04	gb_in.AE003829	AE003829	Drosophila melanogaster	258463	69.00	83.24	2.8e+04	258463
gb_ba.CNSPAX06	AF248288	Pyrococcus abyssi	265118	69.50	84.08	2.5e+04	gb_in.AE003811	AE003811	Drosophila melanogaster	259445	69.00	83.21	2.9e+04	259445
gb_pat.AC041922	AC041922	Sequence 817 from Patent	265118	69.50	84.08	2.5e+04	gb_da.CJ1168X4	CJ1168X4	Campylobacter jejuni	282183	69.00	82.46	3.1e+04	282183
gb_ba.AP000996	AF000996	Thermoplasma volcanum	278604	69.50	83.64	2.7e+04	gb_in.AE003601	AE003601	Drosophila melanogaster	303626	69.00	81.81	3.4e+04	303626
gb_ro.RATCBLP	AC095872	Rattus norvegicus	742	69.00	135.12	36.58	gb_in.AE003477	AE003477	Drosophila melanogaster	304633	69.00	81.78	3.4e+04	304633
gb_pr.BC004335	BC004335	Homo sapiens, chr1	1142	69.00	131.30	59.73	gb_in.AE003437	AE003437	Drosophila melanogaster	305018	69.00	81.77	3.4e+04	305018
gb_pr.AC001217	AC001217	Homo sapiens, chr2	1350	69.00	129.82	72.24	gb_in.AE003593	AE003593	Drosophila melanogaster	313115	69.00	81.54	3.5e+04	313115
gb_pr.AC001217	AC001217	Homo sapiens, chr2	1350	69.00	129.82	72.24	gb_in.AE003593	AE003593	Drosophila melanogaster	313115	69.00	81.54	3.5e+04	313115
gb_pr.BC003605	BC003605	Homo sapiens, chr2	1372	69.00	129.67	73.58	gb_in.AE003843	AE003843	Drosophila melanogaster	316640	69.00	81.44	3.6e+04	316640
gb_ro.BC003430	BC003430	Mus musculus, chr1	1740	69.00	127.57	96.40	gb_pl.CCUI2314	CCUI2314	Cenchrus ciliaris	1335	68.50	128.85	81.78	1335
gb_in.AV061584	AV061584	Drosophila melanogaster	1798	69.00	127.28	100.06	gb_pat.AC023760	AC023760	Sequence 17 from Patent	2877	68.50	122.04	195.77	2877
gb_pl.AV062525	AV062525	Arabidopsis thaliana	2071	69.00	126.02	117.51	gb_ro.SCYDL195W	SCYDL195W	Glaucomyces volans	2890	68.50	122.00	196.77	2890
gb_pat.AY009418	AY009418	Sequence 1 from Patent	2278	69.00	125.18	130.95	gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00	125.18	130.95	gb_vi.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	68.50	121.74	203.44	2976
gb_ro.VI.HHGMIEXE	HHGMIEXE	Human herpesvirus 6	2976	69.00</										

gb_pt:AF126008	68.00	117.44	353.49	4290	AF126008 Homo sapiens breast c	gb_ba:AE001580	67.00	97.81	4.4e+03	30885	AE001580 Borrelia burgdorferi
gb_ba:WBOAPULNS	68.00	117.26	361.46	4375	L07762 Thermoanaerobacterium s	gb_ba:MLCB2548	67.00	95.76	5.7e+03	38916	AL023093 Mycobacterium lep
gb_pt:WBOAPULNS	68.00	116.37	405.26	4838	J012073 Wolbachia sp. Wri gl	gb_ba:AE001584	67.00	93.03	8.1e+03	52971	AL001584 Borrelia burgdorferi
gb_pt:AF387101	68.00	111.44	763.14	8442	AF387101 Homo sapiens protein	gb_hgt:AC100499	67.00	92.13	9.1e+03	58608	AC100499 Mus musculus clon
gb_ba:AB045235	68.00	110.50	860.87	9386	AB045235 Wolbachia sp. wta1 r	gb_pt:SGE9781	67.00	90.77	1.1e+04	68301	U18916 Saccharomyces cerev
gb_pt:AF405992	68.00	110.42	869.43	9468	AF405992 Homo sapiens A-kinase	gb_hgt:AC106273	67.00	90.41	1.1e+04	71188	AC106273 Rattus norvegicus
gb_pt:AB055890	68.00	109.80	941.60	10156	AB055890 Homo sapiens c-lbc n	gb_hgt:AC098320	67.00	90.16	1.2e+04	72456	AC098320 Rattus norvegicus
gb_in:AB001407	68.00	107.32	1.3e+03	13437	AC001407 Plasmodium falcipar	gb_hgt:AC097831	67.00	90.16	1.2e+04	73215	AC097831 Rattus norvegicus
gb_pt:SC23CDS	68.00	99.78	3.4e+03	31431	X86470 S. cerevisiae PWS1, TPM	gb_hgt:AC101587	67.00	90.09	1.2e+04	73789	AC101587 Mus musculus clon
gb_pt:AF135983	68.00	95.33	6.0e+03	51923	AL356983 Human DNA sequence	gb_pt:SCD9461	67.00	89.54	1.3e+04	78500	U33007 Saccharomyces cerev
gb_hgt:AC107592	68.00	92.25	8.9e+03	73497	AL107592 Rattus norvegicus cl	gb_ov:AL591180	67.00	89.34	1.3e+04	80272	AL591180 zebrafish DNA seq
gb_hgt:AC090931	68.00	90.43	1.1e+04	90280	AC090931 Homo sapiens chromos	gb_pt:AB019236	67.00	89.21	1.3e+04	81494	AB019236 Arabidopsis thali
gb_hgt:LMFLCH36_14	68.00	88.68	1.4e+04	101000	Continuation (15 of 36) of I	gb_hgt:AC095541	67.00	89.03	1.4e+04	83131	AC095541 Rattus norvegicus
gb_hgt:OSJN00017	68.00	86.97	1.8e+04	133428	AL606456 Oryza sativa chromo	gb_hgt:AC107555	67.00	88.88	1.4e+04	84519	AC107555 Rattus norvegicus
gb_hgt:AC096100	68.00	85.97	2.0e+04	149325	AC096100 Rattus norvegicus	gb_ov:AL591175	67.00	88.40	1.5e+04	89232	AL591175 zebrafish DNA seq
gb_hgt:AC094715	68.00	85.74	2.1e+04	153223	AC094715 Rattus norvegicus	gb_hgt:AC099305	67.00	88.14	1.5e+04	91953	AC099305 Rattus norvegicus
gb_hgt:AC106404	68.00	85.51	2.1e+04	157373	AC106404 Rattus norvegicus	gb_pt:FBK7	67.00	87.52	1.6e+04	98581	AC097727 Arabidopsis thali
gb_pt:AC1195074	68.00	85.32	2.2e+04	160755	AX195074 Sequence 544 from F	gb_hgt:AC095010	67.00	87.46	1.7e+04	99203	AC095010 Rattus norvegicus
gb_hgt:AC094557	68.00	85.31	2.2e+04	160791	AC094557 Rattus norvegicus	gb_hgt:AC084726	67.00	87.27	1.7e+04	101375	AC084726 Mus musculus chr
gb_hgt:AC007602	68.00	85.31	2.2e+04	160865	AC007602 Homo sapiens chromo	gb_hgt:OSJN00045	67.00	86.67	1.8e+04	108479	AL606610 Oryza sativa chr
gb_vl:AF081810	68.00	85.30	2.2e+04	161046	AF081810 Lymantria dispar nu	gb_hgt:AC094266	67.00	86.15	2.0e+04	115062	AC094266 Rattus norvegicu
gb_hgt:AC080157	68.00	84.83	2.3e+04	169801	AC080157 Rattus norvegicus	gb_pt:AF003049	67.00	86.00	2.0e+04	117000	AP003049 Homo sapiens gen
gb_hgt:AC105656	68.00	84.36	2.5e+04	178982	AC105656 Rattus norvegicus	gb_hgt:AC095745	67.00	85.93	2.0e+04	117980	AC095745 Rattus norvegicu
gb_hgt:AC098141	68.00	84.30	2.5e+04	180313	AC098141 Rattus norvegicus	gb_hgt:AC103239	67.00	84.54	2.4e+04	137897	AC103239 Rattus norvegicu
gb_hgt:AC026802	68.00	83.72	2.7e+04	192386	AC026802 Homo sapiens chromo	gb_hgt:AC094726	67.00	84.21	2.5e+04	143135	AC094726 Rattus norvegicu
gb_hgt:PFMAL13P6	68.00	83.18	2.9e+04	204652	AL049183 Plasmodium falcipar	gb_hgt:AC068373	67.00	83.50	2.7e+04	155186	AC068373 Homo sapiens chr
gb_hgt:AC096325	68.00	82.01	3.1e+04	233362	AC096325 Rattus norvegicus	gb_hgt:AC106473	67.00	83.44	2.8e+04	156169	AC106473 Rattus norvegicu
gb_ba:CU11168X3	68.00	79.28	4.7e+04	317511	AL139076 Campylobacter jejun	gb_hgt:AC094654	67.00	83.42	2.8e+04	156476	AC094654 Rattus norvegicu
gb_pt:AX142405	67.50	133.25	46.52	639	AX142405 Sequence 1127 from Pat	gb_hgt:AC103366	67.00	83.42	2.8e+04	156614	AC103366 Homo sapiens chr
gb_pt:BE39874	67.50	127.57	96.31	1212	E39874 Method for reducing the	gb_hgt:AC051640	67.00	83.31	2.8e+04	158514	AC051640 Homo sapiens chr
gb_ov:DUKARGINX	67.50	125.21	130.38	1582	M35133 Anas platyrhynchos delt	gb_pt:AL499604	67.00	83.18	2.9e+04	160796	AL499604 Human DNA sequen
gb_ba:CATSPD	67.50	124.87	136.30	1645	M18769 Rat liver beta-galactos	gb_hgt:AC103206	67.00	83.04	2.9e+04	163486	AC103206 Rattus norvegicu
gb_in:AV075532	67.50	122.37	187.82	2181	250009 C. acetobutylicum CSPD	gb_hgt:AC094061	67.00	82.93	3.0e+04	165502	AC094061 Rattus norvegicu
gb_ba:AF270077	67.50	119.56	269.36	2395	AY075532 Drosophila melanogast	gb_hgt:AC096596	67.00	82.65	3.1e+04	170674	AC096596 Rattus norvegicu
gb_pt:AF200077	67.50	119.06	287.01	3167	AF270077 Staphylococcus epider	gb_hgt:AC106311	67.00	82.62	3.1e+04	171237	AC106311 Rattus norvegicu
gb_pt:AF362372	67.50	119.06	287.01	3167	AF362372 Dictyostelium discoi	gb_hgt:AC097018	67.00	82.53	3.1e+04	173083	AC097018 Rattus norvegicu
gb_ba:AE006775	67.50	112.05	705.74	6988	AF362372 Dictyostelium discoi	gb_hgt:AC102971	67.00	82.46	3.1e+04	174436	AC102971 Rattus norvegicu
gb_pt:AX353827	67.50	108.24	1.1e+03	10732	AC096775 Sulfolobus solfatar	gb_hgt:AC087156	67.00	82.30	3.2e+04	177630	AC087156 Mus musculus clo
gb_pt:AX353827	67.50	106.35	1.5e+03	13288	AX353827 Sulfolobus solfatar	gb_hgt:AC099102	67.00	82.25	3.2e+04	178544	AC099102 Rattus norvegicu
gb_in:CEY51A2A	67.50	97.44	4.6e+03	35303	AL032835 Caenorhabditis elega	gb_pt:AC009756	67.00	82.25	3.2e+04	178624	AC009756 Homo sapiens, cl
gb_in:AC084445	67.50	92.61	8.5e+03	62584	AC084445 Caenorhabditis brig	gb_hgt:AC084240	67.00	82.12	3.2e+04	18282	AC084240 Rattus norvegicu
gb_pt:AC092223	67.50	89.76	1.2e+04	86372	AC092223 Drosophila melanoga	gb_hgt:AC106452	67.00	82.00	3.3e+04	183818	AC106452 Rattus norvegicu
gb_pt:AF171715	67.50	89.72	1.2e+04	86748	AL031032 Arabidopsis thaliana	gb_hgt:AC094159	67.00	81.96	3.3e+04	184640	AC094159 Rattus norvegicu
gb_hgt:AC017901	67.50	89.43	1.3e+04	89670	AL017901 Drosophila melanogast	gb_hgt:AC095692	67.00	81.30	3.6e+04	198850	AC095692 Rattus norvegicu
gb_hgt:AC020798	67.50	87.22	1.7e+04	114979	AC020798 Mus musculus clone	gb_hgt:AC092296	67.00	81.09	3.7e+04	203650	AC092296 Homo sapiens chr
gb_pt:AL135932	67.50	85.27	2.2e+04	143321	AL135932 Human DNA sequence	gb_ba:AF003192	67.00	77.61	5.8e+04	301550	AP003192 Clostridium perfr
gb_hgt:AC095893	67.50	84.70	2.4e+04	152867	AC095893 Rattus norvegicus	gb_ba:MLEPRTN1	67.00	76.44	6.7e+04	344050	AL583917 Mycobacterium le
gb_hgt:AC095244	67.50	84.48	2.4e+04	156647	AC095244 Rattus norvegicus	em_hgt:inv:AC031479	66.50	128.30	87.75	878	AC031479 Giardia intestinali
gb_in:AC092223	67.50	83.67	2.7e+04	171598	AC092223 Drosophila melanoga	em_hgt:inv:AC078143	66.50	128.08	90.25	900	AC078143 Giardia intestinali
gb_hgt:AC020695	67.50	83.13	2.9e+04	182513	AC020695 Homo sapiens chromo	em_hgt:inv:AC048725	66.50	127.29	99.89	984	AC048725 Giardia intestinali
gb_hgt:AC084393	67.50	83.11	2.9e+04	182742	AC084393 Homo sapiens chromo	em_hgt:inv:AC031137	66.50	127.13	101.97	1002	AC031137 Giardia intestinali
gb_hgt:AC098987	67.50	83.06	2.9e+04	193893	AC098987 Rattus norvegicus	em_hgt:inv:AC047374	66.50	126.12	116.08	1123	AC047374 Giardia intestinali
gb_hgt:AC106311	67.50	83.00	2.9e+04	195162	AL365178 Homo sapiens chromo	gb_pt:AF140553	66.50	125.49	125.88	1206	AF140553 Avena sativa DNA-b
gb_pt:AFCH361780	67.50	82.64	3.1e+04	192861	AL161584 Arabidopsis thalian	gb_ba:AE0011286	66.50	121.43	211.68	1905	AB011286 Candida maltosa EP
gb_hgt:AC017086	67.50	81.82	3.4e+04	211365	AC017086 Homo sapiens chromo	gb_ov:AF332044	66.50	117.78	338.38	2878	AF332044 Scitrus niger BRCA
gb_in:AE003641	67.50	78.73	5.0e+04	299556	AE003641 Drosophila melanoga	gb_ov:BOVPI204	66.50	115.97	436.39	3527	L04797 Bos taurus polymeric
gb_in:DROSADH02	67.50	78.13	5.4e+04	320754	AE003408 Drosophila melanoga	gb_ov:BPPIGR1	66.50	115.72	440.57	3630	X81371 B. taurus mRNA for bo
gb_sts:GL17579	67.00	136.34	31.31	400	GL17579 human STS SHGC-11666 c	gb_pt:AR172654	66.50	115.72	440.57	3630	AR172654 Sequence 5 from pa
gb_ba:CFPOLC	67.00	135.33	35.62	448	X86524 C. perfringens folC gene	gb_pt:SCADR6	66.50	113.19	609.58	4830	X12493 Yeast AD6 gene for
gb_ba:HFU005677	67.00	124.38	145.08	1541	U05677 Helicobacter pylori 87-	gb_pt:SCU15219	66.50	112.00	709.66	5521	U15219 Saccharomyces cerevi
gb_pt:189393	67.00	124.38	145.08	1541	I89393 Sequence 3 from patent	gb_ba:ECOHLY	66.50	108.48	1.1e+03	8211	M10133 E.coli (J96) hlyc, h
gb_pt:AF361830	67.00	122.82	177.16	1937	AF361830 Arabidopsis thaliana	gb_ba:AE0005596	66.50	106.71	1.4e+03	10029	AE0005596 Streptococcus pyo
gb_pt:AV064044	67.00	119.19	282.35	2768	AY054044 Arabidopsis thaliana	gb_ba:AE009152	66.50	105.85	1.6e+03	11049	AE009152 Agrobacterium tum
gb_pt:AV059877	67.00	119.05	287.46	2812	AY059877 Arabidopsis thaliana	gb_ba:AE005969	66.50	105.71	1.6e+03	11225	AD5969 Complete sequence o
gb_ba:AE0007843	67.00	106.00	1.5e+03	12251	AE007843 Clostridium acetobut	gb_vl:FPV11KB	66.50	105.71	1.6e+03	11225	D00295 Fowlpox virus genom
gb_ba:AE000598	67.00	105.79	1.6e+03	12551	AE000598 Helicobacter pylori;	gb_ba:AE006095	66.50	105.69	1.6e+03	11249	AE006095 Pasteurella multo
gb_in:CELC0566	67.00	104.16	1.9e+03	15075	AF045635 Caenorhabditis elega	gb_pt:SCYBL101C	66.50	104.94	1.8e+03	12242	Z35862 S. cerevisiae chromo
gb_ba:AE002154	67.00	101.88	2.6e+03	19497	AE002154 Ureaplasma urealytic	gb_ba:AE008118	66.50	104.68	1.8e+03	12606	AE008118 Agrobacterium tum
gb_in:CBRG01P23	67.00	101.47	2.7e+03	20422	AC084476 Caenorhabditis brig	gb_pt:U33335	66.50	95.49	5.9e+03	35550	U33335 Saccharomyces cerev
gb_ba:AE001578	67.00	98.11	4.2e+03	29838	AE001578 Borrelia burgdorferi	gb_vl:AE0015885	66.50	92.48	8.7e+03	49936	AB015885 faba monkey tumor
gb_ba:AE0001576	67.00	98.00	4.3e+03	30223	AE001576 Borrelia burgdorferi	gb_pt:AF356491	66.50	90.80	1.1e+04	60350	AL356491 Human DNA sequenc
gb_ba:AE001577	67.00	97.98	4.3e+03	30299	AE001577 Borrelia burgdorferi	gb_hgt:AC102251	66.50	90.02	1.2e+04	65903	AC102251 Mus musculus clon
gb_ba:AE001575	67.00	97.85	4.4e+03	30750	AE001575 Borrelia burgdorferi	gb_pt:SCDNC2	66.50	88.46	1.5e+04	78600	X79489 S. cerevisiae genom

gb_hhg:AC096910	gb_hhg:AC097595	-	66.50	86.49	1.9e+04	98153	! AC096910 Rattus norvegicus cl	gb_hhg:AC097595	! AC097595 Rattus norvegicus	66.00	84.15	2.5e+04	113349
gb_hhg:AC097881	gb_hhg:AC097702	+	66.50	86.16	2.0e+04	101857	! AC097881 Rattus norvegicus c	gb_hhg:AC097702	! AC097702 Rattus norvegicus	66.00	84.14	2.5e+04	113510
gb_pr:HS614C15	! AL035250 Human DNA sequence	+	66.50	85.87	2.0e+04	105325	! AL035250 Human DNA sequence	gb_hhg:AC096080	! AC096080 Rattus norvegicus	66.00	84.04	2.6e+04	114725
gb_hhg:AC094512	! AC094512 Rattus norvegicus c	+	66.50	85.62	2.1e+04	108247	! AC094512 Rattus norvegicus c	gb_hhg:AC019814	! AC019814 Drosophila melan	66.00	84.00	2.6e+04	115291
gb_hhg:AC097049	! AC097049 Rattus norvegicus c	+	66.50	85.45	2.1e+04	110382	! AC097049 Rattus norvegicus c	gb_hhg:AC099448	! AC099448 Rattus norvegicus	66.00	83.78	2.6e+04	118157
gb_hhg:AC103287	! AC103287 Rattus norvegicus c	+	66.50	85.13	2.2e+04	114507	! AC103287 Rattus norvegicus c	gb_hhg:AC095525	! AC095525 Rattus norvegicus	66.00	83.75	2.7e+04	118604
gb_hhg:AC107492	! AC107492 Rattus norvegicus c	+	66.50	84.64	2.2e+04	120902	! AC107492 Rattus norvegicus c	gb_hhg:AC094674	! AC094674 Rattus norvegicus	66.00	83.46	2.8e+04	122464
gb_ba:D909901	! D90901 Synchocystis sp. PC	+	66.50	83.95	2.5e+04	130690	! D90901 Synchocystis sp. PC	gb_hhg:AC096240	! AC096240 Rattus norvegicus	66.00	82.91	3.0e+04	130428
gb_hhg:AC096368	! AC096368 Trypanosoma brucei	+	66.50	83.79	2.6e+04	133075	! AC096368 Trypanosoma brucei	gb_ba:D90907	! D90907 Synchocystis sp.	66.00	82.77	3.0e+04	132419
gb_hhg:AC096368	! AC096368 Rattus norvegicus c	+	66.50	83.43	2.8e+04	138663	! AC096368 Rattus norvegicus c	gb_hhg:AC093222	! AC093222 Homo sapiens chr	66.00	82.37	3.2e+04	138635
gb_hhg:AC105378	! AC105378 Trypanosoma brucei	+	66.50	83.32	2.8e+04	140392	! AC105378 Trypanosoma brucei	! AC105378 Trypanosoma brucei	! AC105378 Trypanosoma brucei	66.00	81.92	3.4e+04	145846
gb_ba:D90904	! D90904 Synchocystis sp. PC	+	66.50	82.68	3.1e+04	150894	! D90904 Synchocystis sp. PC	gb_hhg:AC020298	! AC020298 Drosophila melan	66.00	81.90	3.4e+04	145846
gb_hhg:AC094720	! AC094720 Rattus norvegicus c	+	66.50	82.12	3.3e+04	160645	! AC094720 Rattus norvegicus c	gb_hhg:AC098509	! AC098509 Rattus norvegicus	66.00	81.90	3.4e+04	146028
gb_hhg:AC094402	! AC094402 Rattus norvegicus c	+	66.50	82.06	3.3e+04	161856	! AC094402 Rattus norvegicus c	gb_hhg:AC008714	! AC008714 Homo sapiens chr	66.00	81.74	3.4e+04	148846
gb_hhg:AC098137	! AC098137 Rattus norvegicus c	+	66.50	82.05	3.3e+04	162020	! AC098137 Rattus norvegicus c	gb_hhg:AC097979	! AC097979 Rattus norvegicus	66.00	81.58	3.5e+04	151452
gb_hhg:AC027764	! AC027764 Homo sapiens clone	+	66.50	81.94	3.4e+04	163988	! AC027764 Homo sapiens clone	gb_hhg:AC103225	! AC103225 Rattus norvegicus	66.00	81.42	3.6e+04	154256
gb_hhg:AC094400	! AC094400 Rattus norvegicus c	+	66.50	81.80	3.7e+04	180749	! AC094400 Rattus norvegicus c	gb_hhg:AC097588	! AC097588 Sus scrofa clone	66.00	81.23	3.7e+04	157629
gb_hhg:AC058805	! AC058805 Homo sapiens chromo	+	66.50	80.97	3.8e+04	183029	! AC058805 Homo sapiens chromo	gb_hhg:AC066601	! AC066601 Homo sapiens chr	66.00	81.03	3.7e+04	161179
gb_hhg:AC105360	! AC105360 Rattus norvegicus c	+	66.50	80.84	3.9e+04	189853	! AC105360 Rattus norvegicus c	gb_hhg:AC095088	! AC095088 Rattus norvegicus	66.00	80.94	3.8e+04	162875
gb_pr:AF165818	! AF165818 Galliardia theta nu	+	66.50	80.35	4.1e+04	196216	! AF165818 Galliardia theta nu	gb_hhg:AC102984	! AC102984 Rattus norvegicus	66.00	80.87	3.9e+04	164191
gb_hhg:AC0671321	! AC0671321 Mus musculus clone	+	66.50	80.70	4.1e+04	197384	! AC0671321 Mus musculus clone	gb_hhg:AC095076	! AC095076 Rattus norvegicus	66.00	80.80	3.9e+04	165460
gb_hhg:AL671321	! AL671321 Mus musculus chromo	+	66.50	78.37	5.0e+04	234426	! AL671321 Mus musculus chromo	gb_hhg:AC023404	! AC023404 Homo sapiens clo	66.00	80.68	3.9e+04	167659
gb_ba:AL672720	! AL672720 Salmonella enterica	+	66.50	77.65	5.8e+04	266050	! AL672720 Salmonella enterica	gb_hhg:AC024712	! AC024712 Homo sapiens chr	66.00	80.68	3.9e+04	167659
gb_vi:AF192100	! AF198100 Fowlpox virus, comp	+	66.50	76.93	6.3e+04	288539	! AF198100 Fowlpox virus, comp	gb_in:AC104604	! AC104604 Drosophila melan	66.00	80.67	3.9e+04	167901
gb_pi:AF192469	! AF072469 Arabidopsis thaliana F	+	66.00	127.12	102.04	889	! AF072469 Arabidopsis thaliana F	gb_hhg:AC096979	! AC096979 Rattus norvegicus	66.00	80.59	4.0e+04	169239
gb_in:BMX16050	! Y16050 EColi-PvuII fragment of	+	66.00	126.51	108.98	942	! Y16050 EColi-PvuII fragment of	gb_hhg:AC094220	! AC094220 Rattus norvegicus	66.00	80.56	4.0e+04	169867
em_hhg_inv:AC053761	! AC053761 Giardia intestinalis c	+	66.00	126.64	110.03	950	! AC053761 Giardia intestinalis c	gb_in:AC023712	! AC023712 Drosophila melan	66.00	80.58	4.0e+04	170137
gb_pi:ATHASAB	! M9215 Arabidopsis thaliana ad	+	66.00	125.56	124.76	1061	! M9215 Arabidopsis thaliana ad	gb_pr:AC001538	! AC001538 Homo sapiens gen	66.00	80.35	4.1e+04	170431
gb_in:DROCACB	! M97215 Drosophila melanogaster	+	66.00	124.66	139.98	1174	! M97215 Drosophila melanogaster	gb_in:AC007827	! AC007827 Drosophila melan	66.00	80.40	4.1e+04	180946
gb_ba:ECOLITIA	! M17894 E.coli heat-labile ente	+	66.00	124.47	143.51	1200	! M17894 E.coli heat-labile ente	gb_hhg:AC103049	! AC103049 Rattus norvegicus	66.00	79.91	4.3e+04	182795
gb_pi:AF054568	! AF054664 Arabidopsis thaliana	+	66.00	122.78	178.09	1451	! AF054664 Arabidopsis thaliana	gb_hhg:AC095203	! AC095203 Rattus norvegicus	66.00	79.81	4.4e+04	184857
gb_pr:AF285154	! AF285158 Homo sapiens topoisom	+	66.00	121.87	200.16	1608	! AF285158 Homo sapiens topoisom	gb_hhg:AL670838	! AL670838 Mus musculus chr	66.00	79.64	4.5e+04	188488
gb_in:AE069515	! AE069515 Drosophila melanogast	+	66.00	120.18	248.64	1346	! AE069515 Drosophila melanogast	gb_hhg:AL662929	! AL662929 Mus musculus chr	66.00	78.97	4.9e+04	203267
gb_pi:AF400129	! AF400129 Arabidopsis thaliana	+	66.00	114.72	500.53	3601	! AF400129 Arabidopsis thaliana	gb_hhg:CN505TDO	! CN505TDO Homo sapiens chr	66.00	78.76	5.0e+04	208222
gb_ba:AF050327	! AF050327 Helicobacter pylori i	+	66.00	113.85	560.03	3975	! AF050327 Helicobacter pylori i	gb_hhg:AC098287	! AC098287 Rattus norvegicus	66.00	78.18	5.4e+04	222233
gb_ba:AF050319	! AF050319 Helicobacter pylori i	+	66.00	113.81	562.92	3993	! AF050319 Helicobacter pylori i	gb_in:AC003766	! AC003766 Drosophila melan	66.00	78.00	5.5e+04	225894
gb_ba:HP029401	! U29401 Helicobacter pylori vad	+	66.00	113.05	620.48	4350	! U29401 Helicobacter pylori vad	gb_hhg:AL670256	! AL670256 Mus musculus chr	66.00	77.59	5.8e+04	237688
gb_pat:AR032348	! AR032348 Sequence 3 from patent	+	66.00	111.93	716.51	4937	! AR032348 Sequence 3 from patent	gb_hhg:AC096303	! AC096303 Rattus norvegicus	66.00	77.56	5.8e+04	238400
gb_pat:AR083935	! AR083935 Sequence 3 from patent	+	66.00	111.93	716.51	4937	! AR083935 Sequence 3 from patent	gb_in:AE003530	! AE003530 Drosophila melan	66.00	76.16	7.0e+04	270975
gb_pat:AR145899	! AR145899 Sequence 3 from patent	+	66.00	111.93	716.51	4937	! AR145899 Sequence 3 from patent	gb_hhg:AC103203	! AC103203 Rattus norvegicus	66.00	76.10	7.0e+04	281229
gb_pat:BD010356	! BD010356 High molcular weight	+	66.00	111.93	716.51	4937	! BD010356 High molcular weight	gb_hhg:SPNEU1905	! SPNEU1905 Streptococcus pn	66.00	75.61	7.5e+04	297172
gb_pat:135182	! 125182 Sequence 3 from patent	+	66.00	111.93	716.51	4937	! 125182 Sequence 3 from patent	gb_hhg:AC003185	! AC003185 Clostridium perf	66.00	75.48	7.6e+04	301450
gb_pat:135771	! 135771 Sequence 3 from patent	+	66.00	111.93	716.51	4937	! 135771 Sequence 3 from patent	gb_in:AE003434	! AE003434 Drosophila melan	66.00	75.44	7.6e+04	302786
gb_pi:PC00LL2	! X89806 P.lividus cDNA for COL	+	66.00	111.95	811.95	5511	! X89806 P.lividus cDNA for COL	gb_hhg:AC105492	! AC105492 Rattus norvegicus	66.00	74.77	8.3e+04	326514
gb_ba:EC0571MR	! M74821 E.coli genes for eco571	-	66.00	110.54	856.48	5776	! M74821 E.coli genes for eco571	gb_pr:AP001674	! AP001674 Homo sapiens gen	66.00	74.41	8.7e+04	340000
gb_ba:HI008875	! U08875 Haemophilus influenzae	+	66.00	106.62	1.4e+03	8983	! U08875 Haemophilus influenzae	gb_ba:AP003581	! AP003581 Nostoc sp. PC	66.00	74.21	8.9e+04	348050
gb_pat:AR032350	! AR032350 Sequence 6 from patent	+	66.00	106.29	1.5e+03	9323	! AR032350 Sequence 6 from patent	gb_pr:BC009778	! BC009778 Homo sapiens, prot	65.50	124.56	141.81	1053
gb_pat:AR083957	! AR083957 Sequence 6 from patent	+	66.00	106.29	1.5e+03	9323	! AR083957 Sequence 6 from patent	gb_pi:AF0080567	! AF0080567 zea mays pullulana	65.50	123.59	160.64	1175
gb_pat:AR145901	! AR145901 Sequence 6 from patent	+	66.00	106.29	1.5e+03	9323	! AR145901 Sequence 6 from patent	gb_ba:AF005688	! AF005688 Shewanella alga DN	65.50	122.99	173.44	1257
gb_pat:BD010358	! BD010358 High molcular weight	+	66.00	106.29	1.5e+03	9323	! BD010358 High molcular weight	gb_pr:AF040091	! AF040091 Homo sapiens branc	65.50	120.18	248.72	1726
gb_pat:125184	! 125184 Sequence 6 from patent	+	66.00	106.29	1.5e+03	9323	! 125184 Sequence 6 from patent	gb_pi:AF040091	! AF040091 Pichia pastoris di	65.50	119.67	265.33	1827
gb_pat:135773	! 135773 Sequence 6 from patent	+	66.00	106.29	1.5e+03	9323	! 135773 Sequence 6 from patent	gb_pat:AG3710	! AG3710 Sequence 1 from pate	65.50	118.90	292.90	1993
gb_pi:FSR137423	! AJ314222 Pseudomonas stutzeri	+	66.00	106.21	1.5e+03	9408	! AJ314222 Pseudomonas stutzeri	gb_pat:AR161653	! AR161653 Sequence 1 from pa	65.50	118.90	292.90	1993
gb_in:AF147386	! AF177386 Drosophila melanogast	+	66.00	104.38	1.9e+03	11572	! AF177386 Drosophila melanogast	gb_pi:AF0800567	! AF0800567 zea mays pullulana	65.50	114.54	512.66	3261
gb_in:AF146362	! AF146362 Drosophila melanogast	+	66.00	104.37	1.9e+03	11579	! AF146362 Drosophila melanogast	gb_ba:AF364409	! AF364409 Bacteroides fragil	65.50	114.51	514.27	3370
gb_hhg:AC107009	! AC107009 Rattus norvegicus cl	+	66.00	97.83	4.4e+03	24213	! AC107009 Rattus norvegicus cl	gb_ba:AF349974	! AF349974 Bacteriophage pp01	65.50	114.35	525.01	3370
gb_hhg:AC098895	! AC098895 Rattus norvegicus cl	+	66.00	97.09	4.8e+03	26317	! AC098895 Rattus norvegicus cl	gb_in:PRPK4GENE	! PRPK4GENE Homo sapiens	65.50	113.97	551.08	3475
gb_hhg:AC020338	! AC020338 Drosophila melanogast	-	66.00	96.67	5.1e+03	27621	! AC020338 Drosophila melanogast	gb_ba:EC04844	! EC04844 Escherichia coli E10	65.50	110.55	854.85	5113
gb_hhg:AC108536	! AC108536 Rattus norvegicus cl	+	66.00	94.01	7.1e+03	37261	! AC108536 Rattus norvegicus cl	gb_pi:D78169	! D78169 Schizosaccharomyces	65.50	106.81	1.4e+03	7795
gb_hhg:AC097921	! AC097921 Rattus norvegicus cl	+	66.00	93.26	7.9e+03	40555	! AC097921 Rattus norvegicus cl	! AC097721 Clostridium acetob	! AC097721 Clostridium acetob	65.50	106.37	1.5e+03	8198
gb_in:AF147779	! AF147779 Drosophila melanogast	+	66.00	92.72	8.4e+03	43125	! AF147779 Drosophila melanogast	gb_pat:E33749	! E33749 Bacteriocin gene of	65.50	105.64	1.6e+03	8894
gb_in:CBRG17006	! CBRG17006 Caenorhabditis brig	+	66.00	92.07	9.1e+03	46394	! CBRG17006 Caenorhabditis brig	gb_ba:AE006674	! AE006674 Mycolobus solfata	65.50	105.03	1.7e+03	9534
gb_htg:AL606723	! AL606723 Danio rerio chromos	+	66.00	89.09	1.3e+04	64934	! AL606723 Danio rerio chromos	gb_ba:AE000043	! AE000043 Mycolobus solfata	65.50	103.31	2.2e+03	11569
gb_in:AC107510	! AC107510 Rattus norvegicus cl	+	66.00	88.80	1.4e+04	67089	! AC107510 Rattus norvegicus cl	gb_ba:AF057696	! AF057696 Haemophilus ducre	65.50	100.06	3.3e+03	16697
gb_in:AC1025722	! AC1025722 Caenorhabditis elega	+	66.00	88.13	1.5e+04	73235	! AC1025722 Caenorhabditis elega	gb_ba:AE045036	! AE045036 Pectobacterium ca	65.50	99.01	3.8e+03	18791
gb_hhg:AC099881	! AC099881 Mus musculus clone R	-	66.00	87.55	1.6e+04	77270	! AC099881 Mus musculus clone R	gb_pi:SPAC5664	! SPAC5664 S.pombe chromosom	65.50	98.12	4.2e+03	20790
gb_htg:AC103125	! AC103125 Rattus norvegicus cl	+	66.00	86.67	1.8e+04	85255	! AC103125 Rattus norvegicus cl	gb_ba:BSFPBSXSE	! BSFPBSXSE S.pombe chromosom	65.50	95.48	5.9e+03	28000
gb_htg:AC096217	! AC096217 Rattus norvegicus cl	+	66.00	86.40	1.9e+04	87932	! AC096217 Rattus norvegicus cl	gb_pi:SPCC4G3	! SPCC4G3 S.pombe chromosom	65.50	91.90	9.4e+03	41934
gb_htg:AC096435	! AC096435 Rattus norvegicus c	+	66.00	85.16	2.2e+04	10							

gb_hhg:AC092921_1	-	65.50	83.35	2.8e+04	110000	Continuation (2 of 5) of AC093316 Mus musculus chromo	gb_hhg:AC099125	-	65.00	79.27	4.7e+04	154600	AC099125 Rattus norvegicu
gb_hhg:AC093316_0	+	65.50	83.35	2.8e+04	110000	AC093316 Mus musculus chromo	gb_hhg:AC099165	+	65.00	79.11	4.8e+04	157388	AC099165 Rattus norvegicu
gb_hhg:AC095684	-	65.50	83.07	2.9e+04	113543	AC095684 Rattus norvegicus	gb_hhg:AC0106679	+	65.00	79.08	4.8e+04	157913	AC0106679 Rattus norvegicu
gb_pr:AC004930	+	65.50	82.69	3.0e+04	118451	AC004930 Homo sapiens PAC cl	gb_hhg:AC084369	+	65.00	79.00	4.9e+04	159284	AC084369 Homo sapiens chr
gb_pr:AL589706	+	65.50	82.59	3.1e+04	119907	AL589706 Human DNA sequence	gb_hhg:AC095736	+	65.00	78.92	4.9e+04	160845	AC095736 Rattus norvegicu
gb_hhg:OSJN01011	+	65.50	82.51	3.1e+04	120990	AL607103 Oryza sativa chromo	gb_hhg:AC106235	+	65.00	78.82	5.0e+04	160845	AC106235 Rattus norvegicu
gb_hhg:AC096300	+	65.50	82.31	3.2e+04	123763	AL607103 Oryza sativa chromo	gb_hhg:AC106235	+	65.00	78.82	5.0e+04	160845	AC106235 Rattus norvegicu
gb_hhg:AC005959	+	65.50	82.04	3.3e+04	127587	AC005959 Homo sapiens, ** s	gb_hhg:AC103020	+	65.00	78.66	5.1e+04	165585	AC103020 Rattus norvegicu
gb_hhg:AC099196	+	65.50	81.57	3.5e+04	134490	AC099196 Rattus norvegicus	gb_pr:AC019211	+	65.00	78.56	5.1e+04	167471	AC019211 Homo sapiens BAC
gb_pr:HSJ12208	+	65.50	81.20	3.7e+04	140211	AL096678 Human DNA sequence	gb_hhg:AC105549	+	65.00	78.54	5.2e+04	167849	AC105549 Rattus norvegicu
gb_hhg:AC025736	+	65.50	80.93	3.8e+04	144585	AL096678 Human DNA sequence	gb_hhg:AC104786	+	65.00	78.45	5.2e+04	169520	AC104786 Homo sapiens chr
gb_hhg:AC099260	+	65.50	80.83	3.8e+04	146099	AC099260 Rattus norvegicus	gb_hhg:AC098169	+	65.00	78.41	5.2e+04	170378	AC098169 Rattus norvegicu
gb_hhg:OSJN00134	+	65.50	80.82	3.8e+04	146294	AL662944 Oryza sativa chromo	gb_hhg:AC099159	+	65.00	78.30	5.3e+04	172373	AC099159 Rattus norvegicu
gb_hhg:PFMA1381	+	65.50	80.46	4.0e+04	152409	AL031744 Plasmodium falcipar	gb_hhg:AC021696	+	65.00	78.30	5.3e+04	172378	AC021696 Homo sapiens clo
gb_hhg:AC025389	+	65.50	80.17	4.2e+04	157419	AC025389 Homo sapiens chromo	gb_hhg:AC068626	+	65.00	78.23	5.4e+04	173742	AC068626 Rattus norvegicu
gb_hhg:AC013563	+	65.50	80.12	4.2e+04	158281	AC013563 Homo sapiens chromo	gb_hhg:AC098157	+	65.00	78.23	5.4e+04	173742	AC098157 Rattus norvegicu
gb_hhg:AC094457	+	65.50	79.99	4.3e+04	160791	AC094457 Rattus norvegicus	gb_hhg:AC018948	+	65.00	78.15	5.4e+04	175360	AC018948 Homo sapiens chr
gb_hhg:AC094073	+	65.50	79.92	4.3e+04	162000	AC094073 Rattus norvegicus	gb_pr:AC012048	+	65.00	77.97	5.5e+04	178963	AC012048 Homo sapiens chr
gb_hhg:AC097029	+	65.50	79.90	4.4e+04	162408	AC097029 Rattus norvegicus	gb_hhg:AC098556	+	65.00	77.95	5.5e+04	178963	AC098556 Rattus norvegicu
gb_pr:AL353621	+	65.50	79.80	4.4e+04	164115	AL353621 Human DNA sequence	gb_hhg:AC068090	+	65.00	77.47	5.9e+04	189245	AC068090 Homo sapiens chr
gb_hhg:AC094945	+	65.50	79.70	4.4e+04	165989	AC094945 Rattus norvegicus	gb_hhg:AC106227	+	65.00	77.47	5.9e+04	189245	AC106227 Rattus norvegicu
gb_hhg:AC098920	+	65.50	79.16	4.8e+04	176530	AC098920 Rattus norvegicus	gb_hhg:AL671886	+	65.00	77.41	5.9e+04	190708	AL671886 Mus musculus chr
gb_ro:AL590626	+	65.50	79.02	4.8e+04	179282	AL590626 Mouse DNA sequence	gb_hhg:AL606922	+	65.00	77.36	6.0e+04	190708	AL606922 Mus musculus chr
gb_hhg:AL670035	+	65.50	78.91	4.9e+04	181563	AL670035 Mus musculus chromo	gb_pr:AC078851	+	65.00	77.36	6.3e+04	201303	AC078851 Homo sapiens BAC
gb_hhg:AL359264	+	65.50	78.91	4.9e+04	181627	AL359264 Homo sapiens chromo	gb_hhg:AL645586	+	65.00	76.87	6.4e+04	202505	AL645586 Mus musculus chr
gb_hhg:AC108676	+	65.50	78.36	5.3e+04	193103	AC108676 Homo sapiens chromo	gb_hhg:AC094414	+	65.00	76.85	6.4e+04	203023	AC094414 Rattus norvegicu
gb_hhg:AC108416	+	65.50	78.29	5.3e+04	194686	AC108416 Rattus norvegicus	gb_hhg:AL669952	+	65.00	76.84	6.4e+04	203356	AL669952 Mus musculus chr
gb_ba:BSUB00007	+	65.50	77.34	6.0e+04	216750	299110 Bacillus subtilis com	gb_hhg:AC092166	+	65.00	76.51	6.7e+04	210918	AC092166 Homo sapiens chr
gb_hhg:AL606909	+	65.50	77.04	6.2e+04	224061	AL606909 Mus musculus chromo	gb_hhg:AC096324	+	65.00	75.63	7.5e+04	232956	AC096324 Rattus norvegicu
gb_pr:AC012150	+	65.50	76.92	6.3e+04	227305	AC012150 Homo sapiens 12 BAC	gb_hhg:AC095680	+	65.00	75.25	7.8e+04	243167	AC095680 Rattus norvegicu
gb_ba:AP001519	+	65.50	74.35	8.8e+04	303650	AP001519 Bacillus halodurans	gb_hhg:AC106538	+	65.00	74.82	8.3e+04	255336	AC106538 Rattus norvegicu
gb_ba:AP003586	+	65.50	73.11	1.0e+05	349050	AP003586 Nostoc sp. PCC 7120	gb_ba:SMS591785	+	65.00	73.80	9.4e+04	286550	AL591785 Sinorhizobium me
gb_pr:NGA243078	+	65.00	129.48	75.46	536	AJ243078 Nectria galligena part	gb_ba:AP0033190	+	65.00	73.36	9.9e+04	301150	AP0033190 Clostridium perf
gb_pr:NGA243081	+	65.00	129.47	75.46	536	AJ243081 Nectria galligena part	gb_hhg:PFMA113P3	+	65.00	72.87	1.1e+05	318221	AL049184 Plasmodium falci
gb_ba:EKREPCD	+	65.00	127.67	95.10	657	AL2697_3' terminal of Hly A gen	gb_hhg:PFMA14P3	+	65.00	72.79	1.1e+05	321003	AL035476 Plasmodium falci
gb_ph:PF22749	+	65.00	121.28	215.84	1351	M3144 Eikenella corrodens pil	gb_ba:AP003592	+	65.00	72.07	1.2e+05	348250	AP003592 Nostoc sp. PCC 7
gb_pr:AF217185	+	65.00	118.64	302.87	1820	M3144 Eikenella corrodens pil	gb_pr:AC093747	+	64.50	125.37	127.71	755	A93747 Sequence 7 from Pat
gb_in:AF217185	+	65.00	115.60	447.37	2565	AF217249 zea mays kinesin heav	gb_pr:AR148418	+	64.50	125.36	127.90	756	AR148418 Sequence 7 from Pat
gb_pr:AF421953	+	65.00	114.92	488.04	2769	AF217195 Caenorhabditis eleg	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_in:DDIHYHC	+	65.00	110.13	901.80	4752	AF421953 Kluyveromyces lactis	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50	124.65	140.08	819	AX143089 Sequence 1811 from
gb_ba:AE001581	+	65.00	107.11	1.2e+03	6681	M14628 D. discoideum myosin hea	gb_pat:AX143089	+	64.50				

gb_ba:AE0000790	64.50	87.60	1.6e+04	53561	AE0000790 Borrelia burgdorferi	gb_htg:AC103547	-	64.00	83.88	2.6e+04	72205	AC103547 Rattus norvegicus
gb_htg:AL162740	64.50	84.78	2.3e+04	73607	AL162740 Human DNA sequence	gb_pr:AC007022	-	64.00	83.84	2.6e+04	72541	AC007022 Homo sapiens PAC
gb_pr:AP004612	64.50	81.99	3.3e+04	100839	AP004612 Oryza sativa chromo	gb_htg:AC094243	-	64.00	83.31	2.8e+04	77057	AC094243 Rattus norvegicus
gb_pr:AC019127	64.50	81.62	3.5e+04	105118	AC019127 Homo sapiens BAC cl	gb_htg:AC096701	-	64.00	83.15	2.9e+04	78480	AC096701 Rattus norvegicus
gb_ba:AP003366	64.50	81.25	3.6e+04	109589	AP003366 Staphylococcus aure	gb_htg:AC094818	-	64.00	82.71	3.0e+04	82432	AC094818 Rattus norvegicus
gb_ba:AP003138	64.50	80.67	3.9e+04	117016	AP003138 Staphylococcus aure	gb_htg:AC103561	+	64.00	82.27	3.2e+04	86628	AC103561 Rattus norvegicus
gb_htg:OSUN000099	64.50	80.30	4.1e+04	121992	AL066556 Oryza sativa chromo	gb_htg:AC098423	+	64.00	82.07	3.3e+04	88569	AC098423 Rattus norvegicus
gb_htg:AC020029	64.50	79.84	4.4e+04	128469	AC020029 Drosophila melanoga	gb_ro:AF332860S2	+	64.00	81.93	3.4e+04	89594	AF332861 Mus musculus diad
gb_htg:AC105719	64.50	79.62	4.5e+04	131728	AC105719 Rattus norvegicus c	gb_htg:AC108306	+	64.00	81.43	3.6e+04	95187	AC108306 Rattus norvegicus
gb_pr:HS203C2	64.50	78.43	5.2e+04	150620	274695 Human DNA sequence fr	gb_pl:ATW6H20	+	64.00	81.13	3.7e+04	98461	AL096859 Arabidopsis thali
gb_htg:AC097260	64.50	78.24	5.3e+04	153876	AC097260 Homo sapiens chromo	gb_htg:AC091338	+	64.00	80.80	3.9e+04	102195	AC091338 Rattus norvegicu
gb_htg:AC023964	64.50	78.22	5.4e+04	154240	AC023964 Homo sapiens chromo	gb_htg:AC098618	+	64.00	80.33	4.1e+04	107782	AC098618 Rattus norvegicu
gb_pr:AC093901	64.50	77.83	5.6e+04	161153	AC093901 Homo sapiens BAC cl	gb_htg:AC105506	+	64.00	80.29	4.1e+04	108271	AC105506 Rattus norvegicu
gb_in:AC006170	64.50	77.41	5.9e+04	168471	AC006170 Drosophila melanoga	gb_htg:AC106364	-	64.00	80.07	4.2e+04	110875	AC106364 Rattus norvegicu
gb_htg:AC094714	64.50	77.31	6.0e+04	171046	AC094714 Rattus norvegicus c	gb_htg:AC010249	-	64.00	80.08	4.2e+04	111081	AC010249 Homo sapiens chr
gb_htg:AC097394	64.50	77.28	6.0e+04	171508	AC097394 Rattus norvegicus c	gb_htg:AC103074	-	64.00	79.85	4.4e+04	113766	AC103074 Rattus norvegicu
gb_in:AC009203	64.50	77.25	6.1e+04	172061	AC009203 Drosophila melanoga	gb_htg:AC095797	-	64.00	79.61	4.5e+04	116930	AC095797 Rattus norvegicu
gb_pr:AC017089	64.50	76.94	6.3e+04	178320	AC017089 Homo sapiens BAC cl	gb_htg:AC103495	+	64.00	79.53	4.5e+04	118002	AC103495 Rattus norvegicu
gb_htg:AC094933	64.50	76.84	6.4e+04	180191	AC094933 Rattus norvegicus c	gb_htg:AC096140	+	64.00	79.29	4.7e+04	121249	AC096140 Rattus norvegicu
gb_in:AC007817	64.50	76.83	6.4e+04	180499	AC007817 Drosophila melanoga	gb_htg:AC105708	+	64.00	79.04	4.8e+04	124695	AC105708 Rattus norvegicu
gb_htg:AC105841	64.50	76.29	6.9e+04	191747	AC105841 Rattus norvegicus c	gb_pr:HS203C2	+	64.00	78.98	4.9e+04	125487	AL049642 Human DNA sequen
gb_htg:AC021187	64.50	76.14	7.0e+04	195121	AC021187 Homo sapiens chromo	gb_pr:AC002386	+	64.00	78.57	5.1e+04	131458	AC002386 Rattus norvegicu
gb_pr:AC002524	64.50	75.81	7.3e+04	202540	AC002524 Homo sapiens x BAC	gb_htg:AC094240	+	64.00	78.51	5.2e+04	132359	AC094240 Rattus norvegicu
gb_htg:PFWAL13P6	64.50	75.72	7.4e+04	204652	AL049183 Plasmodium falcipar	gb_htg:AC098633	+	64.00	78.40	5.2e+04	134036	AC098633 Rattus norvegicu
gb_htg:AC106680	64.50	75.61	7.5e+04	207064	AC106680 Rattus norvegicus c	gb_htg:AP003368	+	64.00	78.33	5.3e+04	135057	AP003368 Oryza sativa chr
gb_htg:AC0979426	64.50	75.61	7.5e+04	207197	AC107077 Homo sapiens chromo	gb_htg:AC098756	+	64.00	77.82	5.6e+04	143072	AC098756 Rattus norvegicu
gb_htg:AC095246	64.50	75.37	7.7e+04	221668	AC095246 Mus musculus chromo	gb_htg:AC106306	+	64.00	77.81	5.7e+04	143318	AC106306 Rattus norvegicu
gb_in:AE003761	64.50	75.07	8.0e+04	220116	AE003761 Drosophila melanoga	gb_htg:AC105735	-	64.00	77.66	5.8e+04	145680	AC105735 Rattus norvegicu
gb_htg:AC027284	64.50	74.89	8.2e+04	224614	AE003761 Drosophila melanoga	gb_htg:AC103147	+	64.00	77.57	5.8e+04	147237	AC103147 Rattus norvegicu
gb_in:AE003767	64.50	74.88	8.2e+04	224840	AC027284 Mus musculus chromo	gb_ba:D90916	+	64.00	77.51	5.9e+04	148142	D90916 Synchocystis sp.
gb_htg:AC098730	64.50	74.87	8.4e+04	225155	AE003767 Drosophila melanoga	gb_pr:AF274857	+	64.00	77.47	5.9e+04	148526	AF274857 Homo sapiens chr
gb_in:AC003660	64.50	74.69	8.4e+04	229788	AE003767 Mus musculus chromo	gb_htg:AC102240	+	64.00	77.49	5.9e+04	148804	AC102240 Homo sapiens clo
gb_ba:AJ414158	64.50	74.60	8.5e+04	231972	AC003660 Drosophila melanoga	gb_htg:AC106365	+	64.00	77.44	5.9e+04	149352	AC106365 Rattus norvegicu
gb_ba:AP0000984	64.50	74.49	8.6e+04	235050	AJ414158 Yersinia pestis str	gb_pl:AC079128	+	64.00	77.33	6.0e+04	151163	AC079128 Oryza sativa chr
gb_vt:AF198100	64.50	73.83	9.4e+04	253050	AF000984 Sulfolobus tokodai	gb_pl:AC079022	+	64.00	77.31	6.0e+04	151589	AC079022 Oryza sativa chr
gb_pr:AXI196295	64.50	72.67	1.1e+05	288539	AF198100 Fowlpox virus, comp	gb_htg:AP003406	+	64.00	77.25	6.1e+04	152680	AP003406 Oryza sativa chr
gb_pr:PMU98111	64.50	71.32	1.3e+05	335913	AXI196295 Sequence 2 from Pat	gb_htg:AC106397	+	64.00	77.20	6.1e+04	153540	AC106397 Rattus norvegicu
gb_htg:AC1031736	64.00	128.29	87.90	482	U88110 Fusarium merismoides var	gb_htg:AC106212	+	64.00	77.13	6.2e+04	154715	AC106212 Rattus norvegicu
gb_ba:AXI12696	64.00	125.54	125.01	657	AXI12696 3' terminal of Hly A gen	gb_htg:AC097562	+	64.00	77.06	6.2e+04	155909	AC097562 Rattus norvegicu
gb_in:AY070642	64.00	119.95	256.18	1235	AY070642 Drosophila melanogast	gb_htg:AC097002	+	64.00	76.99	6.3e+04	156334	AC097002 Rattus norvegicu
gb_ba:AB047188	64.00	118.70	300.72	1422	AB047188 Marine CFB-group bact	gb_htg:AC106114	+	64.00	76.99	6.3e+04	157179	AC097619 Rattus norvegicu
gb_pl:YSC0TH1	64.00	118.16	321.97	1510	L42133 Saccharomyces cerevisia	gb_htg:AC098073	-	64.00	76.88	6.4e+04	159185	AC074218 Rattus norvegicu
gb_ro:AF121893	64.00	116.05	422.32	1917	AF121893 Rattus norvegicus seq	gb_htg:AC099162	+	64.00	76.71	6.5e+04	162137	AC099162 Rattus norvegicu
gb_ba:AF455356	64.00	113.87	558.43	2451	AF455356 Alicaligenes faecalis	gb_pr:AC026799	+	64.00	76.67	6.5e+04	162918	AC026799 Homo sapiens chr
gb_ba:AF195013	64.00	113.40	593.01	2584	AF195013 Helicobacter pylori s	gb_htg:AC105675	+	64.00	76.62	6.6e+04	163846	AC105675 Rattus norvegicu
gb_ba:AF109145	64.00	113.30	601.10	2615	AF109145 Vibrio cholerae 569B	gb_htg:AC099136	+	64.00	76.58	6.6e+04	164675	AC099136 Rattus norvegicu
gb_pr:BC009895	64.00	112.57	660.24	2840	BC009895 Homo sapiens, phospho	gb_htg:AC102961	+	64.00	76.57	6.6e+04	164714	AC102961 Rattus norvegicu
gb_ov:AB055658	64.00	112.39	675.59	2898	AB055658 Cyprinus carpio GRK7	gb_htg:AC099146	+	64.00	76.56	6.6e+04	165055	AC099146 Rattus norvegicu
gb_ov:XELLTMSR	64.00	111.90	719.22	3052	L42546 Xenopus laevis LIM clas	gb_htg:AC097035	+	64.00	76.42	6.7e+04	167579	AC097035 Rattus norvegicu
gb_ba:AB046568	64.00	108.83	1.1e+03	4330	AB046568 Hydrogenobacter therm	gb_htg:AC094724	-	64.00	76.32	6.8e+04	169452	AC094724 Rattus norvegicu
gb_vt:CVU10029	64.00	108.64	1.1e+03	4420	U10029 Chlorella virus PBCV-1	gb_htg:AC094122	+	64.00	76.32	6.8e+04	169552	AC094122 Rattus norvegicu
gb_pl:AF267125	64.00	107.94	1.2e+03	4783	AF267125 Candida albicans pota	gb_htg:AC099185	+	64.00	76.32	6.8e+04	169565	AC099185 Rattus norvegicu
gb_pr:ARL102577	64.00	105.62	1.6e+03	6216	ARL102577 Sequence 1 from Paten	gb_htg:AC106360	-	64.00	76.28	6.9e+04	170000	AC094951 Rattus norvegicu
gb_ba:AX0079922	64.00	104.64	1.8e+03	6942	AX0079922 Sequence 10 from Paten	gb_htg:AC103047	+	64.00	76.28	6.9e+04	170338	AC106360 Rattus norvegicu
gb_ba:AX004243	64.00	101.23	2.8e+03	10208	AE004243 Vibrio cholerae chro	gb_htg:AC102971	+	64.00	76.07	7.0e+04	173854	AC073047 Homo sapiens chr
gb_ba:AE007784	64.00	100.93	2.9e+03	10553	AE007784 Clostridium acetobut	gb_htg:AC102971	+	64.00	76.07	7.1e+04	174436	AC102971 Rattus norvegicu
gb_ba:AE006197	64.00	100.85	3.0e+03	10655	AE006197 Pasteurella multocid	gb_htg:AC096983	-	64.00	75.92	7.1e+04	174664	AC096983 Rattus norvegicu
gb_ba:AE000566	64.00	99.63	3.5e+03	12216	AE000566 Helicobacter pylori	gb_pr:AC024359	-	64.00	75.92	7.2e+04	177303	AC024259 Homo sapiens chr
gb_ba:U32710	64.00	99.24	3.6e+03	12771	AE002526 Neisseria meningitid	gb_htg:AC095656	+	64.00	75.68	7.4e+04	182146	AC094510 Rattus norvegicu
gb_ba:U32720	64.00	98.54	4.0e+03	13818	U32710 Haemophilus influenzae	gb_htg:AC106074	+	64.00	75.66	7.4e+04	182695	AC095656 Rattus norvegicu
gb_ba:AF0001481	64.00	95.94	5.6e+03	18530	AE001481 Helicobacter pylori,	gb_htg:AC103555	+	64.00	75.64	7.4e+04	183095	AC106074 Rattus norvegicu
gb_ba:AF282852	64.00	94.69	6.5e+03	21347	AF282852 Helicobacter pylori,	gb_ro:AC087416	+	64.00	75.62	7.5e+04	183251	AC013555 Homo sapiens chr
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DEFINITION Escherichia coli (strain 41) heat-labile enterotoxin type IIB
(LT-IIB) A and B chain genes, complete cds.
ACCESSION M28523
VERSION 1 GI:576584
KEYWORDS LT-IIB gene; enterotoxin type IIB.
SOURCE Escherichia coli (strain 41) DNA.
ORGANISM Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
REFERENCE 1 (bases 1 to 1262)
AUTHORS Pickett,C.L., Twiddy,E.M., Coker,C. and Holmes,R.K.
TITLE Cloning, nucleotide sequence, and hybridization studies of the type
IIB heat-labile enterotoxin gene of Escherichia coli
JOURNAL J. Bacteriol. 171 (9), 4945-4952 (1989)
MEDLINE 89359131
COMMENT On Nov 28, 1994 this sequence version replaced gi:341953.
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34 GlyArgTyrSerAsnTyr.....AlaLeuIleSerA 44
|||||..... 39
470 GGCAGGTATAGTCCGTATCCAACTGAAATGATATGCTGCATTAGGTGG 519
40 .....AlaLeuIleSerA 44
520 TATTCCCTCTCACAATAATATTGGTGGTATACAGTATCTTTCGGTGCTA 569
44 laGluGlyGlyMetAsp.....ArgAspLeuPheGly 54
|||||.....
570 TAGAGGGGGGAATGCATCGAAACAGGATTACAGAAGAGATTTATTATGA 619
55 SerAlaAsnIle..... 58
620 GGGTTATCTGCTCTCCTAATAGGATGGCTATCGAATTGCTGGATTTC 669
59 AspGlyPhePro.....GluVal.....ArgGluPhe..... 67
|||||.....
670 CGACGGATTTCCTCGCTGGGAAGAAGTTCCTCGAGAGAATTTCGCGCTA 719
68 ..AsnSerLeuProAsnAsnLysAlaSerSerAspThr.....AlaSer 81
: : : |||||.....
720 ACTCTTGTCTACCAATAATAAAGCTTCCAGTGATACCTACCTGTGCTCT 769
82 Leu...AsnLys.....GlnHisAsp...AlaAspPheLysLysTyrI 94
||| |||||.....
770 TTACAAATAAATATCATCACAGCATGATTTAGCTGATTTTAAGAAATATAT 819
94 eLys.....LeuLeuIleAsnAsnAspGlyP 103
||| |||.....
820 AAAGAGAAAATTTACCTTGATGACTTTTACTAAGTATTAATAATGATGGTT 869
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870 TTTTTCAAATAATGGAGGAAAA 892
seq_name: gb_ba:AE000850
seq_documentation_block:
LOCUS AE000850 11069 bp DNA linear BCT 15-NOV-1997
DEFINITION Methanobacterium thermoautotrophicum from bases 631143 to 642211
(section 56 of 148) of the complete genome.
ACCESSION AE000850 AE000666
VERSION AE000850.1 GI:2621794
KEYWORDS
SOURCE Methanothermobacter thermoautotrophicus
ORGANISM Methanothermobacter thermoautotrophicus
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
REFERENCE 1 (bases 1 to 11069)
AUTHORS Smith,D.R., Doucette-Stamm,L.A., Deloughery,C., Lee,H., Dubois,J.,
Aldredge,T., Bashirzadeh,R., Blakely,D., Cook,R., Gilbert,K.,

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Harrison,D., Hoang,L., Keagle,P., Lumm,W., Pothier,B., Qiu,D., Spadafora,R., Vicaire,R., Wang,Y., Wierzbowski,J., Gibson,R., Jivani,N., Caruso,A., Bush,D., Reeve,J.N. et al.
Complete genome sequence of *Methanobacterium thermoautotrophicum* deltaH: functional analysis and comparative genomics
J. Bacteriol. 179 (22), 7135-7155 (1997)
98037514
2 (bases 1 to 11069)
Smith,D.R.
Direct Submission
Submitted (10-AUG-1997) Genomics and Technology Development, Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154-8448, USA
FEATURES
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/db_xref="taxon:145262"
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98..1009
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98..1009
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complement(3913..4012)
/note="100 bp direct repeat includes part of MTH713
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HIVASESGIIVYPPGKNIGSSYLDVITSYINLLNLKONGYTVENIPANTVILHD
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3078..3533

CDS

gene

CDS

gene

CDS

repeat_region

repeat_region

gene

CDS

gene

Align seg 1/1 to reverse of: CNS07EFS from: 1 to: 155031

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8274 GGTTCCTACCTAGCAATCTTGGTGGTACCAAGGTACACCGTGCTCC 8225

62 ogluValArgGluPhe...AsnSerLeuProAsnAsnLysAlaSerSera 78
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8224 AGAGGTGTAGAGTCTTATCAAGTCTCATGACCGTGAAGCCAGAGG 8175

78 spThrAlaSerLeu.AsnLysGlnHis..... 86
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8174 ACACAACTCTCTGGGATCAACAACATCAAGTGTCTGTGTGAGAAGC 8125

86 ..... 86
8124 AACATGATGGAGAGATGTGAGATAGATCAACATTCCTTGTAGCTGAAG 8075

87 .....AspAlaAspPheLysLysTyrIle..... 94
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95 ...LysLeuLeuIleAsnAsnAsp..... 101
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8024 AGTCCACTGCTAATTCAGGTAGATTATATGAGGACTTACTTTTATATA 7975

102 .....GlyPhePheSerAsnAsnGlyGly 109
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seq_name: gb_in:TAY15795

seq documentation_block:
LOCUS TAY15795 957 bp DNA linear INV 11-MAY-2001

DEFINITION Theileria annulata spm2 gene, partial.
ACCESSION Y15795
VERSION Y15795.1 GI:2673881
KEYWORDS spm2 gene; spm2 protein.
SOURCE Theileria annulata.
ORGANISM Theileria annulata.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae; Theileria.
REFERENCE 1 (bases 1 to 957)
AUTHORS Knight,P.A., Williamson,S.W., Brown,C.G., Bell-Sakyl,L., Kirvar,E., Kinnaird,J., Hussain,K., Hall,R., Boulter,N. and Tait,A.
TITLE Identification of a Theileria annulata antigen expressed in multiple stages of the parasite life cycle
JOURNAL Exp. Parasitol. 90 (1), 110-121 (1998)
MEDLINE 98376467
REFERENCE 2 (bases 1 to 957)
AUTHORS Knight,P.A.
TITLE Direct Submission
JOURNAL Submitted (05-DEC-1997) P.A. Knight, Edinburgh University, Department of veterinary clinical studies, Veterinary field station, Easter Bush Roslin, Midlothian EH25 9RG, UK

Location/Qualifiers
1. .957
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CDS

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BASE COUNT 397 a 150 c 180 g 230 t
ORIGIN

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alignment_scores:
Quality: 76.50 Length: 103
Ratio: 1.297 Gaps: 5
Percent Similarity: 57.282 Percent Identity: 26.214

alignment_block:

US-09-528-682-4 x TAY15795 ..

Align seg 1/1 to: TAY15795 from: 1 to: 957

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24 .....LeuAsnMetGlyAsnGluValAlaLeuA 33
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659 AATACAAATTTTGTAGAGTGTATTTGTTTCAATAGACACCAACAGAT 708

50 ArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgI 66
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709 ...AGTTTATTC.....TACCAGATGAAGAACA 734

66 uPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuA 83
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735 ATTCAATAGTTTGAATAATAATAGTCTGTAAAGAGATGACTTCGCGCTGG 784

83 snLysGlnHisAspAlaAspPheLys...LysTyrIleLysLeuLeuIle 98
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99 AsnAsnAsp 101

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835 AACCAAGAT 843

seq_name: gb_ba:AF160726

seq_documentation_block:

LOCUS AF160726

DEFINITION

peanut witches'-broom phytoplasma heat shock protein GrPE (grpe),

heat shock protein DnaK (dnaK), and heat shock protein DnaJ (dnaJ)

genes, complete cds; and unknown gene.

ACCESSION AF160726

VERSION AF160726.1 GI:9621759

KEYWORDS

SOURCE

ORGANISM

peanut witches'-broom phytoplasma.

peanut witches'-broom phytoplasma

Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;

Acholeplasmatales; Acholeplasmataceae; Phytoplasma; 16SrII (Peanut

WB group).

REFERENCE 1 (bases 1 to 4974)

AUTHORS Chu,P.W. and Lin,C.P.

TITLE Cloning and Analysis of dnaK and dnaJ Genes of Phytoplasma

JOURNAL Associated with Peanut Witches' Broom

REFERENCE 2 (bases 1 to 4974)

Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
 Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
 Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
 Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
 Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
 Louissegh, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
 Ma, J., Maheshwari, M., Mapa, P., Martin, R., Martindale, A.,
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 Mei, G., Metzger, M., Miner, G., Miner, Z., Mitchell, J., Newton, N.,
 Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,
 Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
 Ogulu, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
 Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L.,
 Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M.,
 Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shoostari, N.,
 Sisson, I., Sodergren, E., Sonaik, T., Sparks, A., Stanley, H.,
 Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K.,
 Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N.,
 Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R.,
 Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
 Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S.,
 Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G. and Gibbs, R.

Direct Submission
 Unpublished
 2 (bases 1 to 72729)
 Worley, K.C.

Direct Submission
 Submitted (23-Oct-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Dec 20, 2001 this sequence version replaced gi:16327472.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GFCX
 Center clone name: CH230-11A23
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329First call to
 findPhrapList
 Consensus quality: 69289 bases at least Q40
 Consensus quality: 74341 bases at least Q30
 Consensus quality: 78358 bases at least Q20
 Estimated insert size: 48455; sum-of-contigs estimation
 Quality coverage: 0x in Q20 bases; agarose-fp estimation
 Quality coverage: 0.6x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 42 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1
 * 2113: contig of 2112 bp in length
 * 2212: gap of unknown length
 * 2213: contig of 3049 bp in length
 * 5261: gap of unknown length
 * 5262: gap of unknown length
 * 5362: contig of 2979 bp in length
 * 8341: gap of unknown length
 * 8441: contig of 2558 bp in length
 * 10998: gap of unknown length
 * 11099: contig of 2140 bp in length
 * 13238: gap of unknown length
 * 13239: contig of 2619 bp in length
 * 13339: contig of 2619 bp in length
 * 15958: gap of unknown length
 * 16058: contig of 1978 bp in length

FEATURES
 source

Location/Qualifiers
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 19322 19421: gap of unknown length
 19422 21365: contig of 1944 bp in length
 21366 21465: gap of unknown length
 21466 23677: contig of 2212 bp in length
 23678 23777: gap of unknown length
 23778 26214: contig of 2437 bp in length
 26215 26314: gap of unknown length
 26315 27161: contig of 1302 bp in length
 27162 27716: gap of unknown length
 27717 29080: contig of 1364 bp in length
 29081 29180: gap of unknown length
 29181 31273: contig of 2093 bp in length
 31274 31373: gap of unknown length
 31374 32664: contig of 1291 bp in length
 32665 32764: gap of unknown length
 32765 34090: contig of 1326 bp in length
 34091 34190: gap of unknown length
 34191 35515: contig of 1325 bp in length
 35516 35615: gap of unknown length
 35616 37278: contig of 1663 bp in length
 37279 37378: gap of unknown length
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 39763 39862: gap of unknown length
 39863 41543: contig of 1681 bp in length
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 46888 46987: gap of unknown length
 46988 48064: contig of 1077 bp in length
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 61485 62623: contig of 1139 bp in length
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 64094 64193: gap of unknown length
 64194 65420: contig of 1227 bp in length
 65421 65520: gap of unknown length
 65521 66745: contig of 1225 bp in length
 66746 66845: gap of unknown length
 66846 67973: contig of 1128 bp in length
 67974 68073: gap of unknown length
 68074 69328: contig of 1255 bp in length
 69329 69428: gap of unknown length
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EYCTAVKIDFETRVLSPPAGALAGLAKAYARKVKKLLIAISSGANVQRNLFIY
ERSEIGENREKLISIKPEIPGSLKSRMGSSQVTEFNRYKSLSDAYVLVGVRTK
TEKSPFELKAGFTSDFTRNEISNDHLRMVGGNSDGSNNHNERIFRGEFFE
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DFDQGNKALFIALNLGSLFDAIKTQAGDFKTQDWDGWIARTQKFDGYWSEFFIPW
DVTLMKQPDGDIRKINYALRYSAENSWSSAGTMAARNDYFOELDSLEQNTYKSK
LTFPFISSNKNSTVNOEGSDIGAEIFYSTGKGROIINLAIPDFGOAESDQVWNFSA
QTFYSERARFENQSGSDFISNDYRISVINTRRIGAAPFSNCSESENEEGCEAAKN
YSDIDFALRQKSNNEFEVFASEAEAFSVGRDYYALRSRKLGNKTLGFMVNTV
ENEMGESSTVNDIYINIRSKLITYSDLLASERKNGGLGYRTQFTYLPNKLNSIS
GSLLYFEEDFLQYLRQDWIHAGIGGNRKINEFDNSILLKQIDYCIDLIDADT
AGNSPIGIDQNSFSFSDKNSFOLDNFNRSGSKWTITRKNEAYPFIKSKRRIGITA
DEAKNYIWDVWSEFKCEKDNFDSNGYGRKFYKIAGSIPEPNDLNRNAOYRIR
KENWLIQODNNLASYSRQDTLSFDLWFKNNKHEIRLKSQFVALKAKNPISFSD
ANGLYIKGNINVEENTGVASQYIRKVELAPLSYLFVLSYSGGRIYDEEDRSOSEL
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/evidence=not_experimental
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/protein_id="AAG10441.1"
/db_xref="GI:9971879"
/translation="MVKNKIRKSLFEQGSISDLKSNTSFLIOENVLEKINTHEMQN
IALYFPERNEVTNLLIOAFTKLKNXIPKVIDDEMMAFNLLDEQPNFFINQFGIKE
VKSEYVNIINEIDLMPMTGVDLNGYRLGYSGYFDRLIGSINEVSRPLVLGLCYO
YOICNNHFEGERHDLKYDYVFSNDRMISTSS"
6433..7728
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/transl_table=11
/evidence=not_experimental
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/protein_id="AAG10442.1"
/db_xref="GI:9971880"
/translation="MEKIIFKNRRDSLIKHPKNSALIVPGADLQYRNADSYNLRQE
SSFYLSGFCPESSLLIOWNGKSIDSIFFVPEKDKLPEIMDGYRAGPEKSIDIDG
QAFENKSDALMEILOGLKLYVYSIGKNGGDKQYIDWTCGAANSKDRHSKSIDIDG
SWVGNRLRIKKHEIDINKRACEISASYSIEVMSIKPGDNEQIEALFLYEFKRG
GRPAPYIVAGGACVLHYTENDKELASDILIVDAGECYMTASDITRTFFVSGR
FSDQLOIYIVHKKANLAAIDAVTGNSTIMEQMVSEKVIETGLVELGILSDVQNLH
KNGAFKDYMHKRVHGLGDVHDVGDYMEGDEFMKFKPGMGTITIEPGIYISSAMDVDD
KNKGIGIRIEDDILLVTDSGNINLTKEVPSNPQIEISLMA"
7732..8892
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KIASLTSSFDYLTALTFFVVDIINDSHGKRAHQVSEKGIAPALMPLEGKGMKCIY
VMSIKNOVLGDEPVSEFVNKNSISFSEKLNVSRLKSEILSKLSNHHFENYISGPV
LLGDAHSIHPLAGQINLPADATFCEVSISSYKKGIAFNEKSVLKRKYRIRKSMN
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complement(8900..9136)
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RFVNLKVSAKMRIDIRKGISSEVLKELRAKQKV"
9710..10129
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/evidence=not_experimental
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nucleotidohydrolase"
/protein_id="AAG10445.1"
/db_xref="GI:9971883"
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/evidence=not_experimental
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factor Y) - superfamily II helicase"
/protein_id="AAG10446.1"
/db_xref="GI:9971884"
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SGKTEYLRVAETFIKNNKSVLVLPEINLTQLLSRFRNFNGEIGIYHSHKQTAAR
LKTWLKAFGSIKIIIVTRSSALVPLDNIGLIIIDEEHDQSFROSEGFKFSARDLSIK
RAQLADIPILIGSATPSLOTILKVENKFIIRDIPNRVDGNKPKLIALDINNPLIG
VAKETIEAMQSTIDRQVLVFINRRGFAPLYQSCSGWADCKSDTNLVFHOARN
RLICHRCEASVSNLSCPACKNDFNMVAGTERVEEVKSKSVKFTPIIRVDHDSHTK
VGMEAIVKKIHSDDAAILVGTOMLAKGHDPKVTLVLNADNGLISPEINALEKIS
QLLQVSRAGRNNNLKAVIITQTRYPDIDNINLKTGYMKFASQCLSTNQMNLPFF
TTLCLRCSSPTQKNSDVLLEKAVLILNSRTDINVGIPPLSLVSKSGNYRHQVITIHA
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complement(12428..13510)
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LLIAKELRTLDITYGVRPMIRGDDELDLNNRQDARKYGADIFVSHADGFLSS
VKGASVITWSDSEAVARNLSKQREIRQADIKNLKVPDDEDAARTYPEIKYKI
SESKTLGKILDLQKRDPTKIHKKNAVADPFLKSIDIPSVLSESGFITNPEDAQR
LKGPGRGRIARSVFLGIHNVFKDKPKANTFMSIDPGFVTKIQKGDVLSLSEIRFGV
TVEENTENKLNKPIYPGOLIKINI"
complement(13670..14131)
/codon_start=1
/transl_table=11
/evidence=not_experimental
/product="predicted kinase of the phosphomethylpyrimidine
kinase (Thid) family"
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/db_xref="GI:9971887"
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FISRSIIRKCGMKDLVKSPYTLTCEYDFNNLMFLHIDLYRTNEAEDIDIFLSRKIN
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complement(14128..14985)
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seq_name: gb_pat:190034
seq_documentation_block:
LOCUS I90034 918 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 3 from patent US 5723436.
ACCESSION I90034
VERSION I90034.1 GI:3409974
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 918)
AUTHORS Huang,L. and Cyert,M.S.
TITLE Calcineurin interacting protein compositions and methods
JOURNAL Patent: US 5723436-A 3 03-MAR-1998;
FEATURES
Location/Qualifiers
source
1..918
/organism="unknown"
BASE COUNT 313 a 201 c 163 g 241 t
ORIGIN

alignment_scores:
Quality: 74.50 Length: 95
Ratio: 1.330 Gaps: 2
Percent Similarity: 58.947 Percent Identity: 26.316

alignment_block:
US-09-528-682-4 x I90033 ..
Align seg 1/1 to: I90033 from: 1 to: 1222
13 ProfileAlaAsnThrAspThrThrGlnPheLeuAsnMetGlyAsnG1 29
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
448 CCGAGTGAGACGTTAATTCACACACTCTCTATTTGCGAGCTTTAAAC... 495
29 uValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuLeuSerAlaGluG 46
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
496 .ATGAGCTCTTGATGGAGAGAAAAAATCGTCCAGTCTACACGCAACAT 544
46 lyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePro 62
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545 CAGTGTACCTAGTACAAATAAGACAGACAAT..... 576
63 GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
577 .....CAGCATTTCAATGACATAAACAGATGCTAGGAGTAGTGACGA 620
79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
621 AGATGCCTTTCCCAAAGCCAATCATTAATTTCAATAAGAAACTACCAA 670
96 euLeuIleAsnAspGlyPhePheSerAsnAsn 107
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seq_name: gb_pat:190036
seq_documentation_block:
LOCUS I90036 2745 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 6 from patent US 5723436.
ACCESSION I90036
VERSION I90036.1 GI:3409976
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 2745)
AUTHORS Huang,L. and Cyert,M.S.
TITLE Calcineurin interacting protein compositions and methods
JOURNAL Patent: US 5723436-A 6 03-MAR-1998;
FEATURES
Location/Qualifiers
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/organism="unknown"
BASE COUNT 915 a 587 c 495 g 748 t
ORIGIN

alignment_scores:
Quality: 74.50 Length: 95
Ratio: 1.330 Gaps: 2
Percent Similarity: 58.947 Percent Identity: 26.316

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US-09-528-682-4 x I90036 ..
Align seg 1/1 to: I90036 from: 1 to: 2745
13 ProfileAlaAsnThrAspThrThrGlnPheLeuAsnMetGlyAsnG1 29
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
63 GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
577 .....CAGCATTTCAATGACATAAACAGATGCTAGGAGTAGTGACGA 620
79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
621 AGATGCCTTTCCCAAAGCCAATCATTAATTTCAATAAGAAACTACCAA 670
96 euLeuIleAsnAspGlyPhePheSerAsnAsn 107
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671 TACTTAAATTAATGATAACGTCATACATCAATCAAC 705

seq_name: gb_pat:190033
seq_documentation_block:
LOCUS I90033 1222 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 1 from patent US 5723436.
ACCESSION I90033
VERSION I90033.1 GI:3409973
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 1222)
AUTHORS Huang,L. and Cyert,M.S.
TITLE Calcineurin interacting protein compositions and methods
JOURNAL Patent: US 5723436-A 1 03-MAR-1998;
FEATURES
Location/Qualifiers
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BASE COUNT 313 a 201 c 163 g 241 t
ORIGIN
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gene


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96 euLeu1eAsnAsnAspGlyPhePheSerAsnAsn 107
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seq_name: gb_in:L14324

seq_documentation_block:
LOCUS L14324 38269 bp DNA linear INV 09-AUG-2001
DEFINITION Caenorhabditis elegans cosmid ZK112, complete sequence.
ACCESSION L14324
VERSION L14324.1 GI:289740
KEYWORDS HTG.
SOURCE
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 38269)
The C. elegans Sequencing Consortium.
Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
Science. 282 (5396), 2012-2018 (1998)
99069613
2 (bases 1 to 38269)
Du,Z.
The sequence of C. elegans cosmid ZK112
Unpublished
3 (bases 1 to 38269)
Waterston,R.
Direct Submission
Unpublished
4 (bases 1 to 38269)
Waterston,R.
Direct Submission
Submitted (09-AUG-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
Submitted by:
Genome Sequencing Center
Department of Genetics, Washington University
St. Louis , MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 1RQ, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk

NOTICE: This sequence may not be the entire insert of this clone.
It may be shorter because we only sequence overlapping sections
once, or longer because we provide a small overlap between
neighboring submissions.

This sequence was finished as follows unless otherwise noted: all
regions were double stranded, sequenced with an alternate chemistry
or covered by high quality data (i.e., phred quality >= 30); an
attempt was made to resolve all sequencing problems, such as
compressions and repeats; all regions were covered by sequence from
more than one m13 subclone.

NEIGHBORING COSMID INFORMATION

The clone sequenced to the left is C03B6, 200 bp overlap: the clone
sequenced to the right is ZC97, 1200 bp overlap. Actual start of
this clone is at base position 1 of CELZK112.

NOTES:
Coding sequences below are predicted from computer analysis, using
the program GeneFinder(P. Green and L. Hillier, ms in preparation).
Location/Qualifiers
1. 38269
/organism="Caenorhabditis elegans"
/strain="Bristol N2"
/db_xref="taxon:6239"
/chromosome="III"
/clone="ZK112"

FEATURES
source
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IYMSQIFGAAGRPIPLSTGTAIPNMSGSAVSQPMLAGSGLATPPVPIVEVRPAG
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complement(6683. .6985)
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complement(6683. .6985)
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/translation="MTADDFIETSETSATGEGARANFRLVSLAFOKETDSSILFT
LSQCHIELGGLEKHCGRGRIERKRGREALRLGPGTKYNCPPFIVSRDLSVLLFEED"
8495. .13325
/gene="ZK112.2"
/note="ncl-1"
join(8495. .8511,8563. .8965,9016. .9384,10005. .10091,
10292. .10438,11623. .11790,11858. .12757,12806. .13093,
13149. .13325)
/gene="ZK112.2"
/note="contains similarity to Pfam domain PF00643
(zf-B_box), Score=85.1, E-value=4.7e-22, N=2; coded for by
the following C. elegans cDNAs: yk37d10.3, yk37d10.5,
yk37e12.3, yk37e12.5, yk192e8.5, yk423c1.5, yk536d11.5,
yk661b10.5"
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/db_xref="GI:289745"
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RSVLCLOHRASELVFFVCVSCNLAICRDCVSDHPGSGTHQYELIADVQKMLKMQLI
ADASKHADMLDMFKVDNKKQVLTASLHNAHQAOLETVSNLINVIOQKTKLAKDID
NAFAKQQLTMVDKRIOSMADKLSOTIEFSRRLSMSPASPAEVMVFKOLLRLQLFL
GFNPTDSGLVMTPEIEYLGAGLFNNSASTVSQLGSHGSPSPNNAPANDFLMPQ
AGLAPIGRAIRIPIEQNLARSPHHIAGSLPNMAYSDSNLRLPKDGGSSOSLG
PFNPLGASVPGAAADPFSSQYDKWSLGVPEPSVGLLEGGNVEEKFQTLFFPSRSQIK
RQKMIYHCKFGFVMEQTEPQSVAVNGQDVIYADTNHRIQVDFQKGRFKQFG
ECGRDGLLYPNRVAVNRTGDFVVTERTPTHQIQVYNOYQGFQRKGANTLQHPFG
VCVDSKGRITVVECKVMRVIIFDMEGNLOKESCSRYLEFPNGVCTNDKNETLISDNR
AHCIKVFSYEQQLRQIGCEGVNYPICVGINSGEVVYVADNHNFNLTUTPSQDQTM
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complement(15072. .16630)
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complement(join(15072. .15212,15499. .15561,15628. .15826,
16554. .16630))
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complement(16829. .17084)
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complement(join(16829. .16978,17025. .17084))
/gene="ZK112.6"
/codon_start=1
/product="Hypothetical protein ZK112.6"
/protein_id="AAA28183.1"
/db_xref="GI:289743"
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This sequence is the entire insert of clone RP11-78J21. The true left end of clone RP11-93H24 is at 157212 in this sequence. The true right end of clone RP11-245D16 is at 50244 in this sequence.

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            682..729
                /note="24 copies 2 mer at 100% conserved"
            1368..1676
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            1697..2811
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            2819..2898
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            4522..4829
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            4830..5180
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            5181..5459
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            5460..5670
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            6159..6630
                /note="MER27 repeat: matches 61..565 of consensus"
            6860..7064
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            7131..7326
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            7773..8174
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            8435..8715
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            9060..9264
                /note="AluJo repeat: matches 1..206 of consensus"
            9265..9374
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            9385..10324
                /note="L1MA4A repeat: matches 5319..6299 of consensus"
            10335..10493
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            10510..10624
                /note="AluJb repeat: matches 184..312 of consensus"
            10626..10894
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            10895..11922
                /note="L1MA4A repeat: matches 4289..5331 of consensus"
            11746..11812
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            11923..12216
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            12217..13237
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            13238..13542
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            13543..13928
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            13929..14219
                /note="L1MA4A repeat: matches 2864..3254 of consensus"
            /note="AluJo repeat: matches 1..288 of consensus"
            14220..14776
                /note="L1MA4A repeat: matches 2397..2864 of consensus"
            14777..15079
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            15080..15600
                /note="L1MA4A repeat: matches 1869..2397 of consensus"
            15601..16623
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            16618..17254
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            17257..17563
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            17580..17741
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            21114..21838
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            24587..24666
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            26094..26221
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            26109..26348
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            26380..26559
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            26560..26845
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            26846..27856
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            27860..27991
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            28699..29605
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            29679..31092
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            31019..31117
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            31118..31417
                /note="AluY repeat: matches 3..302 of consensus"
            31418..32834
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            32840..33350
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            36375..36672
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            37931..38257
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            38258..38558
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            38559..39059
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            40071..40341
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ACCESSION   AE008090
VERSION     AE007869
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            Rhizobiaceae; Rhizobium.
            1 (bases 1 to 10473)
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  AUTHORS   Hinkle, G., Slater, S.C. and Goodner, B.
  TITLE     Complete Genome Sequence of Agrobacterium tumefaciens C58
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            Disease in Plants
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 10473)
  AUTHORS   Hinkle, G., Slater, S.C. and Goodner, B.
  TITLE     Direct Submission
JOURNAL     Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street,
            Cambridge, MA 02139, USA
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the identified cDNA sequences using BLASTN 2.0 with the corresponding DBJ accession no. and RCP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein. The orientation of the sequence is from SP6 to T7 of the PAC clone. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/GenomesSeq.html>.

FEATURES

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DEFINITION Homo sapiens chromosome 15 clone RP11-607F22 map 15, WORKING DRAFT
SEQUENCE, 13 unordered pieces.
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VERSION     AC027163.2 GI:10567962
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SOURCE      human.
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            1 (bases 1 to 156690)
AUTHORS     Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
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            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zimmer,A. and Zody,M.
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            On Oct 4, 2000 this sequence version replaced gi:7331476.
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            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            ----- Genome Center
            Center: Whitehead Institute/ MIT Center for Genome Research
            Center code: WIBR
            Web site: http://www-seq.wi.mit.edu
            Contact: sequence_submissions@genome.wi.mit.edu
            ----- Project Information
            Center project name: L6511
            Center clone name: 607_F-22
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            Chemistry: Dye-terminator Big Dye; 100% of reads
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            Quality coverage: 5.0 in Q20 bases; sum-of-contigs
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            * NOTE: This is a 'working draft' sequence. It currently
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            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
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            * 1721 1820: gap of 100 bp

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* 8851 15813: contig of 6963 bp in length
* 15814 15913: gap of 100 bp
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* 23307 23406: gap of 100 bp
* 33171 33270: contig of 9764 bp in length
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* 44223 44522: gap of 100 bp
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                     /note="assembly_fragment"
     misc_feature      96071..106973
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BASE COUNT  47316 a 29721 c 29869 g 48582 t 1202 others
ORIGIN

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                       Ratio: 1.805       Gaps: 1
Percent Similarity: 63.077 Percent Identity: 32.308
alignment_block:
US-09-528-682-4 x AC027163/rev ..

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IPDGFIDKTVSVTKADGYVYVLSLEDKTVPTIKTDLDINIVIGDVLGIDFIVTSDG
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5254..5673
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NSSVQFRAQNLQAEKELQTSQKLSAIAFNKSSSETSLKAAQARRDRYKPLLETG
SISQDFQEQVQALQEQEQLQESQTAANYEQQAIOQKQYAIKAAKARLEGALNLP
SDANVIAQERIAEYAVSEVLSRLNOREQLQKLEQLKQSRQRELNQIMREI
ANTAIRASAGIIQELNRPQAIIIRSGDIVAOISPRKSLPIKALVPASDIRKVTN
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DVTKMLSSFAIYDEKGEQVYFNPVKSDELNLEGLRCPMFPQEKIAKVLRLIT
IVGKSILTAANSQALDKSDRYDRKQGVALLDQWHTLPQDVADKLQLMAHFGLNY
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LAVMGDFWDSLRHAWDDLOKINAAENKLYQLEVAEVLVIPPTLVNPNKPEAREF
FEQVNGRMITKLLPFLSVSMGCSFFMYTSTVKEEDLLDLETLYCPWVFOAQLPKQK
ELRAVYVNGNLFVGLDASSYASTQDMRRANQESCTWQVPELPRKIIHQHDPMARL
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Quality: 74.00 Length: 84
Ratio: 1.510 Gaps: 4
Percent Similarity: 58.333 Percent Identity: 33.333
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US-09-528-682-4 x AP003600 ..
Align seg 1/1 to: AP003600 from: 1 to: 341950
30 ValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluG1 46
::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
224100 ATAGTTTATGACTTTAAAGTATCCGTCACAAGCGAGAGTTGCTGCTTATGC 224149
46 y.....GlyMetAspArgAspLeuPheGlySerAlaAsnIleAspG 60
::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
224150 CAAGTACAAGGCGTATGATGCTGCATATCTTTCGCA.....CCGG 224187
60 LypPheProGluValArgGluPheAsnSerLeuProAsnAsnLysAlaSer 76
||||| ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
224188 GATTTCTGAAATCTGAAGTTTGCAATCTTATGATTTCTCTCAAGACAGT 224237
77 SerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTy 93
||||| ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
224238 AGTGAT....GCTGAACACTCCCGACAAATTTCAACTGTGATCAATAAGAA 224284
93 rleLysLeuIleAAsnAsn.....AspGlyPhePheSerAsnAsnG 108
::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
224285 TTTTCGACTTTTGGGCAATTCAACTGAAGATGGTTCCTTTGGCCCTTCAG 224334
108 ly 108
224335 GG 224336
seq_name: gb_pl:APEL4BXYL
seq_documentation_block:
LOCUS APEL4BXYL 1623 bp DNA linear PLN 01-JUN-1996
DEFINITION A.pisi endo-1,4-betaxyylanase gene.
ACCESSION Z68891
VERSION Z68891.1 GI:1359485
KEYWORDS
SOURCE
ORGANISM
Ascochyta pisi.
Ascochyta pisi.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Dothideales; Didymella; Ascochyta.
REFERENCE
1 (bases 1 to 1623)
Lubeck,P.S., Paulin,L., Degefu,Y., Lubeck,M. and Collinge,D.
Molecular cloning and DNA sequencing of a xylanase gene from the
phytopathogenic fungus Ascochyta pisi Lib
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1623)
Paulin,L.
Direct Submission
JOURNAL Submitted (25-JAN-1996) Paulin L., Institute of Biotechnology,
Viikinkaari 9, Helsinki, Finland
FEATURES
Location/Qualifiers
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/db_xref="SPTREMBL:O00263"
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/product="unnamed"
1125. .1179
Intron 391 a 518 c 368 g 346 t
BASE COUNT
ORIGIN

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  Ratio: 1.065        Gaps: 4
Percent Similarity: 59.483 Percent Identity: 21.552

alignment_block:
US-09-528-682-4 x APEI4BXYL ..
Align seg 1/1 to: APEI4BXYL from: 1 to: 1623

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1262 GAGTACTAGTAGTCGAGCAACTTCGGCACCTACGACCCCTCTTCCAGGC 1311
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
17 rAsnThrThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspG 34
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1312 C.....ACCGTCAGGGCTCCGTGACCGCCGACG 1340
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
34 lyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyGlyMetAspArg 50
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1341 GC.....TCCTCGTACAAAGATTGCACAGACCCAG..... 1369
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
51 AspteuPheGlySerAlaAsnIleaspGlyPheProGluValArgGluPh 67
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1370 ...CGCACCAACCGCCCTCCATCGACGGCACCCACAGACCTTCCAGCAGTA 1416
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
67 eAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnL 84
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1417 CTGGTCTGTGGCCAGACAGCGGCGGCTCTTCCAGCGGCGGCTCAG 1466
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
84 ysGlnHisAspAlaAspPheLysTyrIleLysLeu..... 96
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1467 CTCACCTTCGACGCGCTGGCTGCAAGGCATGAGCTCGGAACGACACAAC 1516
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
97 .....LeuIleAsnAspGlyPhePheSerAsnAsnGlyGlyLys 110
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1517 TACCAGATCGTGGCTACCGGGGCTACTTCTCCAGCGGCGGCTCAG 1564
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seq_name: gb_htg:AC103259

seq_documentation_block:
LOCUS AC103259 112484 bp DNA linear HTG 21-DEC-2001
DEFINITION Rattus norvegicus clone CH230-166J4, *** SEQUENCING IN PROGRESS
***, 47 unordered pieces.
ACCESSION AC103259
VERSION AC103259.2 GI:17974771
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 112484)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,

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Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
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Ogih,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojokan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoshitari,N.,
Slisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmami,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Washington,S., Williams,G., Williamson,A., Wleczyk,R., Woodden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 112484)
Worley,K.C.
Direct Submission
Submitted (24-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 21, 2001 this sequence version replaced gi:17062919.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GJQF
Center clone name: CH230-166J4
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 101125 bases at least Q40
Consensus quality: 106675 bases at least Q30
Consensus quality: 112029 bases at least Q20
Estimated insert size: 98310; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.3x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 47 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 6637: contig of 6637 bp in length
* 6638 6737: gap of unknown length
* 6738 12170: contig of 5433 bp in length
* 12171 12270: gap of unknown length
* 12271 17400: contig of 5130 bp in length
* 17401 17500: gap of unknown length

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* 17501 21260: contig of 3760 bp in length
* 21261 21360: gap of unknown length
* 21361 25621: contig of 4261 bp in length
* 25622 25721: gap of unknown length
* 25722 28629: contig of 2908 bp in length
* 28630 28729: gap of unknown length
* 28730 32777: contig of 4048 bp in length
* 32778 32877: gap of unknown length
* 32878 36763: contig of 3886 bp in length
* 36764 36863: gap of unknown length
* 36864 40444: contig of 3581 bp in length
* 40445 40544: gap of unknown length
* 40545 43316: contig of 2772 bp in length
* 43317 43416: gap of unknown length
* 43417 45217: contig of 1801 bp in length
* 45218 45317: gap of unknown length
* 45318 47947: contig of 2630 bp in length
* 47948 48047: gap of unknown length
* 48048 49760: contig of 1713 bp in length
* 49761 49860: gap of unknown length
* 49861 53475: contig of 3615 bp in length
* 53476 53575: gap of unknown length
* 53576 56062: contig of 2487 bp in length
* 56063 56162: gap of unknown length
* 56163 57968: contig of 1806 bp in length
* 57969 58068: gap of unknown length
* 58069 60331: contig of 2263 bp in length
* 60332 60431: gap of unknown length
* 60432 63276: contig of 2845 bp in length
* 63277 63376: gap of unknown length
* 63377 66146: contig of 2770 bp in length
* 66147 66246: gap of unknown length
* 66247 69089: contig of 2843 bp in length
* 69090 69189: gap of unknown length
* 69190 72282: contig of 3093 bp in length
* 72283 72382: gap of unknown length
* 72383 74056: contig of 1674 bp in length
* 74057 74156: gap of unknown length
* 74157 75678: contig of 1522 bp in length
* 75679 75778: gap of unknown length
* 75780 77374: contig of 1596 bp in length
* 77375 77474: gap of unknown length
* 77475 78813: contig of 1339 bp in length
* 78814 78913: gap of unknown length
* 78914 80091: contig of 1178 bp in length
* 80092 80191: gap of unknown length
* 80192 82494: contig of 2303 bp in length
* 82495 82594: gap of unknown length
* 82595 84666: contig of 2072 bp in length
* 84667 84766: gap of unknown length
* 84767 86385: contig of 1619 bp in length
* 86386 86485: gap of unknown length
* 86486 88016: contig of 1331 bp in length
* 88017 88116: gap of unknown length
* 88117 89618: contig of 1502 bp in length
* 89619 89718: gap of unknown length
* 89719 91240: contig of 1522 bp in length
* 91241 91340: gap of unknown length
* 91341 92765: contig of 1425 bp in length
* 92766 92865: gap of unknown length
* 92866 93910: contig of 1045 bp in length
* 93911 94010: gap of unknown length
* 94011 95627: contig of 1617 bp in length
* 95628 95727: gap of unknown length
* 95728 97031: contig of 1304 bp in length
* 97032 97131: gap of unknown length
* 97132 98216: contig of 1085 bp in length
* 98217 98316: gap of unknown length
* 98317 99761: contig of 1445 bp in length
* 99762 99861: gap of unknown length
* 99862 101661: contig of 1800 bp in length
* 101662 102845: contig of 1084 bp in length

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* 102846 102945: gap of unknown length
* 102946 104489: contig of 1544 bp in length
* 104490 104589: gap of unknown length
* 104590 105923: contig of 1334 bp in length
* 105924 106023: gap of unknown length
* 106024 107098: contig of 1075 bp in length
* 107099 107198: gap of unknown length
* 107199 108498: contig of 1300 bp in length
* 108499 108598: gap of unknown length
* 108599 109659: contig of 1061 bp in length
* 109660 109759: gap of unknown length
* 109760 111265: contig of 1506 bp in length
* 111266 111365: gap of unknown length
* 111366 112484: contig of 1119 bp in length.
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                     /db_xref="taxon:10116"
                     /clone="CH230-166J4"
BASE COUNT   33579 a 20234 c 19473 g 34521 t 4677 others
ORIGIN

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    Ratio: 1.413       Gaps: 4
    Percent Similarity: 52.525    Percent Identity: 29.293

alignment_block:
US-09-528-682-4 x AC103259 ..

Align seg 1/1 to: AC103259 from: 1 to: 112484

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22 n.....PheLeuAsnMetGlyAsnGluValAlaL 32
7582 AGATATGCAAAACAGAAATGCTCTCACCCAAACATACAGGAATAC 7631
32 euAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGlyGlyMet 48
||| ||| ||| |||::: |||::: |||:::
7632 AGGACACAGGAGATCAAAACCTAAGAATAATAGGTTTACAGAGAGTAA 7681
49 AspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluVal 65
||| ::::: ||| |||::: |||::: |||:::
7682 GACTCCCAAGTTAAAGGGTCAGTAATATG.....TTCGAAACAATCAT 7725
65 gGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerL 82
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7726 AGAAGAAAC...TTACCTAAC.....C 7745
82 euAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysLeuLeu 97
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seq_name: gb_vi:AF325155

seq_documentation_block:
LOCUS      AF325155
DEFINITION Spodoptera litura nucleopolyhedrovirus strain G2, complete genome.
ACCESSION  AF325155
VERSION    AF325155.1 GI:15553210
KEYWORDS
SOURCE
ORGANISM   Spodoptera litura nucleopolyhedrovirus.
            Viruses: dsDNA viruses, no RNA stage; Baculoviridae;
            Nucleopolyhedrovirus.
REFERENCE  1 (bases 1 to 139342)
AUTHORS   Pang,Y., Yu,J., Wang,L., Hu,X., Bao,W., Li,G., Chen,C., Han,H.,
            Hu,S. and Yang,H.
TITLE     Sequence Analysis of the Spodoptera litura Multicapsid

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Consensus quality: 148585 bases at least Q40
Consensus quality: 157081 bases at least Q30
Consensus quality: 164382 bases at least Q20
Estimated insert size: 152520; sum-of-ctg-estimation
Quality coverage: 0x in Q20 bases; agarose-1p estimation
Quality coverage: 2.3x in Q20 bases; sum-of-ctg-estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 67 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
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* 136498: 138689: contig of 2192 bp in length
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alignment_scores:
Quality: 73.50 Length: 67
Ratio: 1.670 Gaps: 2
Percent Similarity: 65.672 Percent Identity: 32.836

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US-09-528-682-4 x AC095438/rev ..

Align seg 1/1 to reverse of: AC095438 from: 1 to: 187586

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BASE COUNT 2911 a 1385 c 1625 g 2034 t
ORIGIN

alignment_scores:
Quality: 72.50 Length: 85
Ratio: 1.394 Gaps: 3
Percent Similarity: 61.176 Percent Identity: 27.059

Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:16874678.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GHAN
Center clone name: CH230-117A22
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to findPhrapList

Consensus quality: 140999 bases at least Q40
Consensus quality: 148978 bases at least Q30
Consensus quality: 156080 bases at least Q20
Estimated insert size: 147801; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently consists of 55 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1
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7905: gap of unknown length
17053: contig of 9148 bp in length
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17154: contig of 7193 bp in length
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seq_name: gb_htg:AC099184

seq_documentation_block:
LOCUS AC099184 166852 bp DNA linear HTG 20-DEC-2001
DEFINITION Rattus norvegicus clone CH230-117A22, *** SEQUENCING IN PROGRESS
***, 55 unordered pieces.
ACCESSION AC099184
VERSION AC099184.2 GI:17973062
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 166852)
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Weinstock,G. and Gibbs.R.
Direct Submission
Unpublished
2 (bases 1 to 166852)
Worley,K.C.
Direct Submission
Submitted (09-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One

Hernandez, J., Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseghe, H., Lozado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenwo, S., Ogutu, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Rives, Y., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Slisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Direct Submission
Unpublished
2 (bases 1 to 172199)

Worley, K. C.

Direct Submission

Submitted (15-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:16930859.

COMMENT

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GIID
Center clone name: CH230-62L13
----- Summary Statistics

Assembly program: Phrap; version 0.990329First call to findPhrapList
Consensus quality: 138342 bases at least Q40
Consensus quality: 145173 bases at least Q30
Consensus quality: 150824 bases at least Q20
Estimated insert size: 142168; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 2.4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 63 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 7563: contig of 7563 bp in length
* 7564 7663: gap of unknown length
* 7664 17066: contig of 9403 bp in length
* 17067 17166: gap of unknown length
* 17167 23634: contig of 6488 bp in length
* 23635 23754: gap of unknown length
* 23755 31080: contig of 7326 bp in length
* 31081 31180: gap of unknown length
* 31181 36505: contig of 5325 bp in length
* 36506 36605: gap of unknown length
* 36606 40235: contig of 3630 bp in length
* 40236 40335: gap of unknown length

40336 44553: contig of 4218 bp in length
44554 44653: gap of unknown length
44654 47729: contig of 3076 bp in length
47730 47829: gap of unknown length
47830 52693: contig of 4864 bp in length
52694 52793: gap of unknown length
52794 56955: contig of 4162 bp in length
56956 61317: contig of 4262 bp in length
61318 61417: gap of unknown length
61418 64575: contig of 3158 bp in length
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68717 72927: contig of 4211 bp in length
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101426 101525: gap of unknown length
101526 103718: contig of 2193 bp in length
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120099 122191: contig of 2093 bp in length
122192 122291: gap of unknown length
122292 125454: contig of 3163 bp in length
125455 125554: gap of unknown length
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127056 128648: contig of 1593 bp in length
128649 128748: gap of unknown length
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131399 134230: contig of 2832 bp in length
134231 134330: gap of unknown length
134331 136037: contig of 1707 bp in length
136038 136137: gap of unknown length
136138 138225: contig of 2088 bp in length
138226 138325: gap of unknown length
138326 140301: contig of 1976 bp in length
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* 142115 142214: gap of unknown length
* 142215 143450: contig of 1236 bp in length
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* 145813 147823: contig of 2011 bp in length
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* 147924 149107: contig of 1184 bp in length
* 149108 149207: gap of unknown length
* 149208 151034: contig of 1827 bp in length
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* 152241 152340: gap of unknown length
* 152341 154103: contig of 1763 bp in length
* 154104 154203: gap of unknown length
* 154204 155590: contig of 1387 bp in length
* 155591 155690: gap of unknown length
* 155691 156842: contig of 1152 bp in length
* 156843 156942: gap of unknown length
* 156943 158009: contig of 1067 bp in length
* 158010 158109: gap of unknown length
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US-09-528-682-4 x AC099452/rev ..

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22 nPheLeu.....AsnMetGlyAsnGluValAlaL 32
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32 euAspGlyArgTyrgSerAsnTyrrAlaLeuIleSerAlaGluGlyMet 48
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49 AspArgAspLeuPheGlySerAlaAsnIle.....As 59
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59 pGlyPheProGluValArg..... 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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66 .....GluPhe..... 67
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67 ..... 67
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68 .AsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnL 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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84 ysGlnHisAspAlaAspPheLysLysTyrrIleLysLeuLeuIleAsnAsn 100
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101 Asp.....GlyPhe 103

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28614 GATCAAGTAGGCTTC 28600

seq_name: gb_htg:AC094036

seq_documentation_block:

LOCUS AC094036

DEFINITION Rattus norvegicus clone CH230-34118, *** SEQUENCING IN PROGRESS

ACCESSION AC094036

VERSION AC094036.2 GI:17975630

KEYWORDS HTG; HTGS PHASE1.

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 182583)

AUTHORS

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Briefe,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C., Caron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyile,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Homs,F., Howard,S., Huber,J., Huiyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loisedge,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,N., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojuben,I., Rolfe,M., Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I., Sodergren,E., Sonaiker,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tameriss,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalobos,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstein,G. and Gibbs,R.

TITLE Direct Submission

REFERENCE 2 (bases 1 to 182583)

Worley,K.C.

Direct Submission

AUTHORS

TITLE

JOURNAL

COMMENT

Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

Submitted (14-SEP-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

On Dec 21, 2001 this sequence version replaced gi:15617897.

----- Genome Center


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----- Project Information
Center project name: GPHK
Center clone name: CH230-34L18
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 140876 bases at least Q40
Consensus quality: 157668 bases at least Q30
Consensus quality: 167320 bases at least Q20
Estimated insert size: 163483; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-1p estimation
Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
  (see http://www.hqsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
* NOTE: This is a 'working draft' sequence. It currently
  consists of 71 contigs. The true order of the pieces
  is not known and their order in this sequence record is
  arbitrary. Gaps between the contigs are represented as
  runs of N, but the exact sizes of the gaps are unknown.
  * This record will be updated with the finished sequence
  * as soon as it is available and the accession number will
  * be preserved.
*
* 1
* 6527: contig of 6527 bp in length
* 6528: gap of unknown length
* 6628: contig of 4663 bp in length
* 11290: gap of unknown length
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* 11390: gap of unknown length
* 11391: contig of 3428 bp in length
* 14818: gap of unknown length
* 14819: contig of 4684 bp in length
* 14918: gap of unknown length
* 19602: contig of 4684 bp in length
* 19603: gap of unknown length
* 19702: contig of 4421 bp in length
* 24123: gap of unknown length
* 24124: gap of unknown length
* 24224: contig of 4447 bp in length
* 28670: contig of 4447 bp in length
* 28671: gap of unknown length
* 28770: gap of unknown length
* 33216: contig of 4446 bp in length
* 33217: gap of unknown length
* 33316: gap of unknown length
* 33317: contig of 3491 bp in length
* 36807: gap of unknown length
* 36808: gap of unknown length
* 40610: contig of 3703 bp in length
* 40710: gap of unknown length
* 44497: contig of 3787 bp in length
* 44597: gap of unknown length
* 44598: gap of unknown length
* 44599: contig of 3172 bp in length
* 47769: gap of unknown length
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* 52630: contig of 4761 bp in length
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* 52731: gap of unknown length
* 55734: contig of 3024 bp in length
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* 94795: contig of 2492 bp in length
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* 157959: contig of 1645 bp in length
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  US-09-528-682-4 x AC094036
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VERSION X77733.1 GI:456671
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SOURCE bread wheat.
ORGANISM Mitochondrion Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
Breiman,A.
REFERENCE 1 (bases 1 to 1159)
AUTHORS Direct Submission
TITLE Submitted (17-FEB-1994) A. Breiman, Tel Aviv University, Tel Aviv,
JOURNAL 69978, ISRAEL
2 (bases 1 to 1159)
AUTHORS Elkeles,A., Devos,K.M., Graur,D., Zizi,M. and Breiman,A.
TITLE Multiple cDNAs of wheat voltage-dependent anion channels (VDAC):
isolation, differential expression, mapping and evolution
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seq_documentation_block:	10328 bp	DNA linear	BCT 28-MAR-2001
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VERSION			
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SOURCE	Caulobacter crescentus		
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REFERENCE	1 (bases 1 to 10328)		
AUTHORS	Nierman, W.C., Feldblyum, T.V., Laub, M.T., Paulsen, I.T., Nelson, K.E., Eisen, J., Heidelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Venter, J.C., Shapiro, L. and Fraser, C.M.		
TITLE	Complete genome sequence of Caulobacter crescentus		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (7), 4136-4141 (2001)		
MEDLINE	21173698		
REFERENCE	2 (bases 1 to 10328)		
AUTHORS	Nierman, W.C., Feldblyum, T.V., Paulsen, I.T., Nelson, K.E., Eisen, J., Heidelberg, J.F., Alley, M.R.K., Ohta, N., Maddock, J.R., Potocka, I., Nelson, W.C., Newton, A., Stephens, C., Phadke, N.D., Ely, B., Laub, M.C., DeBoy, R.T., Dodson, R.J., Durkin, A.S., Gwinn, M.L., Haft, D.H., Kolonay, J.F., Smit, J., Craven, M., Khouri, H., Shetty, J., Berry, K., Utterback, T., Tran, K., Wolf, A., Vamathevan, J., Ermolaeva, M., White, O., Salzberg, S.L., Shapiro, L., Venter, J.C. and Fraser, C.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (31-JAN-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA		
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ORIGIN

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1653 CCAGGAACCTTCAACCTGTTGCGCAACACACACACCCCGGCCCA 1604

23 heLeuAsnMetGlyAsnGlu.....ValAlaLeuAspGlyArgTyr 36

1603 AGATCCAGCTGGGTGACGGCGAGCAGTACCTGCTGCTGGACGCGCTC 1554

37 SerAsnTyrAlaLeu.....IleSerAlaGluClyGlyMetA 49

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1453 GCCGCGACCGCCCTGACCGCGAGCGTTTCGGTGATCTGGGCTAT 1404

62 ProGluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAs 78

1403 CCGCGCGTGGTGGTCTG.....CTGCGCTGCAAC.....CTGCGCGA 1366

78 pThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleL 95

1365 CACCACCGACCTCGAGCAG.....TTCACCGACGAACTGC 1331

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seq_documentation_block:

LOCUS U39725 12844 bp DNA linear BCT 19-OCT-2000
DEFINITION Mycoplasma genitalium section 47 of 51 of the complete genome.

ACCESSION U39725 U39730 L43967

VERSION U39725.1 GI:3845017

KEYWORDS

SOURCE Mycoplasma genitalium.

ORGANISM Mycoplasma genitalium.

REFERENCE 1 (bases 1 to 12844)

1 (bases 1 to 12844)

Fraser, C.M., Gocayne, J.D., White, O., Adams, M.D., Clayton, R.A.,

Fleischmann, R.D., Bult, C.J., Kerlavage, A.R., Sutton, G.G.,

Kelly, J.M., Fritchman, J.L., Weidman, J.F., Small, K.V., Sandusky, M.,

Fuhrmann, J.L., Nguyen, D.T., Utterback, T., Saudek, D.M.,

Phillips, C.A., Merrick, J.M., Tomb, J., Dougherty, B.A., Bott, K.F.,

Hu, P.C., Lucier, T.S., Peterson, S.N., Smith, H.O. and Venter, J.C.

The minimal gene complement of Mycoplasma genitalium

Science 270 (5235), 397-403 (1995)

96026346

2 (bases 1 to 12844)

Fraser, C.M., Gocayne, J.D., White, O., Adams, M.D., Clayton, R.A.,

Fleischmann, R.D., Bult, C.J., Kerlavage, A.R., Sutton, G.G.,

Kelly, J.M., Fritchman, J.L., Weidman, J.F., Small, K.V.,

Sandusky, M., Fuhrmann, J.L., Nguyen, D.T., Utterback, T.R.,

Saudek, D.M., Phillips, C.A., Merrick, J.M., Tomb, J.-F.,

Dougherty, B.A., Bott, K.F., Hu, P.-C., Lucier, T.S., Peterson, S.N.,

Smith, H.O., Hutchinson, C.A. III and Venter, J.C.

Direct Submission

Submitted (29-Oct-1995) The Institute for Genomic Research, 9712

Medical Center Drive, Rockville, MD 20850, USA

3 (bases 1 to 12844)

Fraser, C.M., Gocayne, J.D., White, O., Adams, M.D., Clayton, R.A.,

Fleischmann, R.D., Bult, C.J., Kerlavage, A.R., Sutton, G.G.,

Kelly, J.M., Fritchman, J.L., Weidman, J.F., Small, K.V., Sandusky, M.,

Fuhrmann, J.L., Nguyen, D.T., Utterback, T., Saudek, D.M.,

Phillips, C.A., Merrick, J.M., Tomb, J.-F., Dougherty, B.A., Bott, K.F.,

TITLE
JOURNAL

Submitted (19-Oct-1998) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA

COMMENT
On Oct 19, 2000 this sequence version replaced gi:1046149

FEATURES

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE AUTHORS

1 (bases 1 to 19894)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Alsbrooks, S.L., Anaratunge, H.C., Are, J.R., Banks, T., Barbara, J.,
Bentons, J., Blinag, K., Blankenburg, K., Bonnin, D., Bouck, J.,
Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
Chen, Z., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Cher, M., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,
Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,
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Hamilton, K., Harris, C., Harris, K., Hart, M., Haviak, P., Hawes, A.,
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Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
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Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,
Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
Ogulu, M., Okunolu, O., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L.,
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Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S.,
Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 19894)
Worley, K.C.

Direct Submission
Submitted (24-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GJSR
Center clone name: CH230-133B12
----- Summary Statistics
Sequencing vector: Plasmid; M7789
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 43731 bases at least Q40
Consensus quality: 50503 bases at least Q30
Consensus quality: 55212 bases at least Q20
Estimated insert size: 31598; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0.3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces

TITLE JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 2635: contig of 2635 bp in length
2636 2735: gap of unknown length
2736 6146: contig of 3411 bp in length
6147 6246: gap of unknown length
6247 8732: contig of 2486 bp in length
8733 8832: gap of unknown length
8833 10847: contig of 2015 bp in length
10848 13180: contig of 2233 bp in length
13181 13280: gap of unknown length
13281 15312: contig of 2032 bp in length
15313 15412: gap of unknown length
15413 17562: contig of 2150 bp in length
17563 17662: gap of unknown length
17663 19894: contig of 2232 bp in length.

FEATURES

source

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/clone="CH230-133B12"

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ORIGIN

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Ratio: 1.075 Gaps: 4

Percent Similarity: 48.551 Percent Identity: 23.913

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38 AsnTyrAlaLeuIleSerAlaGluGlyMetAspArgAspLeuPheG1 54
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87 pAlaAspPheLysLysTyrIleLysLeuLeuIleAsnAspGlyPheP 104
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seq_name: gb_pl:SPAC4G8

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 DEFINITION S.pombe chromosome I cosmid c4G8.
 ACCESSION Z56276
 VERSION Z56276.2 GI:4584696
 KEYWORDS condensation-specific protein homologue; leucyl tRNA synthetase;
 MAK32 homologue; mitochondrial carrier protein; nuclease;
 regulatory protein; SEC61 homologue; serine threonine protein
 kinase; SMP3 homologue; zinc finger protein.
 fission yeast.

SOURCE

ORGANISM Schizosaccharomyces pombe

Eukaryote; Fungi; Ascomycota; Schizosaccharomycetes;

Schizosaccharomycetales; Schizosaccharomycetaceae;

Schizosaccharomycetes.

1 (bases 1 to 36776)

Badcock,K., Churcher,C.M., Barrell,B.G., Rajandream,M.A. and

Walsh,S.V.

Direct Submission

Submitted (16-OCT-1995) Schizosaccharomyces pombe chromosome I
 sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge
 CB10 1RQ E-mail: barrell@sanger.ac.uk

On Apr 14, 1999 this sequence version replaced gi:1022345.

Notes:

Details of yeast sequencing at the Sanger Centre are available on
 the World Wide Web.

(URL, <http://www.sanger.ac.uk/Projects/S-pombe>)

Protein coding regions (CDS) have been predicted with the help of
 computer analysis using the GeneFinder program in Pombase (an ACEDB
 database) with additional predictions for the branch-acceptor sites
 supplied by the program Sp3splice. CAUTION: It is possible that for
 any individual CDS we may have underestimated or overestimated the
 number of introns/exons or we may not have chosen the correct
 splice donor/acceptor sites.

CDS are numbered using the following system eg SPAC5H10.01c. SP (S.
 pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c
 (complementary strand).

The more significant matches with motifs in the PROSITE database
 are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the

sequenced clone. It may be shorter because we only sequence

overlapping sections once, or longer, because we arrange for a

small overlap between neighbouring submissions.

Cosmid c4G8 overlapped by c22G7, EMBL:SPAC22G7, Z54328, at the 5',

end and c16C9, EMBL:SPAC16C9, Z54366, at the 3' end.

FEATURES

source

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/note="SPAC4G8.01c, len85, low similarity to N-term of N.

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/note="nominal overlap with SPAC22G7, EM:254328 S. pombe

chromosome 1"

complement(join(1352..1364,1533..1635,1743..1839))

/gene="SPAC4G8.02c"

complement(join(1352..1364,1533..1635,1743..1839))

/gene="SPAC4G8.02c"

/note="SPAC4G8.02c, len:70, SIMILARITY:Canis familiaris,

S61G-CANFA, protein transport protein sec61 gamma

subunit., (68 aa), fasta scores: opt: 245, E():5.6e-13,

(49.3% identity in 67 aa)"

/codon_start=1

/label="SPAC4G8.02c"

/product="putative protein transport protein sec61-gamma

subunit"

/protein_id="CAA91203.1"

/db_xref="GI:1022347"

/db_xref="SWISS-PROT:Q09827"

/translation="MADNADDLFOIPKMFYKSGSHFIKRCVKPDRKEFLSISKAVATG

FVLMGLIGYIIKLHIPIKVLVGA"

complement(1365..1382)

/gene="SPAC4G8.02c"

/note="splice branch and acceptor sequence,

tactaataataatat tag"

complement(1365..1532)

/gene="SPAC4G8.02c"

/note="confirmed intron"

complement(1527..1532)

/gene="SPAC4G8.02c"

/note="splice donor sequence, gtaagt"

complement(join(1532..1635,1743..1800))

/gene="SPAC4G8.02c"

/note="Match to PF00584 SecE, SecE/Sec61-gamma subunits of

protein translocation complex Score 57.34"

complement(1636..1649)

/gene="SPAC4G8.02c"

/note="splice branch and acceptor sequence,

tactaataagaacag"

complement(1636..1742)

/gene="SPAC4G8.02c"

/note="confirmed intron"

complement(1737..1742)

/gene="SPAC4G8.02c"

/note="splice donor sequence, gtagag"

complement(2962..5304)

/gene="SPAC4G8.03c"

complement(2962..5304)

/gene="SPAC4G8.03c"

/note="SPAC4G8.03c, len:780,

SIMILARITY:Schizosaccharomyces pombe, YDHE_SCHPO,

hypothetical 73.3 kd protein c699.14 in chromosome 1.,

(681 aa), fasta scores: opt: 858, E():0, (32.3% identity

in 598 aa)"

/codon_start=1

/label="SPAC4G8.03c"

/product="pumilio domain containing protein"

/protein_id="CAA91204.1"

/db_xref="GI:1022348"

/db_xref="SWISS-PROT:Q09829"

/translation="MVNRDAYNELNLNKKSOETNRKPSPLSYTSISRELDYANOSPF

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FPSSVTVSPSEETPLTSGMKNKSVEHYFTLSESAISSSHKSSIPERNFSSVSVN

PLLHWNNDVTLRLDPSLENVANSRQDLQPYKTFSTISNSDFLHRESSFSLDDEES

KLASLRNUNIDRPLVYLKNSERLRLQLLNHPFSSQNNVSTNSKNYSTDFTK

IQSSSLIQNRQNRHRIETDLSHPDHLDPSPSPSPSPSPSPSPSPSPSPSPSPSP

SKKLNSQLNPILRSENVLDNHHSLSDMDNPTNVSTKNRNNQTVGEHPYVDNK

KKKGPAPKEKATLGKTVNSFFGSHSTSNYSKVLAKLTGEKSDLSLLKNGKK

KSDNQIPHLVGLHSLTICKQYGRYLRQLLDENPKVNASLFFPIRQSVQVLM

DPFGNMQCKLFVYASRQKLSMLNGIGEVLDICSNLYGTRSMQNIKDTSVQVLM

LLKLTIPSLTTLACDNNHTVLQKCIAPFPEKLEPLFLSNEENLITLATNRHGCCI

LQCLDRNTGDIQERLVNSIIKSCULLVQNAVGNVYLVQHVLELNIQPYTERIEFFG

OM of: US-09-528-682-4 to: N_Geneseq_032802: * out_format : pfs

Date: Jun 18, 2002 7:54 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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-O=/cgn2_1/USPTO.spool/US09528682/runat_18062002_082444_7843/app_query.fasta_1.689
-DB=N_Geneseq_032802 -QPMT=fastap -SUFFIX=p2n.rng -GAPOP=12.000
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-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LISP=1000 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL -OUTFMT=pfs
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-528-682-4

Query length: 110

Database: N_Geneseq_032802: *

Database sequences: 1736436

Database length: 85845721

Search time (sec): 554.690000

score_list:

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/SID55/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AAV25018	61.00	117.35	344.96	23	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AAH567818	60.00	108.73	1.0e+03
/SID55/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV25018	61.00	115.39	443.36	28	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AAH567818	60.00	108.73	1.0e+03
/SID55/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV25018	61.00	115.39	443.36	28	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AAH567818	60.00	108.73	1.0e+03
/SID55/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV25018	61.00	113.81	542.92	33	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AAH567818	60.00	108.73	1.0e+03
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:ABR45476	61.00	113.23	584.93	33	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AAH567818	60.00	108.73	1.0e+03
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:ABR45476	61.00	112.48	644.20	33	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AAH567818	60.00	108.73	1.0e+03
/SID55/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAH14547	61.00	103.81	2.0e+03	87	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	108.15	1.1e+03
/SID55/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAH25091	61.00	103.81	2.0e+03	87	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	107.39	1.2e+03
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:ABR45476	61.00	93.45	7.4e+03	2	/SID55/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:AAH567818	60.00	107.30	1.3e+03
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:ABR45476	61.00	86.90	1.7e+04	2	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH567818	60.00	107.06	1.3e+03
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH68398	61.00	65.21	2.7e+05	3	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AAH567818	60.00	106.72	1.3e+03
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH68398	61.00	65.21	2.7e+05	3	/SID55/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:AAH567818	60.00	99.99	3.2e+03
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
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/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
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/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
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/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00	90.45	1.1e+04
/SID55/gcgdata/geneseq/geneseqn-emb1/NA2000A.DAT:AAH68398	60.50	128.52	82.29	73	/SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH567818	60.00</		

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/SID55/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:AAO241170 +	59.00	100.77	2.9e+03	72	/SID55/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAO13237 -	58.50	106.05	1.5e+03
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/SID55/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:AAO66626 +	59.00	100.77	2.9e+03	72	/SID55/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:AAO33524 +	58.50	105.60	1.6e+03
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/SID55/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:AAO36651 +	59.00	100.74	2.9e+03	73	/SID55/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAO298281 +	58.50	105.60	1.6e+03
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/SID55/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:AAO66631 +	59.00	100.63	2.9e+03	73	/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABO25867 +	58.50	103.16	2.1e+03
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/SID55/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAO16961 +	59.00	100.40	3.0e+03	75	/SID55/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:AAO41967 -	58.50	95.13	6.0e+03
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/SID55/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAO16937 +	59.00	100.37	3.1e+03	76	/SID55/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:AAO10190 +	58.50	87.22	1.6e+04
/SID55/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:AAO66629 +	59.00	100.16	3.1e+03	77	/SID55/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAO9469 +	58.50	79.20	4.6e+04
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/SID55/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAO57904 +	59.00	98.20	4.0e+03	93	/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABO25063 +	58.00	119.51	261.34
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/SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:ABO13578 +	59.00	94.06	6.8e+03	11	/SID55/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:ABO47072 +	58.00	119.32	267.93
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seq_documentation_block:

XX AAF28528:

04-APR-2001 (first entry)

Genomic fragment #15.

Genomic library; bacte

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XX

TAYLOR & FRANCIS

Taylor & Francis

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DT
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Diet + C
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XX
WPT: 2001-041437/05

Genomic library for identifying diagnostic and therapeutic

PT elements and drug targets, comprises Moraxella catarrhalis nucleic acid compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic acid compositions.

XX PS Claim 1; Page 128-135; 545pp; English.

The present invention relates to *Moraxella catarrhalis* genomic library comprising a combination of 41 nucleic acid molecules (see AAF28514-AAF28559). The library has a number of uses described in the specification (e.g.) is useful for identifying diagnostic and therapeutic associations. *M. catarrhalis* (*Branhamella catarrhalis*) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. *M. catarrhalis* is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary

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Ratio:	1.397	Gaps:
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alignment_block:
US-09-528-682-4 x AAF28544

Align seg 1/1 to: AAF28544 from: 1 to: 65792

PT synthetase - useful to diagnose, treat or prevent bacterial
XX infection, especially meningitis

PS Claim 4; Page 37-38; 44pp; English.

XX The present sequence encodes alanyl tRNA synthetase (alas) from
CC Streptococcus pneumoniae. The polynucleotide encoding alas can be used
CC for the recombinant production of alas, which can be used to treat
CC conditions requiring alas activity. Sequences antisense to the
CC polynucleotide can be used to control alas expression. Alas, or alas
CC expressing vectors can be used to induce an immune response, i.e. an
CC antibody (Ab) and/or T cell response, against S. pneumoniae to protect
CC against infection, or to screen for antagonists or agonists of the
CC polynucleotide encoding alas or alas's activity, i.e. antibacterials.
CC The antagonist, e.g. an anti-alas Ab, can be used to treat conditions
CC requiring alas inhibition, e.g. an S. pneumoniae infection, particularly
CC meningitis. A fragment of the polynucleotide encoding alas can be used as
CC a probe to isolate full length or related sequences, or diagnose, e.g.
CC by polymerase chain reaction, infection stage and type, including
CC mutation and polymorphism detection. Diagnosis may also be achieved by
CC detecting alas gene overexpression, e.g. by immunoassay. The Ab can be used
CC to treat infection, isolate or identify alas expressing clones, purify
CC alas and as an immunoassay reagent. More generally, the products can
CC prevent adhesion of bacteria to wounds and in dwelling devices, block
CC alas protein mediated invasion of mammalian cells and block the normal
CC progression of infection.

SQ Sequence 2619 BP; 766 A; 570 C; 607 G; 676 T; 0 other;

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30  lAlaLeuAspGlyArgTyrSerAsn...TyrAlaLeuIleSerAlaGluG 46
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1990 AGTCACCGATATCTACGACACCAAGTCCCTGCCGTATTCACCGAAG 1941
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1940 AGGCGGATAGCTCCCATTTCTTTAGCAGTGTCAATATC..... 1903
    ::::::::::|
63  GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
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79  rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96
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seq_documentation_block:

ID AAA60446 standard; cDNA: 6585 BP.

XX AAA60446;

XX 09-OCT-2000 (first entry)

XX

DE Murine factor V encoding cDNA SEQ ID NO:4.

XX Murine; factor V; FV; activated protein C; APC; anticoagulant;
KW activated protein C resistant factor V; thrombosis; screening;
KW thrombophilia; ds.

OS Mus sp.

XX Key Location/Qualifiers

FT CDS 6..6557

FT /*tag= a

FT /product= "Factor V"

PN US6066778-A.

PD 23-MAY-2000.

XX 06-NOV-1996; 96US-0746111.

XX 06-NOV-1996; 96US-0746111.

XX (UNMI) UNIV MICHIGAN.

XX Ginsburg D, Cui J;

XX WPI; 2000-410682/35.

XX P-PSDB; AAB03533.

XX New transgenic mice expressing activated protein C resistant factor V
PT and factor V null transgenic mice useful for screening anticoagulants,
PT as models for human thrombophilia and as models for testing in utero
PT gene therapy protocols -

XX Example 1; Fig 2; 76pp; English.

XX The present invention describes transgenic mice (I) and (II) containing
CC modifications in the factor V gene, where (I) expresses an activated
CC protein C (APC) resistant factor V and (II) lacks the ability to express
CC wild-type factor V. The transgenic animals (I) and (II) are useful for
CC screening compounds with anticoagulant activity. Methods from the present
CC invention, and the transgenic animals, are also useful in providing
CC models for human thrombophilia. These models are useful in providing
CC insight into the basic regulatory mechanisms of blood coagulation and
CC pathogenesis of human thrombosis. In addition, factor V null transgenic
CC mice, especially pregnant females may be used as a model system to test
CC in utero gene replacement therapy protocols. The present sequence
CC encodes murine factor V, which is used in an example from the present
CC invention.

SQ Sequence 6585 BP; 1946 A; 1675 C; 1432 G; 1532 T; 0 other;

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Ratio: 1.169 Gaps: 4
Percent Similarity: 61.321 Percent Identity: 25.472

alignment_block:

US-09-528-682-4 x AAA60446 ..

Align seg 1/1 to: AAA60446 from: 1 to: 6585

```

1  AspTyrPheThrValArgIleGlnAspAlaTyrGluProIleAlaAsnTh 17
    ||||| ::::::::::|
2058 GATTATGACANTGAGGACTCATATGAGNTTATGAACCTCTCGACCTAC 2107
    ::::::::::|
17  rAsnThrThrThrGlnPheLeu.....AsnMetGlyAsnGluValAlaL 32
    ::::::::::|
2108 ATCCATGACAACTCGGAGAAATTCATGATTCCTTAGAATAATGATTTGGCA 2157
    ::::::::::|
32  euAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyMet 48
    ::::::::::|
2158 TAGACAACGAAGATGATGATTACCACTACTTACTGCGGTTCATCATTTAGGA 2207
    ::::::::::|

```


CC nucleic acid may be used in expression vectors for gene therapy to
CC potentiate the immunosuppressive effects of immunosuppressant drugs.
CC This DNA may be expressed recombinantly to prepare a CNI protein
CC and also be used to form a fusion protein which consists of a CNI
CC subunit and this CNI polypeptide.
XX
SQ Sequence 3500 BP; 1135 A; 754 C; 605 G; 1006 T; 0 other;

alignment_scores:
Quality: 74.50 Length: 95
Ratio: 1.330 Gaps: 2
Percent Similarity: 58.947 Percent Identity: 26.316

alignment_block:

US-09-528-682-4 x AAT18500 ..

Align seg 1/1 to: AAT18500 from: 1 to: 3500

13 ProIleAlaAsnThrAsnThrThrThrGlnPheLeuAsnMetGlyAsnG1 29

2650 CCGAGTGAGACGCTTAATTCACACACTCTCTATTTTGCAGTCTTTAAAC... 2697

29 uValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluG 46

2698 .ATGAGTCTTGATGGGAGAAAAAATCGCCAGCTACAGCGCAACAT 2746

46 lYcGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePro 62

2747 CAGTGTCTTACTAGTACATAAAGACAGAACAA... 2778

63 GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79

2779CAGATTTCATGACATAAACACAGATCTAGGAGTAGTACCGA 2822

79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96

2823 AGATGCTTTCCCAAGGCAATCATTAATTTCAATAAGAACTACCAA 2872

96 eUleuIleAsnAsnAspGlyPhePheSerAsnAsn 107

2873 TACTTAAATTAATGATAACGTCATACAATCAAAAC 2907

seq_name: /SID85/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:AAQ57972

seq_documentation_block:

ID AAQ57972 standard; DNA; 3300 BP.

XX AC AAQ57972;

XX DT 14-SEP-1994 (first entry)

XX DE rsaA gene.

XX KW C. crescentus; rsaA; paracrystalline; S-layer; protein; heterologous;

KW cellulase; xylase; metallothionein; restriction site;

KW reading frame; fusion protein; bioreactor; toxic metal; sewage;

XX waste water; wood pulp suspension; cell surface; vaccine; fish; ss.

OS Caulobacter crescentus.

XX PH key Location/Qualifiers

FT -35_signal 4..7 /tag= a

FT -10_signal 28..31 /tag= b

FT RBS 88..92 /tag= c

FT CDS 101..3181 /tag= d

FT /product= rsaA protein

FT 3223..3258

FT terminator

FT /tag= e

FT /rpt_type= TERMINAL

XX CA2090549-A.

XX 10-DEC-1993.

XX 26-FEB-1993; 93CA-2090549.

XX 09-JUN-1992; 92US-0895367.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Bingle WH, Smit J;

XX WPI; 1994-066249/09.

XX P-PSDB; AAR48993.

XX Prodn. of heterologous polypeptides in bacteria, partic.
PT Caulobacter - by expression of a fusion prod. of the polypeptide
PT sequence and a bacterial S-layer protein gene
XX
PS Claim 17; Fig 6; 27pp; English.

XX This sequence represents the C. crescentus rsaA gene which encodes
CC the paracrystalline S-layer protein. This gene was used in the
CC production of the heterologous protein of the invention. The
CC heterologous protein is produced by cloning a polypeptide coding
CC sequence, eg cellulase, xylase or a metallothionein, into a
CC restriction site within the rsaA gene which preserves the rsaA reading
CC frame and expressing the fusion sequence in Caulobacter. This S-
CC layer protein bacterial system can be used in bioreactors, eg. to
CC bind toxic metals in sewage waste water etc. or for the treatment of
CC wood pulp suspensions. The system can be used to produce heterologous
CC proteins at the cell surface for use in vaccines, partic. fish
CC vaccines. The S-layer protein is synthesised in large quantities and
CC has a general repetitive sequence, permitting the synthesis of large
CC amounts of heterologous protein as a fusion product and presentation at
CC the cell surface.
XX
SQ Sequence 3300 BP; 548 A; 1238 C; 985 G; 529 T; 0 other;

alignment_scores:

Quality: 74.00 Length: 112

Ratio: 1.194 Gaps: 5

Percent Similarity: 55.357 Percent Identity: 28.571

alignment_block:

US-09-528-682-4 x AAQ57972 ..

Align seg 1/1 to: AAQ57972 from: 1 to: 3300

1 AspTyrPheThrValArgIleGlnAspAlaTyrGluProIleAlaAsnTh 17

608 GACTACTGACCGCCTTCGTGCGC.....GCCAACAC 639

17 rAsn...ThrThrThrClnPheLeuAsnMetGlyAsnGluValAlaLeuA 33

640 GCGGTTCACGGCGCGCCGACATCGATCTCGCGCTCAAGGCGCCCTGA 689

33 spGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGly..... 47

690 TCGGCACCATCTCTGAACGCCGCCACCGGTGTCGGGCATCGGTGTACGCG 739

48MetAspArgAspLeuPhe...GlySerAlaAsnI1 58

740 ACCGCCACCGCGCGATGATCAACGACCTGTCGGACGCGCCCTGTGCGAG 789

58 eAspGlyPheProGluValArgGluPheAsnSerLeuProAsnAsnLysA 75

790 CGAACACGGCGGTGGCGTGAACTGTTTACCCGCTATCCGTCGTCGGCGG 839

75 laSerSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLys 91


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PR 07-OCT-1998; 98US-0167568.
XX 08-DEC-1998; 98US-0206942.
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Loosmore SM, Yang Y, Klein MH;
XX
XX WPI; 2000-303789/26.
DR P-PSDB; AAB01837.
XX
XX Nucleic acid molecule for producing recombinant high molecular weight
PT proteins of Haemophilus which are used as a vaccine to provide
PT protection against Haemophilus induced diseases in humans -
XX
PS Claim 7; Fig 23A-P; 307pp; English.
CC
CC The invention relates to the recombinant production of Haemophilus
CC influenzae high molecular weight (HMW) proteins in Escherichia coli. The
CC expression construct used to effect recombinant expression comprises a
CC promoter functional in E. coli (e.g., the T7 promoter) operably linked
CC to a modified hmWABC operon from a non-typeable (non-encapsulated) H.
CC influenzae (NTHi). Most HMW-expressing NTHi strains contain two hmw gene
CC clusters termed hmw1ABC and hmw2ABC. Each hmWABC operon comprises hmWA,
CC hmWB and hmWC genes. The hmWA genes encode the structural HMWA proteins
CC and the hmWB and hmWC genes encode accessory proteins which are
CC responsible for post-translational processing and secretion of the HMWA
CC proteins. The modified hmWABC operon used in the expression construct of
CC the invention contains an A gene modified such that it encodes only the
CC mature HMWA. The invention also discloses hmWA genes (AAAS2175-A52198)
CC and HMWA proteins (AAB01824-B01849) from the non-typeable H. influenzae
CC strains Joysc, KI, K21, LDC2, PMH1, 15 and 12. The nucleic acids and
CC vectors are used for the production of recombinant H. influenzae HMW
CC proteins which can be used as vaccines to mediate a humoral or
CC cell-mediated immune response to provide protection against diseases in
CC humans caused by H. influenzae (e.g., otitis media, epiglottitis,
CC pneumonia and tracheobronchitis). The HMW proteins are also useful as
CC antigens in immunoassays for detecting antibodies against Haemophilus,
CC HMW proteins and/or HMW peptides. The nucleotide sequences encoding the
CC HMW proteins can be used to isolate and clone hmw genes from other
CC non-typeable strains of Haemophilus via hybridisation reactions. The
CC present sequence represents a modified NTHi hmWA gene encoding a mature
CC HMWA protein.
XX
SQ Sequence 3222 BP; 1179 A; 599 C; 659 G; 785 T; 0 other;

alignment_scores:
  Quality: 73.00 Length: 82
  Ratio: 1.352 Gaps: 3
  Percent Similarity: 65.854 Percent Identity: 28.049

alignment_block:
US-09-528-682-4 x AAAS2186 ..
Align seg 1/1 to: AAAS2186 from: 1 to: 3222
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||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
508 AACAAATGTGCTTTAAATGGAGCGGGTAAAGTCTAAGTATTATTCAAC 557
44 aGluGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyP 61
:||||:||||:||||:||||:||||:||||:||||:||||:||||:
558 AGCAAGCAATTTATCATAGACTTGACGGTGAATTAATGATCTGGAA 607
61 heProGluValArgGluPhe.....AsnSerLeuProAsnAsnLysAla 75
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
608 ATGTAACAATTAATCAACACCGACGCAAAACATTCGAATCTGGAAGCT 657
76 SerSerAspThr.....AlaSerLeuAsnLysGlnHisAspAl 88
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
658 AGCAGCGATTCATTATGGAAATGTCATCTCTTTAAATTTGAGAGAATTC 707
88 aAspPheLys.....LysTyrIleLysLeuLeuIleAsnAsnAsp 101
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seq_name: /SIDSS/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAAS2185
seq_documentation_block:
ID AAAS2185 standard; DNA; 3240 BP.
XX
AC AAAS2185;
XX
DT 11-SEP-2000 (first entry)
XX
DE Haemophilus influenzae strain LDC2 hmW2A gene, SEQ ID NO:46.
XX
KW HMW protein; hmW gene; hmWA1; hmWA2; high molecular weight;
KW non-typeable Haemophilus influenzae; NTHi; non-encapsulated;
KW recombinant production; Escherichia coli; antibacterial; vaccine;
KW human disease; otitis media; epiglottitis; pneumonia; tracheobronchitis;
KW detection; diagnosis; ds.
XX
OS Haemophilus influenzae strain LDC2.
XX
PN WO200020609-A2.
XX
PD 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-CA00938.
XX
PR 07-OCT-1998; 98US-0167568.
PR 08-DEC-1998; 98US-0206942.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Loosmore SM, Yang Y, Klein MH;
XX
XX WPI; 2000-303789/26.
DR P-PSDB; AAB01836.
XX
XX Nucleic acid molecule for producing recombinant high molecular weight
PT proteins of Haemophilus which are used as a vaccine to provide
PT protection against Haemophilus induced diseases in humans -
XX
PS Claim 12; Fig 23A-P; 307pp; English.
CC
CC The invention relates to the recombinant production of Haemophilus
CC influenzae high molecular weight (HMW) proteins in Escherichia coli. The
CC expression construct used to effect recombinant expression comprises a
CC promoter functional in E. coli (e.g., the T7 promoter) operably linked
CC to a modified hmWABC operon from a non-typeable (non-encapsulated) H.
CC influenzae (NTHi). Most HMW-expressing NTHi strains contain two hmw gene
CC clusters termed hmw1ABC and hmw2ABC. Each hmWABC operon comprises hmWA,
CC hmWB and hmWC genes. The hmWA genes encode the structural HMWA proteins
CC and the hmWB and hmWC genes encode accessory proteins which are
CC responsible for post-translational processing and secretion of the HMWA
CC proteins. The modified hmWABC operon used in the expression construct of
CC the invention contains an A gene modified such that it encodes only the
CC mature HMWA. The invention also discloses hmWA genes (AAAS2175-A52198)
CC and HMWA proteins (AAB01824-B01849) from the non-typeable H. influenzae
CC strains Joysc, KI, K21, LDC2, PMH1, 15 and 12. The nucleic acids and
CC vectors are used for the production of recombinant H. influenzae HMW
CC proteins which can be used as vaccines to mediate a humoral or
CC cell-mediated immune response to provide protection against diseases in
CC humans caused by H. influenzae (e.g., otitis media, epiglottitis,
CC pneumonia and tracheobronchitis). The HMW proteins are also useful as
CC antigens in immunoassays for detecting antibodies against Haemophilus,
CC HMW proteins and/or HMW peptides. The nucleotide sequences encoding the
CC HMW proteins can be used to isolate and clone hmw genes from other
CC non-typeable strains of Haemophilus via hybridisation reactions. The
CC present sequence represents an hmWA gene from a non-typeable strain of H.
CC influenzae.
XX
SQ Sequence 3240 BP; 1185 A; 600 C; 665 G; 790 T; 0 other;
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alignment_scores:
  Quality: 73.00      Length: 82
  Ratio: 1.352        Gaps: 3
  Percent Similarity: 65.854  Percent Identity: 28.049

alignment_block:
US-09-528-682-4 x AAA52185 ..
Align seg 1/1 to: AAA52185 from: 1 to: 3240

28 AsnGluValAlaLeuAspGlyArgTySerAsnTyrAlaLeuLeuSerAl 44
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
526 AACAAATGCTTTAAATGGACGGGTAATGGTCTAAGTATTATTTCAC 575
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
44 aGluGlyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGly 61
:||||:||||:||||:||||:||||:||||:||||:||||:||||:
576 AGCAAGCAATTTATCTCATGACTTGACGGTGAAATTAATGTATCTGAA 625
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
61 heProGluValArgGluPhe.....AsnSerLeuProAsnAsnLysAla 75
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
626 ATGTAACAATTAATCAACACGACGACAAACATTTGATCTGCAAGGCT 675
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
76 SerSerAspThr.....AlaSerLeuAsnLysGlnHisAspAl 88
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
676 AGCAGCGATTCTTATGGAATGTCTACTCTTTTAAATTTGAGAGAAGATC 725
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
88 aAspPheLys.....LysTyrIleLysLeuLeuIleAsnAsnAsp 101
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
726 AAGTTTACCTTTATCAATACGTTAACTCTGCCAGAAATGGTGAT 771
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AA58840
seq_documentation_block:
ID AAT58840 standard; DNA; 580073 BP.
XX
AC
AT58840;
XX
DT 27-MAR-1997 (first entry)
XX
DE Mycoplasma genitalium genome.
XX
KW M. genitalium; DNAA; DNA gyrase; origin of replication;
KW megabase shotgun sequencing method; open reading frame; ORF; ss.
XX
OS Mycoplasma genitalium.
XX
FH Key Location/Qualifiers
CDS 8552..9184
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FT /label= MG006
FT /note= "Previously identified as MORF-20076, the
FT encoded protein shows 27.59 percentage
FT identity to thymidylate kinase (CDC8)
FT from Saccharomyces cerevisiae"
CDS 11252..12040
FT /*tag= b
FT /label= MG009
FT /note= "Previously identified as MORF-20078, the
FT encoded protein shows 35.43 percentage
FT identity to the Bacillus subtilis hypothetical
FT protein covered in accession number
FT GB:D26185_102"
CDS 12069..12725
FT /*tag= c
FT /label= MG010
FT /note= "Previously identified as MORF-20079, the
FT encoded protein shows 25.73 percentage
FT identity to DNA primase (dnaE) from
FT Clostridium acetobutylicum"
CDS complement (13570..14247)
FT /*tag= d
FT /label= MG012

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FT FT /note= "Previously identified as MORF-20080, the
FT encoded protein shows 31.50 percentage
FT identity to the ribosomal protein S6
FT modification protein (rimK) from Escherichia
FT coli"
FT complement (14396..15217)
FT /*tag= e
FT /label= MG013
FT /note= "Previously identified as MORF-19823, MORF-20080
FT and MORF-20081, the encoded protein shows 33.04
FT percentage identity to 5,10-methylene-tetra-
FT hydrofolate dehydrogenase (fold) from E. coli"
CDS 17474..19243
FT /*tag= f
FT /label= MG015
FT /note= "Previously identified as MORF-20084, the
FT encoded protein shows 32.23 percentage
FT identity to transport ATP-binding protein
FT (msbA) from E. coli"
CDS 26478..27344
FT /*tag= g
FT /label= MG023
FT /note= "Previously identified as MORF-20092, the
FT encoded protein shows 45.96 percentage
FT identity to fructose-bisphosphate aldolase
FT (tsr) from B. subtilis"
CDS 27345..28448
FT /*tag= h
FT /label= MG024
FT /note= "Previously identified as MORF-19826 and
FT MORF-20093, the encoded protein shows 46.84
FT percentage identity to GTP-binding protein
FT from E. coli"
CDS 36987..38978
FT /*tag= i
FT /label= MG032
FT /note= "Previously identified as MORF-20099, the
FT encoded protein shows 26.82 percentage
FT identity to ATP-dependent nuclease (addA)
FT from B. subtilis"
CDS 39242..39904
FT /*tag= j
FT /label= MG033
FT /note= "Previously identified as MORF-20100, the
FT encoded protein shows 35.90 percentage
FT identity to glycerol uptake facilitator
FT (glpF) from B. subtilis"
CDS complement (39873..40514)
FT /*tag= k
FT /label= MG034
FT /note= "Previously identified as MORF-20101, the
FT encoded protein shows 48.13 percentage
FT identity to thymidylate kinase (tdk)
FT from B. subtilis"
CDS 40543..41787
FT /*tag= l
FT /label= MG035
FT /note= "Previously identified as MORF-20102, the
FT encoded protein shows 30.71 percentage
FT identity to histidyl-trNA synthetase (hiss)
FT from Mycobacterium leprae"
CDS complement (44751..46277)
FT /*tag= m
FT /label= MG038
FT /note= "Previously identified as MORF-20105, the
FT encoded protein shows 46.83 percentage
FT identity to glycerol kinase (glpK)
FT from E. coli"
CDS complement (46268..47422)
FT /*tag= n
FT /label= MG039
FT /note= "Previously identified as MORF-19831 and
FT MORF-20106, the encoded protein shows 43.20

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FT      percentage identity to glycerol-3-phosphate
FT      dehydrogenase (GUT2) from S. cerevisiae"
FT      49377..49643
FT      /*tag= O
FT      /label= MG041
FT      /note= "The encoded protein shows 48.86 percentage
FT      identity to phosphohistidinoprotein-hexose
FT      phosphotransferase (ptsH) from Mycoplasma
FT      capricolum"
FT      CDS
FT      50060..51520
FT      /*tag= P
FT      /label= MG042
FT      /note= "Previously identified as MORF-19832 and
FT      MORF-20108, the encoded protein shows 41.92
FT      percentage identity to spermidine/
FT      putrescine transport ATP-binding protein
FT      (potA) from E. coli"
FT      CDS
FT      51525..52382
FT      /*tag= q
FT      /label= MG043
FT      /note= "Previously identified as MORF-20110, the
FT      encoded protein shows 26.51 percentage
FT      identity to spermidine/putrescine transport
FT      system permease protein (potB) from E. coli"
FT      CDS
FT      52366..53220
FT      /*tag= r
FT      /label= MG044
FT      /note= "Previously identified as MORF-20111, the
FT      encoded protein shows 29.45 percentage
FT      identity to spermidine/putrescine transport
FT      system permease protein C (potC) from E. coli"
FT      CDS
FT      54658..55605
FT      /*tag= s
FT      /label= MG046
FT      /note= "Previously identified as MORF-20112, the
FT      encoded protein shows 36.60 percentage
FT      identity to sialoglycoprotease (gcp)
FT      from Pasteurella haemolytica"
FT      CDS
FT      complement (56970..58310)
FT      /*tag= t
FT      /label= MG048
FT      /note= "Previously identified as MORF-19834,
FT      MORF-20114 and MORF-20115, the encoded protein
FT      shows 43.02 percentage identity to signal
FT      recognition particle protein (ffh) from B.
FT      subtilis"
FT      CDS
FT      58117..59079
FT      /*tag= u
FT      /label= MG049
FT      /note= "Previously identified as MORF-20114 and
FT      MORF-20115, the encoded protein shows 44.78
FT      percentage identity to purine-nucleoside
FT      phosphorylase (deod) from E. coli"
FT      CDS
FT      59083..59754
FT      /*tag= v
FT      /label= MG050
FT      /note= "Previously identified as MORF-20117, the
FT      encoded protein shows 83.03 percentage
FT      identity to deoxyribose-phosphate aldolase
FT      (deoc) from Mycoplasma pneumoniae"
FT      complement (64898..65731)
FT      /*tag= w
FT      /label= MG056
FT      /note= "Previously identified as MORF-20122, the
FT      encoded protein shows 30.25 percent
FT      identity to the protein disclosed in
FT      GB:D26185_99 from B. subtilis"
FT      CDS
FT      complement (65713..66249)
FT      /*tag= x
FT      /label= MG057
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FT      encoded protein shows 38.90 percentage
FT      identity to the protein disclosed in
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FT      81047..82597
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FT      /label= MG067
FT      /note= "Previously identified as MORF-19845, the
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FT      (SPase) from Staphylococcus aureus"
FT      CDS
FT      91065..91919
FT      /*tag= z
FT      /label= MG070
FT      /note= "Previously identified as MORF-20136, the
FT      encoded protein shows 34.8 percentage
FT      identity to ribosomal protein S2 (rps2)
FT      from Spirulina plantensis"
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FT      Quality: 72.00 Length: 129
FT      Ratio: 1.180 Gaps: 6
FT      Percent Similarity: 47.287 Percent Identity: 27.132
FT      alignment_block:
FT      US-09-528-682-4 x AAT58840/rev ..
FT      Align seg 1/1 to reverse of: AAT58840 from: 1 to: 580073
FT      7 IleGlnAspAlaTyrGluProIleAlaAsnThrAsnThrThrGlnPh 23
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      535817 APTTTTGATGCACATCCAAATCTTAATGATCCTACTATCAGCA 535768
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      23 eLeu.....AsnMetGlyAsnGluValAlaLeuAspG 34
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      535767 ATTAGAACAACTAAATAAACAATCCATCCTGTTATTGCTGATA 535718
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      34 lyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyGlyMetAspArg 50
FT      :: ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      535717 ATGTTTTTCAACAAACAGCTTTAATGTTTAGTGAA.....ATGGATGAT 535674
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      51 AspLeuPheGlySerAlaAsnIleAsp..... 59
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      535673 AGTATTTTAAAGAACGCCAGTCAGTATATATTAGATTTACACCAAGGCT 535624
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      60 ....GlyPheProGluValArgGluPheAsnSerLeu..... 70
FT      ::||| ||||| ||||| ||||| ||||| ||||| |||||
FT      535623 CTTAAGTTATTTAACCTGGAGTAGTAAACTTAATGATTTAATCAGGATTAAAA 535574
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      71 .....ProAsnAsnLysAlaSerSerAspThrAlaSer 81
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      535573 GTGATGTCATTATAGTAGCTAATGATTTAACACCAAGTCACACGCAACT 535524
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      82 LeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLeuLeuIle 98
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      535523 CTTAAT.....AAAAGATATGTCAG..... 535503
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      98 eAsnAsnAspGlyPhePheSerAsnAsnGlyGlyLys 110
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT      535502 .....GCTTTTAACTGAGAGTGGTGTAA 535476
FT      ||||| ||||| ||||| ||||| ||||| ||||| |||||
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FT      seq_documentation_block:
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FT      XX
FT      AC AAC90510;
FT      XX
FT      DT 15-MAR-2001 (first entry)
FT      XX
FT      DE Mouse factor VIII CDNA.
FT      XX
FT      KW Mouse; factor VIII; fVIII; coagulant; clotting factor; haemophilic;
FT      KW Immune detection evasion; ss.
FT      XX
FT      OS Mus musculus.
```


3793 GGTCTTAAAGACCAATGGAATAAATTCCTTGAACCTCTGAGCAAGAACAT 3842
 89 Asp.....PheLysLysTyrIle..... 94
 3843 AGTCCAAAGCAATTAGTATATTTAATGTTTAAAAAATATGTAATAATCA 3892
 95LysLeuLeuIleAsnAspGlyPheP 104
 3893 AAGTTTCTTGTGACAGAGAAAAAATAAGTCACAGTAGAACAGGATGGAATTA 3942
 104 heSerAsnAsnGlyGlyLys 110
 3943 CAAAGAACATAGGACTTAAA 3962

seq_name: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAx91164

seq_documentation_block:
 ID AAX91164 standard; cDNA to mRNA; 7493 BP.

AC AAX91164;
 XX
 DT 26-NOV-1999 (first entry)
 XX
 DE Mouse factor VIII protein encoding nucleotide sequence.
 XX
 KW Factor VIII protein; hybrid protein; porcine; mouse; immunogenicity;
 KW antigenic; procoagulant; factor X activation; haemophilia; human; ds.
 XX
 OS Mus musculus.
 XX
 PN W09946274-AL.
 XX
 PD 16-SEP-1999.
 XX
 PF 10-MAR-1999; 99WO-US05193.
 XX
 PR 10-MAR-1998; 98US-0037601.
 XX
 XX (UYEM-) UNIV EMORY.
 XX
 PI Lollar JS;
 XX
 DR WPI; 1999-551355/46.
 DR P-PSDB; AAY31596.
 XX
 PT New porcine and modified human factor VIII proteins for treating
 PT hemophilia -
 XX
 PS Examples; Page 131-136; 187pp; English.
 XX
 CC The invention provides DNA encoding porcine factor VIII, hybrid porcine
 CC /human factor VIII, or modified human factor VIII having reduced
 CC immunogenicity. Active factor VIII increases catalytic efficiency of
 CC factor IXa towards factor X activation. The factor VIII proteins of the
 CC invention can be produced by standard recombinant methodology and have
 CC less antigenic activity, or greater procoagulant activity, than prior art
 CC factor VIII. The invention is used to treat haemophilia. The present
 CC sequence represents the nucleotide sequence encoding the A and C domains
 CC of mouse factor VIII protein.
 XX
 SQ Sequence 7493 BP; 2487 A; 1503 C; 1436 G; 2067 T; 0 other;

alignment_scores:
 Quality: 71.50 Length: 140
 Ratio: 0.993 Gaps: 5
 Percent Similarity: 51.429 Percent Identity: 21.429

alignment_block:
 US-09-528-682-4 x AAX91164 ..

Align seg 1/1 to: AAX91164 from: 1 to: 7493

4 ThrValArgIleGlnAspAlaTyrGluProIle....AlaAsnThrAsnTh 19
 3543 ACAACAGACTTCAGATGCCATATATAAGTCATAGTACAGATTCACAAGA 3592
 19 rThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgT 36
 3593 AGTACAGCGCTTTCATTCATGATGGACACTTTTGTAGGCAAAAATCTACAT 3642
 36 Yr.....SerAsnTyrAlaLeuIleSerAlaGluGlyGlyMetAspArg 50
 3643 ATTGAGACTTAACCATATGCTAAATAGAACTACCTCAACAAAAATAAA 3692
 51 AspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgGluPh 67
 3693 GACATATTTCATAGAAAAGATGAAGATCCTATATCCACAAGATGAAGAGAA 3742
 67 eAsnSerLeuProAsnAsn..... 73
 3743 TACAATCATGCCATTTTCCAAAGATGTTGTTCTGTGAGAACTTCAAAT 3792
 74LysAlaSerSerAspThrAlaSerLeuAsnLysGlnHisAspAla 88
 3793 GGTTTAAAAAGCAATGGAATAATTCCTTGAACCTCTGAGCAAGAACAT 3842
 89 Asp.....PheLysLysTyrIle..... 94
 3843 AGTCCAAAGCAATTAGTATATTTAATGTTTAAAAAATATGTAATAATCA 3892
 95LysLeuLeuIleAsnAsnAspGlyPheP 104
 3893 AAGTTTCTTGTGACAGAGAAAAAATAAGTCACAGTAGAACAGGATGGAATTA 3942
 104 heSerAsnAsnGlyGlyLys 110
 3943 CAAAGAACATAGGACTTAAA 3962

seq_name: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:AA17717

seq_documentation_block:

ID AA17717 standard; DNA; 3300 BP.
 XX
 AC AA17717;
 XX
 DT 21-MAY-1996 (first entry)
 XX
 DE Caulobacter rsaa gene.
 XX
 KW S-layer; rsaa gene; surface protein; biofilm; vaccine; ds.
 XX
 OS Caulobacter crescentus strain CB15.
 XX
 FH Key Location/Qualifiers
 FT 5..7
 FT -35_signal /tag= a
 FT 28..31 /tag= b
 FT -10_signal /tag= c
 FT 88..91 /tag= d
 FT RBS 101..3181
 FT CDS /tag= d
 FT /transl_except= pos:1229..1231; aa:Gly
 FT /transl_except= pos:2627..2629; aa:Gly
 FT /transl_except= pos:2630..2632; aa:Ser
 FT 3214..3230
 FT terminator /tag= e
 FT /note= "putative transcription terminator
 FT palindromic"
 FT 3233..3248
 FT terminator /tag= f
 FT /note= "putative transcription terminator
 FT palindromic"
 XX
 PN US5500353-A.


```

XX 19-MAR-1996.
XX 09-JUN-1992; 92US-0895367.
XX 09-FEB-1994; 94US-0194290.
XX 09-JUN-1992; 92US-0895367.
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX Bingle WH, Smit J;
XX WPI; 1996-171046/17.
XX P-PSDB; AAR94014.
XX Expression and presentation of polypeptide heterologous to
XX Caulobacter S-layer protein to bacterium's environment - by cloning
XX in-frame into Caulobacter rsaA gene, and expressing as fusion prod.
XX with S-layer protein
XX Example 2; Fig 6a-c; 22pp; English.
XX The rsaA gene (AAT17717) of Caulobacter crescentus CB15 codes for
XX the paracrystalline S-layer protein (AAR94014). Restriction
XX sites within the gene permit the insertion of heterologous DNA.
XX The encoded polypeptide is then expressed and presented on the
XX surface of the Caulobacter as a fusion protein with the S-layer
XX protein. The bacterium is cultured as a biofilm in a bioreactor
XX or may be used to present an antigenic epitope (see AAR94016 and
XX (AAR94016) to the environment e.g. for use as a vaccine.
XX Sequence 3300 BP; 548 A; 1218 C; 1005 G; 529 T; 0 other;

alignment_scores:
  Quality: 71.00 Length: 112
  Ratio: 1.164 Gaps: 5
  Percent Similarity: 54.464 Percent Identity: 28.571

alignment_block:
US-09-528-682-4 x AAT17717 ..
Align seg 1/1 to: AAT17717 from: 1 to: 3300

1 AspTyrPheThrValArgIleGlnAspAlaTyrGluProIleAlaAsnTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
608 GACTACCTGACCGCCTTCGTGCGC.....GCCAACAC 639

17 rAsn...ThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuA 33
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
640 GCCGTTACGCGCGTCGCCACATCGATCTGCGCGTCAAGCGCGCCTGA 689

33 spGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGly..... 47
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
690 TCGGCACCATCTCTGAACCGCGCCACGGTGTGCGGCATCGGTGTACGCG 739

48 .....MetAspArgAspLeuPhe....GlySerAlaAsnIle 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
740 ACCGCCACGCGCGCGATGATCAACAGACCTTCGCGACGCGCCTGTGCGAC 789

58 eAspGlyPheProGluValArgGluPheAsnSerLeuProAsnAsnLysA 75
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
790 CGACACGCGCGTGGGTGAACCTGTTCACCGCCTATCCCTGTCGCGGCG 839

75 laSerSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLys 91
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
840 TGTGCGGTTCGACCTCTCTGCTGACCCACCGCGCACCGACCC..... 880

92 LysTyrIleLysLeuLeuIleAsnAsnAspGlyPhe 103
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
881 .....CTGACGGGACCGCGCAACACGACGACGTTTC 910

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA1197.DAT:AARV01866

```

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seq_documentation_block:
ID AAV01866 standard; DNA; 3300 BP.
XX
AC AAV01866;
XX
DT 20-APR-1998 (first entry)
XX
DE Caulobacter crescentus S-layer rsaA gene.
XX
KW S-layer; rsaA gene; Caulobacter; vaccine; antigenic; ligand; enzyme;
KW metallothionein; heavy metal; water; sewage; xylanase; cellulase;
KW wood pulping; ss.
XX
OS Caulobacter crescentus.
XX
FH Key Location/Qualifiers
FT -35_signal 5..7
FT /*tag= a
FT -10_signal 28..31
FT /*tag= b
FT RBS 3292..91
FT /*tag= c
FT /*tag= Shine_Dalgarno_sequence
FT CDS 101..3181
FT /*tag= d
FT /*product= "S-layer protein"
XX
PN WO9734000-A1.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-CA00167.
XX
PR 12-MAR-1996; 96US-0614377.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Bingle WH, Nomellini JF, Smit J;
XX
DR WPI; 1997-470880/43.
DR P-PSDB; AAW37490.
XX
PT New DNA containing sequence for C-terminal region of Caulobacter
PT S-layer protein expressed as fusion proteins containing antigenic
PT peptides in Caulobacter, useful as live vaccines
XX
PS Example 2; Fig 6; 58pp; English.
XX
CC The present sequence encodes a Caulobacter S-layer protein used in an
CC example of the present invention. A new DNA construct has been developed
CC which contains at least one restriction site for insertion of DNA
CC upstream of DNA encoding a C-terminal region of at least the last 82
CC amino acids (aa) of Caulobacter S-layer protein. Caulobacter containing
CC the DNA constructs above additionally containing a sequence encoding a
CC heterologous polypeptide, are particularly useful in live vaccines
CC (where the heterologous polypeptide is an antigen). They can also be
CC used for production of e.g. ligands, enzymes or other proteins, e.g.
CC metallothioneins to remove heavy metals from water or sewage, or
CC xylanase or cellulase for use in wood pulping. All known Caulobacter
CC strains are harmless, and stable in outdoor environments, including
CC water (so suitable for vaccinating fish) or soil. They are well suited
CC for growing in biofilm reactors and produce S-layer proteins, which is
CC an ideal system for presentation of antigens, at high level.
XX
SQ Sequence 3300 BP; 548 A; 1218 C; 1005 G; 529 T; 0 other;

alignment_scores:
  Quality: 71.00 Length: 112
  Ratio: 1.164 Gaps: 5
  Percent Similarity: 54.464 Percent Identity: 28.571

```


CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence encodes an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 3057 BP; 1244 A; 491 C; 619 G; 703 T; 0 other;

alignment_scores:
 Quality: 70.50 Length: 105
 Ratio: 1.282 Gaps: 3
 Percent Similarity: 52.381 Percent Identity: 25.714

alignment_block:

US-09-528-682-4 x AAS55103 ..

Align seg 1/1 to: AAS55103 from: 1 to: 3057

15 AlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluValAl 31

1036 GCCAATTTAAATGATCGATTGAGACATTTAATAAAGCGAAT..... 1077

31 aLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyGlyM 48

1078AATAGATTTTCGCATGTTGCATTTTAAACCTAATAATGGTA 1120

48 etAspArgAsp.....LeuPheGlySerAlaAsn 57

1121 AAACGACAAAGTGTGACTGTTACTGGAACCTTTAATGAAAGGTAGTAATCAG 1170

58 IleAspGlyPheProGluValArgGluPheAsnSerLeuProAsnAsnLy 74

1171 AATGGAATCAACCAAGATAGTAGTGGGAATTTGAATACTTGGGTAATAATGA 1220

74 sAlaSerSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheL 91

1221 AGACATACGCAAGAGTGTATATGCAATACGACAGATACITCTTAATTTA 1270

91 yLysTyrIle.....LysLeuLeuIleAsnAsnAspGly 102

1271 AAGAAGTCACAAGTAATATGATGCGGAATTTGAATTTACAAAATAATGGA 1320

103 PhePheSerAsnAsn 107

1321 AGCTATTTCATTGAAT 1335

seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT: AAN82053

seq_documentation_block:

ID AAN82053 standard; DNA; 3280 BP.

XX AC AAN82053;

XX 05-JAN-1990 (first entry)

DE DNA encoding fibronectin binding protein.

XX Fibronectin binding protein; S.aureus; immunisation;

KW mastitis; ruminants; wound infection; diagnosis.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

FT CDS 57..313

FT /*tag= a

PN EP294349-A.

XX 07-DEC-1988.

XX

XX 30-MAY-1988; 88EP-0850188.

XX 01-JUN-1987; 87SE-0002272.

XX (ALFA) ALFA-LAVAL AGRI INTERNATIONAL AB.

XX Hook M, Lindberg MK, Signas LC, Wadstrom TM, Froman G;

XX WPI: 1988-347978/49.

XX P-PSDB; AAP82115.

XX Hybrid DNA encoding Staphylococcus aureus fibronectin binding protein -
 PT useful for immunisation and topical application to prevent
 PT staphylococcal infections.

XX Disclosure; Fig. 8A:1-8A:2; 23pp; English.

XX The DNA encodes a S.aureus fibronectin binding protein which may be
 CC included in a hybrid protein. The protein may be used to immunise
 CC ruminants against staphylococcal mastitis, pref. when given at
 CC 0.5-5 microg/kg, using 3 doses at 1-3 week intervals; and for
 CC topical applicn. to prevent wound infection, pref. using an
 CC isotonic saline soln. of concn. 25-250 microg/mg. The DNA and the
 CC hybrid protein may be immobilised on a carrier and used to diagnose
 CC staphylococcal infections.

XX Sequence 3280 BP; 1327 A; 509 C; 652 G; 792 T; 0 other;

alignment_scores:

Quality: 70.50 Length: 105
 Ratio: 1.282 Gaps: 3
 Percent Similarity: 52.381 Percent Identity: 25.714

alignment_block:

US-09-528-682-4 x AAN82053 ..

Align seg 1/1 to: AAN82053 from: 1 to: 3280

15 AlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluValAl 31

1092 GCCAATTTAAATGATCGATTGAGACATTTAATAAAGCGAAT..... 1133

31 aLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyGlyM 48

1134AATAGATTTTCGCATGTTGCATTTTAAACCTAATAATGGTA 1176

48 etAspArgAsp.....LeuPheGlySerAlaAsn 57

1177 AAACGACAAAGTGTGACTGTTACTGGAACCTTTAATGAAAGGTAGTAATCAG 1226

58 IleAspGlyPheProGluValArgGluPheAsnSerLeuProAsnAsnLy 74

1227 AATGGAATCAACCAAGATAGTAGTGGGAATTTGAATACTTGGGTAATAATGA 1276

74 sAlaSerSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheL 91

1277 AGACATACGCAAGAGTGTATATGCAATACGACAGATACITCTTAATTTA 1326

91 yLysTyrIle.....LysLeuLeuIleAsnAsnAspGly 102

1327 AAGAAGTCACAAGTAATATGATGCGGAATTTGAATTTACAAAATAATGGA 1376

103 PhePheSerAsnAsn 107

1377 AGCTATTTCATTGAAT 1391

seq_name: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT: AAV74365

seq_documentation_block:

ID AAV74365 standard; DNA; 13740 BP.

XX

AC AAV74365;
 XX 16-MAR-1999 (first entry)
 XX Staphylococcus aureus contig SEQ ID #54.
 DE
 XX Computer readable medium; vaccine; S.aureus infection; Immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome; ds.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1141..1200
 FT /tag= a
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 FT misc_feature 2941..3000
 FT /tag= b
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 FT misc_feature 4741..4800
 FT /tag= c
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 FT misc_feature 6541..6600
 FT /tag= d
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 FT misc_feature 8341..8400
 FT /tag= e
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 FT misc_feature 10141..10200
 FT /tag= f
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 FT misc_feature 11941..12000
 FT /tag= g
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 XX EP786519-A2.
 XX 30-JUL-1997.
 XX
 XX 07-JAN-1997; 97EP-0100117.
 XX
 XX 05-JAN-1996; 96US-0009861.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
 XX Rosen CA;
 XX WPI; 1997-374922/35.
 XX
 XX Polynucleotide(s) and proteins derived from Staphylococcus aureus

PT stored on computer readable medium and used in the production of
 PT anti-S.aureus vaccines
 XX
 PS Claim 1; Page 413-420; 3271pp; English.
 XX
 CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
 CC of the invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random access
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the S.aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against S.aureus infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the S.aureus DNA sequences contained on the
 CC computer readable medium.
 XX
 SQ Sequence 13740 BP; 3728 A; 2620 C; 1977 G; 4992 T; 423 other;

alignment_scores:
 Quality: 70.50 Length: 105
 Ratio: 1.282 Gaps: 3
 Percent Similarity: 52.381 Percent Identity: 25.714
 alignment_block:
 US-09-528-682-4 x AAV74365/rev ..
 Align seq 1/1 to reverse of: AAV74365 from: 1 to: 13740
 15 AlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluValAl 31
 7235 GCCAATTAATGCGTGGATTGAGACATTTAATAAGCGAAT..... 7194
 31 aLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyGlyM 48
 7193AATAGATTTTCGCATCTTGCATTTATTAAACCTAATAATGTA 7151
 48 etAspArgasp.....LeuPheGlySerAlaAsn 57
 7150 AAACGACAGTGTGCTGTTACTGGAACTTTAATGAAGGTAGTAATCAG 7101
 58 IleAspGlyPheProGluValArgGluPheAsnSerLeuProAsnAsnLy 74
 7100 AATGGAATCAACCAAAAGTAGGATATTTGAATCTTGGTAAATATGA 7051
 74 sAlaSerSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPhel 91
 7050 AGACATAGCGAAGAGTGTATATGCAATACGACAGATACTTCTAAATTTA 7001
 91 ysLysTyrIle.....LysLeuLeuIleAsnAsnAspGly 102
 7000 AAGAAGTCACAAGTAATATGATGGGAATTTGAATTTACAAAATAATGGA 6951
 103 PhePheSerAsnAsn 107
 6950 AGCTATTCATTTGAAT 6936
 seq_name: /SID85/gcgdata/geneseq/geneseq-emb1/NA1999.DAT: AAX91726
 seq_documentation_block:
 ID AAX91726 standard; DNA; 2601 BP.
 XX
 XX AC AAX91726;
 XX
 XX DT 25-AUG-1999 (first entry)

US-09-528-682-4 x AAZ29207/rev ..

Align seg 1/1 to reverse of: AAZ29207 from: 1 to: 3564

2 TyrPheThrValArgIleGlnAspAlaTyrClnpProIleAlaAsnThrAs 18
3348 TATTTTTCAGCGCGGTAGCCATCTCCATTTTCCCCCATATGATCCAGCA 3299
18 nThrThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyA 35
3298 TCCCACTACTGGGTATTTATCCAAAGGAAATGAAATCAGTATGTCAACA 3249
35 rGlyTyr 36
3248 AATAT 3244

seq_name: /SIDS5/qcdata/geneseq/geneseq-emb1/NA2000.DAT:AAZ29219

```
seq_documentation_block:
ID   AAZ29219 standard; DNA; 4090 BP.
```

AC	AAZ29219;
XX	
XX	21-FEB-2000 (first entry)
DT	
XX	
XX	Human genomic IFNA2 DNA, 5'to the ORF including partial coding region.
DE	
XX	
KW	Interferon alpha 2; IFNA2; genomic sequence; transcription start site;
KW	upstream; targeting sequence; regulatory sequence; marker gene;
KW	homologous recombination; recombinant cell; gene therapy; DNA construct;
KW	Papilloma virus; Hepatitis B virus; Hepatitis C virus; Vaccinia virus;
KW	Herpes simplex virus; Herpes zoster varicellous virus; Rhinovirus; ds.
XX	
XX	
OS	Homo sapiens.

Key	Location/Qualifiers
misc_feature	1..278
FT	/*tag= a
FT	/note= "5'end of the genomic sequence upstream to the coding region of Interferon alpha 2"
FT	279..3491
FT	/*tag= b
FT	/note= "Genomic sequence upstream to the coding region of Interferon alpha 2"
FT	3492..3564
FT	/*tag= c
FT	/note= "Novel genomic sequence upstream to the coding region of Interferon alpha 2"
FT	3565..4074
FT	/*tag= d
FT	/note= "Sequence immediately upstream the coding region of Interferon alpha 2"
FT	4075..4090
FT	/*tag= e
FT	/label= Partial_Interferon_alpha_2_protein
FT	/note= "no stop codon given"
FT	
CDS	

WO9957292-A1.

11-NOV-1999

05-MAY-1999: 99WO-US09925.

07-MAY-1998: 98IIS-0084648

21-MAY-1998; 98US-0086555.

(TRAN-) TRANSKARYOTIC THERAPIES INC.

Treco DA, Heartlein MW, Selden RF;

WPI; 2000-072236/06.

PT Novel genomic sequences used to treat human diseases and disorders

XX PS XX CC CC CC CC CC CC CC CC CC CC CC CC CC CC XX SQ

Disclosure; Fig 6; 68pp; English.

CC The present DNA sequence is the human genomic sequence upstream of the
CC transcription start site of Interferon alpha-2 (IFNA2), including a
CC part of the coding region. A DNA construct comprising a targeting
CC sequence homologous to the region upstream of the coding sequence of
CC IFNA2, a transcriptional regulatory sequence that differs from the
CC endogenous IFNA2 gene, and a selectable marker gene for selection of
CC recombinant cells is generated. It can be used by homologous
CC recombination, to modify the expression of endogenous IFNA2.
CC These recombinant cells which express IFNA2 are useful for in vitro
CC production of the protein and gene therapy. Such cells may be used in a
CC delivery system for treating infections caused by viruses such as
CC Papilloma virus, Hepatitis B and C virus, Vaccinia virus, Herpes simplex
CC virus, Herpes zoster varicellous virus and Rhinovirus and other
CC conditions that can be treated with IFNA2.

Sequence 4090 BP; 1564 A; 650 C; 695 G; 1181 T; 0 other;

alignment_scores:		
Quality:	70.00	Length: 35
Ratio:	2.692	Gaps: 0
Percent Similarity:	74.286	Percent Identity: 37.143

alignment_block:

US-09-528-682-4 x AAZ29219/rev ..

Align seg 1/1 to reverse of: AAZ29219 from: 1 to: 4090

2 TyrPheThrValArgIleGlnAspAlaTyrGluProIleAlaAsnThrAs 18
||||| :||| :: :||| :||| :|||
3348 TATTTTGAGCCGGTAGGCATCTCCATTTTCCCCCATATGATCCAGCAA 3299

18 nThrThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyA 35
- | ||||| :::::||::: |||||||::::::::::: ;
3298 TCCCACTACTGGGTATTTATCCAAAGGAATGAAATCAGTATGTCAACAA 3249

35 rqrtyr 36

3248 AATAT 3244

seq name: /SID5/acadata/geneseq/geneseq-emb1/NA2000.DAT:AAA09032

seq documentation block:

seq_documentation_block:
ID AAA09032 standard: PNA: 663 BP.

AA
AC
AAA09032:

01-AUG-2000 (first entry)

XX DE Human CSAPT-4 open reading frame.

Cardiovascular system associated protein tyrosine phosphatase 4;
CSAPP-4; cytostatic; immunomodulatory; antidiabetic; virucide;
hypotensive; cardiant; tyrosine phosphatase modulator; ss.

XX Homo sapiens.

XX PN WO200018890-A2

XX
PD
06-APR-2000XX
PF 30-SEP-1999. 99W0-1152292AXX
30-SEP-1998. 0805-0163833
DB

PR 30-SEP-1998; 9805-0164193.

PA (MILL-) MILLENNIUM PHARM INC.

PI Acton S;


```

XX 26-JUN-2001 (first entry)
XX Human cDNA sequence SEQ ID NO:11150.
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX Homo sapiens.
XX EP1074617-A2.
XX 07-FEB-2001.
XX 28-JUL-2000; 2000EP-0116126.
XX 29-JUL-1999; 95JP-0248036.
XX 27-AUG-1999; 99JP-0300259.
XX 11-JAN-2000; 2000JP-0118776.
XX 02-MAY-2000; 2000JP-0183767.
XX 09-JUN-2000; 2000JP-0241899.
XX (HELI-) HELIX RES INST.
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602
XX full-length cDNAs defined in the specification, and for the detection
XX and/or diagnosis of the abnormality of the proteins encoded by the
XX full-length cDNAs -
XX
XX Claim 8; SEQ ID 11150; 2537pp + CD ROM; English.
XX
XX The present invention describes primer sets for synthesising 5602
XX full-length cDNAs defined in the specification. Where a primer set
XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary
XX to the complementary strand of a polynucleotide which comprises one of
XX the 5602 nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in
XX the specification. The primer sets can be used in antisense therapy and
XX in gene therapy. The primers are useful for synthesising polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
XX AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
XX represent oligonucleotides, all of which are used in the exemplification
XX of the present invention.
XX
XX Sequence 1350 BP; 324 A; 418 C; 310 G; 298 T; 0 other:

```

```

alignment_scores:
  Quality: 69.00      Length: 72
  Ratio: 1.683       Gaps: 4
  Percent Similarity: 56.944      Percent Identity: 31.944

```

```
alignment_block:
```

```
US-09-528-682-4 x AAH14036 ..
```

```
Align seg 1/1 to: AAH14036 from: 1 to: 1350
```

```

13 ProfileAlaAsnThrAsnThrThrThrGlnPheLeuAsnMetGlyAsnG1 29
||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

585 CCGCAGATTCAACAATTCAGTGACAAACATCTACACAAATGATTATATCC 634
29 uValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeu..... 41
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
635 AGTGGCCCTGGAGGAGCGGTCCTCAACTTCCCGATGGTCCCGGCTCGG 684
42 .....IleSerAlaGluGlyGlyMetAsp.....ArgAsp 51
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
685 ACGTCCGATGGCGGCATGGTGGCATGGAGCCACACACATGAATGGA 734
52 LeuPheGlySerAlaAsnIleAspGlyPheProGluValArgGluPheAs 68
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
735 TCATTAGGTGTCAGGCGACATAGACGGACTTCCAAAA.....AA 772
68 nSerLeuProAsnAsn 73
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||
773 TTCT...CCTAACAC 785

```

```
seq_name: /SID85/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AA234611
```

```
seq_documentation_block:
```

```
ID AA234611 standard; cDNA; 1943 BP.
```

```
XX
```

```
AC AA234611;
```

```
XX
```

```
DT 15-FEB-2000 (first entry)
```

```
XX
```

```
DE Human receptor molecule (REC) Incyte clone 2121924.
```

```
XX
```

```
KW Receptor; REC; human; diagnosis; therapy; neoplastic disorder;
```

```
XX
```

```
KW immunological disorder; reproductive disorder; nervous disorder;

```

```
XX
```

```
KW gastrointestinal disorder; smooth muscle disorder;

```

```
XX
```

```
KW musculoskeletal disorder; ss.
```

```
XX
```

```
OS Homo sapiens.
```

```
XX
```

```
PH Key
```

```
XX
```

```
FT CDS
```

```
XX
```

```
FT Location/Qualifiers
```

```
XX
```

```
95..1180
```

```
/*tag= a
```

```
XX
```

```
PN WO9557270-A2.
```

```
XX
```

```
PD 11-NOV-1999.
```

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XX
```

```
PD 28-APR-1999; 99WO-US09191.
```

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XX
```

```
PR 01-MAY-1999; 98US-0071822.
```

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XX
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```
PA (INCY-) INCYTE PHARM INC.
```

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XX
```

```
PI Hillman JL, Bandman O, Tang YT, Yue H, Lal P, Corley NC;
```

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XX
```

```
PI Guegler KJ, Patterson C;
```

```
XX
```

```
DR WPI; 2000-052971/04.
```

```
XX
```

```
DR P-P8DB; AAY32202.
```

```
XX
```

```
PT Novel human receptor molecules used in the diagnosis, treatment and
```

```
XX
```

```
PT prevention of neoplastic, immunological, reproductive gastrointestinal,
```

```
XX
```

```
PT nervous, smooth muscle and musculoskeletal disorders -
```

```
XX
```

```
PS Claim 7; Page 88-89; 94pp; English.
```

```
XX
```

```
CC This is the nucleotide sequence of Incyte cDNA clone 2121924
```

```
XX
```

```
CC encoding a novel human receptor molecule (REC, see AAY32202). The
```

```
XX
```

```
CC invention provides human RECs and polynucleotides which identify
```

```
XX
```

```
CC and encode REC, as well as vectors, host cells, antibodies,

```

```
XX
```

```
CC agonists and antagonists. Human RECs appear to play a role in
```

```
XX
```

```
CC neoplastic, immunological, reproductive gastrointestinal, nervous,

```

```
XX
```

```
CC smooth muscle and musculoskeletal disorders. The protein, antagonists
```

```
XX
```

```
CC and agonists, and compositions can be used to treat: a reproductive
```

```
XX
```

```
CC disorder, including but not limited to, prolactin production disorders,

```

```
XX
```

```
CC infertility including tubal disease, ovulatory defects, endometriosis,

```

```
XX
```

```
CC disruptions of the oestrous and menstrual cycles, polycystic ovary
```


sndrome, ovarian hyperstimulation syndrome, endometrial and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic pregnancy, teratogenesis, breast cancer, fibrocystic breast disease, galactorrhoea, disruptions of spermatogenesis, abnormal sperm physiology, testis cancer, prostate cancer, benign prostatic hyperplasia, prostatitis, Peyronie's disease, male breast carcinoma and gynaecomastia: gastrointestinal disorders including, but are not limited to, dysphagia, peptic oesophagitis, oesophageal spasm and stricture, oesophageal carcinoma, dyspepsia, indigestion, gastritis, gastric carcinoma, anorexia, nausea, emesis, gastroparesis, intestinal tract infection, peptic ulcer, colitis, Whipple's disease, Mallory-Weiss syndrome, irritable bowel syndrome, short bowel syndrome, diarrhoea, constipation, cirrhosis, jaundice, and hepatic vein thrombosis; nervous disorders including, but are not limited to, Alzheimer's disease, amnesia, bipolar disorder, catatonia, cerebral neoplasms, Down's syndrome, and dystonias; smooth muscle cell disorders including, but not limited to, angina, anaphylactic shock, arrhythmia, cardiovascular shock, migraine, and pheochromocytoma; musculoskeletal disorders including muscular dystrophy, central core disease, nemaline myopathy, centronuclear myopathy, lipid myopathy, inclusion body myositis, thymotonic myoapathy, and ethanol myopathy; immunological disorders including AIDS, Addison's disease, adult respiratory distress syndrome, allergy, ankylosing spondylitis, amyloidosis, anaemia, asthma, atherosclerosis, autoimmune hemolytic anaemia, autoimmune thyroiditis, bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, haemodialysis, and extracorporeal circulation; viral, fungal, bacterial or protozoan infections; trauma; and neoplastic disorders including adenocarcinoma, leukemia, melanoma, myeloma, sarcoma, and various cancers. The REC polynucleotide is a source of probes and primers which bind may be used to detect REC in a sample from a patient (claimed). They may also be administered as part of a gene therapy regime.

Sequence 1943 BP: 515 A; 537 C; 473 G; 418 T; 0 other:

```

alignment_scores:
  Quality: 69.00      Length: 72
  Ratio: 1.683       Gaps: 4
  Percent Similarity: 56.944  Percent Identity: 31.944

alignment_block:
  US-09-528-682-4 x AAZ34611 ..

Align seg 1/1 to: AAZ34611 from: 1 to: 1943

13 ProfileAlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnCl 29
   ||| :|||:|||||: :|||: :|||: |||
863 CCGCAGATTTCACAAATTCACAGTGCACATCTCACAAATGATTAATCC 912
   ||| ||| ||| |||: :|||: |||
29 uValAlaLeuAspGlyArgTyrSerAsnThrAlaLeu..... 41
   ||| ||| ||| |||: :|||: |||
913 ATGTCGCCCTGGAGGACGGCGTCCACTTCCCGATGGGTCCCGGCTCGG 962
   ||| ||| ||| |||: :|||: |||
42 .....lIeSerAlaGluGlyGlyMetAsp.....ArgAsp 51
   :|||: :|||: ||| |||: :|||:
963 ACGTCCGATGGCGGCATGGGTGGCATGGAGCCACACCATGATGAATGGA 1012
   :|||: :|||: ||| |||: :|||: |||
52 LeuPheGlySerAlaAsnIleAspGlyPheProGluValArgGluPheAs 68
   :|||: :|||: ||| |||: :|||: |||
1013 TCATTAGGGTCAGCGCACATAGACGGACTTCCAAA.....AA 1050
   ||| ||| ||| |||: :|||: |||
68 nSerLeuProAsnAsp 73

```

```

||||| |||||||||
1051 TTCT...CCTAACAC 1063

seq_name: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:AA08098
seq_documentation_block:
ID_ AA08098 standard; DNA; 2278 BP.
XX
XX AA08098;
XX
DT 04-JUL-1996 (first entry)
XX
DE Enterohaemorrhagic E.coli hlyA gene.
XX
KW Enterohaemorrhagic Escherichia coli; virulent; EHEC; O157:H7 serotype;
KW detection; hlyA gene; probe; primer; enterohaemorrhagic colitis;
KW haemolytic uremic syndrome; mesenteric adenitis; ss.
XX
XX Escherichia coli (enterohaemorrhagic).
XX
XX Key Location/Qualifiers
FH CDS 2..2278
FT FT /*tag= a
FT FT /product= hlyA_gene_product
FT FT /note= "incomplete CDS; does not include start
FT FT codon"
XX
PN US5475098-A.
XX
XX 12-DEC-1995.
XX
XX 14-JUN-1994; 94US-0258188.
XX
XX 14-JUN-1994; 94US-0258188.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Hall RH, Xu JG;
XX
XX WPI; 1996-048546/05.
XX
XX P-PSDB; AAR86998.
XX
XX Entero:haemorrhagic E. coli (EHEC) nucleic acid sequences - useful
XX for probe and primer design for sensitive and specific detection of
XX EHEC
XX
XX Claim 6; Columns 31-38; 32pp; English.
XX
XX Enterohaemorrhagic E.coli (EHEC) associated with enterohaemorrhagic
XX colitis, haemolytic uremic syndrome and mesenteric adenitis have
XX been found to carry a hlyA gene and a hlyB gene, separated by an
XX intergenic region. The hly genes and the intergenic region are
XX absent from bacteria not associated with these diseases and so
XX provide a useful target for detecting EHEC pathogens, esp. O157:H7
XX serotype E.coli. The present sequence is the EHEC hlyA gene.
XX
XX Sequence 2278 BP; 745 A; 344 C; 550 G; 639 T; 0 other;
XX

```

```

alignment_scores:
  Quality: 69.00      Length: 98
  Ratio: 1.211      Gaps: 4
  Percent Similarity: 58.163      Percent Identity: 25.510

alignment_block:
  US-09-528-682-4 x AAT08098 ..

Align seg 1/1 to: AAT08098 from: 1 to: 2278

23 PheLeuAsn.....MetGlyAsnGluValAlaLeuAspGlyArgTyrSe 37
|||||.....:|||||:.....: |||:
1745 TATCTGAATGGTGGTTTTCGTAATGATATTTATGTTTATGGGCAAAACTA 1794

```



```

1008 GAGCATTGGCTGTGATATACCGGATCCAGTTCATCCACCGATGACAC 1057
79 rlaSerLeuAsnLys.....GlnHisAspAlaAspPheLysLysTyri 94
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1058 GGCTTCACGTGGACCGACATCTTCTCATCGCAGTGATGTCTCTCTCC 1107
94 leLysLeuLeuIleAsnAsn.....AspGlyPhe 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1108 AGATTTTAAAGCCAAACAGGTCAAGAGATCGCAAGACCTTGATGGATTC 1157
104 PheSerAsnAsnGlyCly 109
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1158 TACAGCCATGGGATGGGA 1175

```

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:AA569724

seq_documentation_block:

ID AA569724 standard; cDNA; 4290 BP.

XX AC AA569724;

DT 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #5528.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

DR P-PSDB; ABG05537.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 1; SEQ ID No 5528; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AA564197-AA594564 represent novel human
 CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 4290 BP: 1315 A; 944 C; 1137 G; 894 T; 0 other;

alignment_scores:

Quality: 68.00 Length: 106
 Ratio: 1.172 Gaps: 6
 Percent Similarity: 54.717 Percent Identity: 29.245

alignment_block:

US-09-528-682-4 x AA569724 ..

Align seg 1/1 to: AA569724 from: 1 to: 4290

```

23 PheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArg.....TyrSe 37
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
97 TTCTCTGGATGTTGGACTG.....GGCAGAGAGTGTACCTC 131
37 rAsnTyrAlaLeuIleSerAlaGluGlyMetAspArgAspLeuPheG 54
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
132 AAACAAGGTGTACTTAAAGAGATCTGGGAGTGATCTGACCTCTTC 181
54 lySerAlaAsnIleAspGly.....PheProGluValArgGlu 66
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
182 ACTCACCCAGTGTGACATGGACGATCATCTTCCCAAAGCCAGAGAA 231
67 .....PheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
232 GAGCATTGGCCCTGTGATATCATCCGGATCCAGTTCATCCACCGATGAC 281
79 rlaSerLeuAsnLys.....GlnHisAspAlaAspPheLysLysTyri 94
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
282 GGCTTCACGTGGACCGACATCTTCTCATCGCAGTGATGTCTCTCTCC 331
94 leLysLeuLeuIleAsnAsn.....AspGlyPhe 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
332 AGATTTTAAAGCCAAACAGGTCAAGAGATCGGCAAGACCTTGATGGATTC 381
104 PheSerAsnAsnGlyCly 109
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
382 TACAGCCATGGGATGGGA 399

```

seq_name: /SID55/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AAA70204

seq_documentation_block:

ID AAA70204 standard; DNA; 4317 BP.

XX AC AAA70204;

DT 07-NOV-2000 (first entry)

XX Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:337.
 KW Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine;
 KW antimalarial; malaria; protozoacide; infection; insecticide; ds.

XX Plasmodium falciparum.

XX WO200025728-A2.

XX 11-MAY-2000.

XX 05-NOV-1999; 98WO-US26796.

XX 05-NOV-1998; 98US-0107131.

XX (HOFF/) HOFFMAN S.

XX (CARU/) CARUCCI D.

XX (GARD/) GARDNER M.

XX (VENT/) VENTER J C.

PI Hoffman S, Carucci D, Gardner M, Venter JC;
 XX WPI: 2000-365347/31.
 XX
 XX Proteins encoded by chromosome 2 of the human malarial parasite,
 PT Plasmodium falciparum, useful as antimalarial vaccines and in the
 PT diagnosis of P.falciparum infection -
 XX
 XX
 PS Disclosure; Page 530-531; 577pp; English.
 XX
 CC The present invention describes proteins and their fragments (I) encoded
 CC by chromosome 2 of the human malarial parasite, Plasmodium falciparum.
 CC Also described are: (i) nucleotide sequences (II) encoding (I); and (2)
 CC vaccines against P. falciparum infection comprising (I) or (II).
 CC (i) and (ii) are useful for the development of vaccines against
 CC P. falciparum infection. (I) and polyclonal antisera or a monoclonal
 CC antibody raised to immunogens comprising the sequences of (I), are
 CC useful in the detection of infection with P. falciparum. Furthermore,
 CC (I) (especially when they are rifins or secreted or membrane proteins)
 CC can aid the identification of drugs to treat or prevent P. falciparum
 CC infection, or they can be used to identify drug resistance in
 CC P. falciparum. Sequencing of the Plasmodium chromosome 2 and the
 CC subsequent identification of proteins encoded by it will help to expand
 CC our understanding of parasite biology, a process hampered by the
 CC complexity of the parasitic life cycle, and provide new targets for
 CC vaccine and drug development. Parasite resistance to drugs and mosquito
 CC resistance to insecticides have led to a resurgence of malaria in many
 CC parts of the world, and there is a pressing need for vaccines and new
 CC drugs. AAT70078 to AAT70287 and AAT8144 to AAT8352 represent nucleotide
 CC and protein sequences given in the present invention, but which are not
 CC specifically mentioned within the specification.
 XX
 SQ Sequence 4317 BP; 1862 A; 543 C; 582 G; 1330 T; 0 other;

alignment_scores:
 Quality: 68.00 Length: 55
 Ratio: 1.943 Gaps: 2
 Percent Similarity: 63.636 Percent Identity: 34.545

alignment_block:

US-09-528-682-4 x AAT70204 ..

Align seg 1/1 to: AAT70204 from: 1 to: 4317

61 PheProGluValArgGluPheAsnSerLeuProAsnAsnLys.....AL 75
 |||:||||| |||:|||||
 3679 TTTCAGATATTCANAATGTTGATCTCTCCACCAAGAAATAAATCAATC 3728

75 aserSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLysL 92
 : |||:|||||:||||| ||| |||:|||||
 3729 CATATCTTCAAGCGCAATTTGAATTATCAATGATAATCAATTTAACA 3778

92 ysTyr.....:|||||:||||| ||| |||:|||||
 || :||:|||||:||||| ||| |||:|||||
 3779 AAAGAGAAATGATGGAACACCATGATATCTATGACTAACCAGTCATCT 3828

103 PhePheSerAsnAsn 107

3829 ATGTTTTCGATGAAAC 3843

seq_name: /SIDSS/gcgdata/geneseq/geneseq-emb1/NA1999.DAT: AAX24044

seq_documentation_block:

ID AAX24044 standard; cDNA; 5276 BP.

XX

AC AAX24044;

XX

DT 30-JUN-1999 (first entry)

XX

DE Human brx cDNA.

XX

KW Brx protein; breast cancer; nuclear receptor-binding auxiliary protein;

KW anti-cancer; anti-proliferative; mitogen; transcription factor; human;
 KW tumour suppressor; ovarian cancer; proliferative disorder; treatment;
 KW immune tissue; prevention; reproductive tissue; ss.
 XX Homo sapiens.
 OS
 XX WO9915544-A1.
 PN
 XX PD 01-APR-1999.
 XX
 XX PF 23-SEP-1998; 98WO-US19782.
 XX
 XX PR 23-SEP-1997; 97US-0059621.
 XX
 XX PA (DRIG/) DRIGGERS P H.
 PA (RUBL/) RUBINO D M.
 PA (SEGE/) SEGERS J.
 XX
 XX Driggers PH, Rubino DM, Segers J;
 DR WPI: 1999-254688/21.
 DR P-PSDB; AAW93941.
 XX
 XX Breast cancer gene encoding a nuclear receptor-binding auxiliary
 PT protein, brx
 XX
 XX Claim 5; Page 63-64; 69pp; English.
 XX
 CC This invention describes a novel human breast cancer gene encoding a
 CC nuclear receptor-binding auxiliary protein, brx. The brx encoded protein
 CC has anti-cancer, anti-proliferative and mitogenic activity and acts as a
 CC transcription factor and tumour suppressor. Levels of expression of brx
 CC can be detected using the primers, probes and antibodies (contained in
 CC the kit) to determine a predisposition to breast and ovarian cancer and
 CC other proliferative disorders of immune tissues. Vectors containing the
 CC brx gene can be used for prevention and treatment of cancers and
 CC proliferative diseases of mammalian reproductive and immune tissues.
 XX
 SQ Sequence 5276 BP; 1564 A; 1182 C; 1361 G; 1169 T; 0 other;

alignment_scores:

Quality: 68.00 Length: 106
 Ratio: 1.172 Gaps: 6
 Percent Similarity: 54.717 Percent Identity: 29.245

alignment_block:

US-09-528-682-4 x AAX24044 ..

Align seg 1/1 to: AAX24044 from: 1 to: 5276

23 PheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArg.....TyrSe 37
 |||||:|||||:||||| ||| |||:|||||
 351 TTCTCGATGTTGGAGCTG.....GGCAGAGAGTGTCACCTC 385

37 rAsnTyrAlaLeuIleSerAlaGluGlyMetAspArgAspLeuPheG 54
 :||:|||||:||||| ||| |||:|||||
 386 AAACAAGGCTGACTTAAAGAGAACTGGAGTGATCTGACCTCTTC 435

54 lySerAlaAsnIleAspGly.....PheProGluValArgGlu 66
 ||| :||:|||||:||||| ||| |||:|||||
 436 ACTCACCCAGTGATGACATGGACAGCATCATCTTCCCAAGCCAGAGAA 485

67PheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
 :||:|||||:||||| ||| |||:|||||
 486 GAGCATTTGGCTGTGATATCACCAGGATCCAGTTCAATCCAGCATGACAC 535

79 rAlaSerLeuAsnLys.....GlnHisAspAlaAspPheLysLysTyrI 94
 |||||:|||||:||||| ||| |||:|||||
 536 GGCTTCACCTGGACCGACATCTTCTCATGGCAGTGATGTCTCTCTCCC 585

94 leLysLeuLeuIleAsnAsn.....AspGlyPhe 103
 ||| :||:|||||:||||| ||| |||:|||||

586 AGATTTTAAAGCCAAACAGAGTCAAGAGATCGGAAAGCCCTTGATGGATTC 635

104 PheSerAsnGlyGly 109

636 TACAGCCATGGATGGGA 653

seq_name: /SIDS5/gcgdata/geneseq/geneseq-n-emb1/NA2001B.DAT:AAH88704

seq_documentation_block:

ID AAH88704 standard; DNA; 160755 BP.

XX AC AAH88704;

XX DT 26-FEB-2002 (first entry)

XX DE Human DNA sequence SEQ ID 544.

XX KW Single nucleotide polymorphism; SNP; biallelic marker; human;

XX KW central nervous system disorder; CNS; ds.

XX OS Homo sapiens.

XX PN WO200151659-A2.

XX PD 19-JUL-2001.

XX PF 11-JAN-2001; 2001WO-IB00116.

XX PR 13-JAN-2000; 2000US-0175854.

XX PA (GEST) GENSET.

XX PI Chu T, Blumenfeld M, Cohen D;

XX DR WPI; -2001-483085/52.

XX PT Isolated polynucleotides, useful for genotyping nucleic acids for

XX PT biallelic markers for the diagnosis of depression, comprises central

XX PT nervous system disorder related biallelic marker .

XX PS Disclosure; Page 476-519; 519pp; English.

XX CC The present invention relates to biallelic markers derived from human

XX CC genes involved in central nervous system (CNS) disorders (see

XX CC AAH88161-AAH88702). The markers have a single nucleotide polymorphism

XX CC (SNP) and are useful in determining the genetic predisposition of

XX CC individuals to CNS disorders, by identifying the nucleotides at a set of

XX CC genetic markers in a biological sample, where the markers comprise at

XX CC least one CNS disorder related marker. The present sequence was used

XX CC to illustrate the invention.

XX SQ Sequence 160755 BP; 43057 A; 36601 C; 38189 G; 42727 T; 181 other;

alignment_scores:

Quality: 68.00 Length: 114

Ratio: 1.214 Gaps: 4

Percent Similarity: 49.123 Percent Identity: 26.316

alignment_block:

US-09-528-682-4 x AAH88704 ..

Align seg 1/1 to: AAH88704 from: 1 to: 160755

2 TyrPheThrValArgIleGlnAspAlaTyrGluProIleAlaAsnThrAs 18

||| :: :: :: :: :: ||| :: :: :: :: ::

88256 TACCAATCAAAAAAGTCTGGATCAGATTAATTCACGCCAAATTCAC 88305

18 nThrThrThr.....GlnPheLeuAsnMetGlyAsnGluV 30

::||| ||| ||| ||| ||| ||| ||| ||| ||| |||

88306 CACATGTACAAGAGAACTGACCAATTC..... 88336

30 aIalaLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGly 46

88337TACTGAACACTATTCCAAAGAAATCCAAAGAGGAG 88369

47 GlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProG1 63

88370 GGACTCTCTCTAACTATTCTATGAAGCCAGCATCAGCCTAATGCCAA 88419

63 u.....ValArgGluPheAsnSerLeuProAsnAsnLysA 75

88420 ATCTGGAAGAGTCACAAATGAAAAAATACTTCTGGCTAATATCCCTGA 88469

75 laSerSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLys 91

88470 TGAACATAGACACAAAAATCTCAACAAAAATACCAGAAACCAAAATGCAG 88519

92 LysTyrIleLysLeuLeuIleAsnAsnAsp.....GlyPhe 103

88520 CGGCACATCAAAATGTTAATAACGATGATCAAGTAGGCTTC 88561

seq_name: /SIDS5/gcgdata/geneseq/geneseq-n-emb1/NA2001A.DAT:AAH52867

seq_documentation_block:

ID AAH52867 standard; DNA; 639 BP.

XX AC AAH52867;

XX DT 03-SEP-2001 (first entry)

XX DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:1127.

XX KW Staphylococcus epidermidis SRI strain; infection; diagnosis;

XX KW vaccination; endocarditis; ds.

XX OS Staphylococcus epidermidis.

XX PN WO200134809-A2.

XX PD 17-MAY-2001.

XX PF 09-NOV-2000; 2000WO-US30782.

XX PR 09-NOV-1999; 99US-0164258.

XX PA (GLAX) GLAXO GROUP LTD.

XX PI Kimmerly WJ;

XX DR WPI; 2001-316495/33.

XX DR P-PSDB; AAG82017.

XX PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,

XX PT useful for vaccinating against infections, e.g. endocarditis -

XX PS Claim 8; Page 326; 2188pp; English.

XX CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides

XX CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

XX CC (I) and (II) can have antibacterial activity and therefore can be used

XX CC in vaccination. The nucleic acids (I) may be used to produce the

XX CC S. epidermidis polypeptides (II) via the production of vectors

XX CC containing them which are used to produce hosts cells which express the

XX CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be

XX CC used to vaccinate subjects and to raise antibodies against the bacteria.

XX CC The polypeptides may also be used to assay for other inhibitors of their

XX CC activity and therefore identify compounds that may be used for the

XX CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to

XX CC AAH55090 represent specifically claimed S. epidermidis genomic DNA

XX CC polynucleotide sequences from the present invention. AAH55091 to

XX CC AAH55098 represent oligonucleotide sequences and primers which are used

XX CC in the exemplification of the present invention.

XX CC N.B. The present invention specifically claims all the polynucleotide

XX CC sequences given in the sequence listing of the present specification,

XX CC however the sequence listing only goes up to SEQ ID NO:4454 so even

CC though sequences are given in the disclosure for SEQ ID NO:4465 to 4472.
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
SQ Sequence 639 BP: 286 A: 66 C: 96 G: 191 T: 0 other:
XX

alignment_scores:		
Quality:	67.50	Length: 126
Ratio:	1.023	Gaps: 5
Percent Similarity:	52.381	Percent Identity: 20.635

alignment block:

Align seq 1/1 to: AAH52867 from: 1 to: 639

```

1 AspTyrPheThrValArgIleGlnAspAlaTyrGluProIleAlaAsnTh 17
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
73 AATTATTTTAAATTTGCTGTATGAT...TTTCAAAAGAGAGATCAAA 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
17 rAsnThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAsp 34
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
120 GAGACTAGACATTCATATATGATGATCGAAGCTAGATAGCA..... 162
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
34 lyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyMetAspArg 50
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
163 ..AAATATTGGAGCGAAGGATTTTATCAATTTATCCGTTGAGAGATAAT 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
51 AspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgGlu 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
211 GAATTAATACTAATGATATATTAACTCTTTAAAAGAAATACTCTGTT 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
67 eAsnSerLeuProAsn.....AsnLysAlaSerSerA 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
261 CAATCAATTAACCTTAATATACAGAAAAGATCTTAATCAATCTACTAAT 310
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
78 spThrAlaSer..... 81
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
311 ACTTTTCAAGTGATAATAGAGAAATTTTCATTTGTAATAATTACAGATCAT 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
82 LeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysLeuLeu 98
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
361 ATTAATCAGCGCTTTGAAACAGACTTCAA..... 390
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
98 eAsnAsnAspGlyPhePheSerAsnAsn 107
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
391 ...AATGATGAACATATTATTAAGATGAC 414
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

seq_name: /SIDS5/qcadata/qeneseq/qeneseqn-emb1/NA2001A.DAT:AAF82337

seq_documentation_block:

XX
ID AAF02337 SCANDIAU; DNA; 1212 BF.

AC
AAF82337;
XX

DT 22-JUN-2001 (first entry)
XX

DE Human alpha-Z
yy

KW Human; beta-1,3-N-acetylglucosamine transfer

KW Siat; alpha-2,6

OS Homo sapiens

[illegible]

OM of: US-09-528-682-4 to: EST:* out_format : pfs

Date: Jun 18, 2002 6:27 PM

About: Results were produced by the GenCore software, version 4.5.
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Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q/cgn2.1/USPTO.spool/US09528682/runat_18062002_082443_7797/app_query.fasta_1.689
-DB=EST -QWMT=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -GAPOP=6.000
-FGAPEXT=7.000 -YGAPO=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blossum62 -TRANS=human40.cdi
-LIST=1000 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=50 -MODE=LOCAL -OUTFWT=pfs -NORM=ext -HEAPSIZ=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09528682@cgn1_1_5309
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-528-682-4

Query length: 110

Database: EST:

Database sequences: 13736207

Database length: -1841457050

Search time (sec): 4056.470000

score_list:

Sequence	Strd Orig	zScore	EScore	Len	Documentation
gb_est2:B1813876	+ 82.00	186.62	0.3786	487	I B1813876 pFEST0a91d05.y1 Plasm
gb_est1:BE061488	+ 78.50	178.34	1.110	471	I BE061488 MRO-BF0248-091299-103-
gb_est2:BM169137	+ 78.50	173.99	1.91	720	I BM169137 ESTP571660 PyBS Plasmid
gb_gss:CNS04594	+ 78.00	168.85	3.770	1055	I AL275743 Tetradon nigroviridis
gb_gss:CNS080F0V	+ 76.50	165.89	5.41	982	I AL396677 T3 end of clone A0AA0
gb_gss:BA483045	+ 76.00	165.65	5.57	891	I BH483045 BOHQU12TR BOHQ Brassic
gb_est2:BF496463	+ 74.00	168.62	3.81	412	I BP496463 AT10383 Sprime AT droe
gb_est2:BF239368	+ 74.00	164.03	6.86	645	I BF239368 O67PBR01 Pb CDNA #20,
gb_est2:BF232289	+ 74.00	162.46	8.39	752	I BF232289 ESTP43194 tomato callu
gb_gss:BAH30987	+ 73.50	161.62	9.35	816	I BAH30987 CH230-58G18.TVB CHORI-
gb_gss:BA292928	+ 73.00	161.36	9.77	801	I BA292928 BOHKF67TR BOHK Brassic
gb_gss:BA2523935	+ 72.50	158.12	14.65	801	I BH552001 BOHMW73TF BOHM Brassic
gb_est1:AV919718	+ 72.50	157.96	14.95	721	I AV919718 AV919718 K. Sato unpub
gb_est1:AW257463	+ 72.50	163.17	7.66	489	I AW257463 NF009030RT1F1023 Davel
gb_est2:BG674231	+ 72.50	160.18	11.25	655	I AW257463 EST305600 KV2 Medica9
gb_gss:BAH48660	+ 72.50	158.98	13.11	736	I BG674231 ESTP08850 HOGA Medica9
gb_gss:BAH52001	+ 72.50	158.12	14.65	801	I BH552001 BOHMW73TF BOHM Brassic
gb_est2:BG032307	+ 72.50	150.22	40.37	1733	I BF032307 601452770F1 NIH.MGC
gb_est1:AV916505	+ 72.00	159.51	12.26	620	I AV916505 AV916505 K. Sato unpub
gb_est1:AV916629	+ 72.00	159.30	12.60	633	I AV916629 AV916629 K. Sato unpub
gb_est1:AV917534	+ 72.00	158.05	14.78	715	I AV917534 AV917534 K. Sato unpub
gb_gss:BAH457228	+ 72.00	157.99	14.89	719	I BAH457228 BOHK53TF BOHK Brassic
gb_est2:BG296887	+ 72.00	157.96	14.95	721	I AV919718 AV919718 K. Sato unpub
gb_est2:BG23671	+ 71.50	156.70	17.58	816	I BG296887 HVSME002F14f Hordeum
gb_est2:BF637831	+ 71.50	165.71	5.53	300	I BG26371 see09406.y1 Gm-cl067 C
gb_est2:BF299122	+ 71.50	158.53	13.90	605	I BF637831 NF043050F1F1036 Phose
gb_gss:BA2906675	+ 71.50	158.31	14.30	618	I BF299122 O68PBC11 Pb CDNA #20,
gb_est2:BF366639	+ 71.50	157.96	14.89	719	I BAH457228 BOHK53TF BOHK Brassic
gb_gss:CNS023J6	+ 71.50	157.54	15.77	666	I BF366639 P11_35.D02.g1.A002 Pat
gb_est1:AV917617	+ 71.00	154.41	23.56	904	I AL219733 Tetradon nigroviridis
gb_gss:BA2408211	+ 71.00	158.27	14.37	557	I AW37167 IL3-CF0220-091199-026-
gb_gss:BAH37653	+ 71.00	157.96	14.95	587	I AZ408211 IM0179K18F Mouse 10kb
gb_gss:BAH456623	+ 71.00	157.47	15.93	595	I BH37653 CH230-169119.TJ CHORI-
gb_gss:BAH00761	+ 71.00	156.38	16.11	600	I BAH456623 BOGLO21TF BOGL Brassic
gb_gss:CNS03535	+ 71.00	157.85	17.24	632	I BH300761 CH230-109J14.TJ CHORI-
gb_gss:BAH593625	+ 71.00	154.41	23.56	904	I AL219733 Tetradon nigroviridis
gb_gss:CNS023J6	+ 71.00	157.96	14.37	557	I AW37167 IL3-CF0220-091199-026-
gb_est1:AL1907481	+ 71.00	152.74	29.21	944	I AL21891 T7 end of clone A0AA0
gb_est2:BE581548	+ 70.50	157.97	14.93	502	I AL907481 RC-BT144-190399-038 BT
gb_est2:BJ172105	+ 70.50	155.62	20.20	632	I BJ172105 BJ172105 full length d

gb_est2:BJ164638	- 70.50	154.87	22.23	680	I BJ164638 BJ164638 full lengt
gb_est1:AW448595	+ 70.50	153.99	24.89	741	I AW448595 BRY 735 BRY Triticu
gb_gss:BH350007	+ 70.50	153.88	25.24	749	I BH350007 CH230-198K12.TJ CHO
gb_est2:BG603389	- 70.00	160.15	11.30	360	I BG603389 EST502479 Plasmodiu
gb_est2:199973	- 70.00	158.18	14.53	436	I Y99973 yeg99a11.r1 Soares fet
gb_gss:BH287081	+ 70.00	157.59	15.68	462	I BH287081 CH230-113M2.TV CHOR
gb_gss:BH260957	+ 70.00	156.42	18.22	518	I BH260957 CH230-90H4.TJ CHORI
gb_gss:BH260164	+ 70.00	154.80	22.43	607	I BH260164 CH230-90E16.TJ CHOR
gb_est2:BM1887904	+ 70.00	154.78	22.48	608	I B1887904 ZF637-1-002159 zebrr
gb_gss:AZ523131	+ 70.00	154.65	22.87	616	I AZ523131 Z15PB007 Pb MBN #21
gb_gss:AZ526651	+ 70.00	154.56	23.11	621	I AZ526651 Z58PB005 Pb MBN #21
gb_est2:BJ0609077	+ 70.00	153.91	25.14	662	I BJ0609077 BJ060907 NIBB Mochi
gb_gss:CNS07A5A	+ 70.00	149.26	45.61	1042	I AL436976 T3 end of clone BC
gb_gss:BM163086	+ 69.50	152.77	29.09	656	I BM163086 EST565609 PyBS Plas
gb_est2:BM163086	+ 69.50	150.59	38.50	812	I BM163086 EST565609 PyBS Plas
gb_gss:CNS01KDN	+ 69.50	148.68	49.15	978	I AL148204 Anopheles gambiae G
gb_est1:BB484810	- 69.00	160.59	10.67	271	I BB484810 BB484810 RIKEN full
gb_gss:AZ735725	+ 69.00	156.25	18.62	414	I AZ735725 RPCI-24-150M24.TV R
gb_est1:AW217002	+ 69.00	155.49	20.53	446	I AW217002 EST295716 tomato ca
gb_est2:BF227138	+ 69.00	155.17	21.38	460	I AW227869 up15c10.y1 NCI-CGAP
gb_est2:BF722398	+ 69.00	155.13	21.50	462	I BF722398 kx15c10.y1 Parastro
gb_est1:AI960861	+ 69.00	154.71	22.67	481	I BF722398 mab18604.y1 Soares
gb_est2:BJ032596	+ 69.00	154.40	23.60	496	I AI960861 sc91f04.y1 Gm-cl019
gb_gss:BM308205	+ 69.00	153.98	24.92	517	I BM308205 BJ032596 NIBB Mochi
gb_est2:BG802008	+ 69.00	153.88	25.24	522	I BG802008 0123-16 Mouse E14.5
gb_gss:BM311505	+ 69.00	153.80	25.50	526	I BM311505 CH230-3J3.TV CHORI-
gb_gss:BM324755	+ 69.00	153.21	27.49	557	I BM324755 CH230-31M8.TV CHORI
gb_est1:AW377200	- 69.00	153.14	27.75	561	I AW377200 IL3-CF0220-111199-0
gb_est2:BF1332174	+ 69.00	153.08	27.94	564	I BH287875 CH230-113024.TV CHO
gb_est2:BF1332174	+ 69.00	153.01	28.20	568	I BF1332174 G02981623F1 NCI-CGA
gb_est2:BF0202689	+ 69.00	152.98	28.33	570	I BF0202689 h13c02.x1 NCI-CGAP
gb_est1:AL519195	- 69.00	152.76	29.12	582	I AL519195 AL519195 LTI.NFL011
gb_gss:BM354348	+ 69.00	152.68	29.45	587	I BM354348 CH230-94J7.TV CHORI
gb_est1:AW035781	+ 69.00	152.43	30.37	601	I AW035781 EST281935 tomato ca
gb_est1:AL633862	+ 69.00	151.84	32.78	637	I AL633862 AL633862 XGC-gastru
gb_gss:BM307082	+ 69.00	151.69	33.39	646	I BM307082 CH230-10L17.TJ CHOR
gb_est2:BG694683	+ 69.00	151.48	34.35	660	I BG694683 NISC-lv06h02.w2 Soa
gb_est2:BM014203	+ 69.00	151.43	34.55	663	I BM014203 G0363902F1 NIH.MGC
gb_est2:BI916705	+ 69.00	151.34	34.96	669	I BI916705 G0317860F1 NIH.MGC
gb_est2:BM166061	+ 69.00	150.83	37.31	703	I BM166061 EST5658584 PyBS Plas
gb_gss:BF343724	+ 69.00	150.73	37.80	710	I BF343724 CH230-128B8.TV CHOR
gb_est1:AL644418	+ 69.00	150.66	38.15	715	I AL644418 AL644418 XGC-neurol
gb_est2:BE542200	+ 69.00	150.61	38.36	718	I BE542200 G01567501F1 NIH.MGC
gb_est2:BE542200	+ 69.00	150.49	39.00	727	I BE542200 G01066532F1 NIH.MGC
gb_est2:BG674067	+ 69.00	150.10	40.98	755	I BG674067 G01299527F1 NIH.MGC
gb_est2:BG674498	+ 69.00	149.78	42.70	779	I BG674498 G02620533F1 NCI-CGA
gb_est2:BF343724	+ 69.00	149.13	46.41	830	I BF343724 G02015382F1 NCI-CGA
gb_est2:BF582638	+ 69.00	148.30	51.61	900	I BF582638 G02094029F1 NCI-CGA
gb_est2:BE791748	+ 69.00	148.12	52.82	916	I BE791748 G01581568F1 NIH.MGC
gb_est2:BF138699	+ 69.00	147.99	53.73	928	I BF138699 G01781882F1 NCI-CGA
gb_est2:BF233109	+ 69.00	147.82	54.88	943	I BF233109 G02023850F1 NIH.MGC
gb_est2:BG749394	+ 69.00	147.55	56.79	968	I BG749394 G02070884F1 NIH.MGC
gb_hc:AK011509	+ 69.00	142.21	112.77	1632	I AK011509 Mus musculus 10 da
gb_hc:AK011853	+ 69.00	140.20	145.93	1986	I AK011853 Mus musculus 10 da
gb_hc:AK011711	+ 69.00	139.85	152.62	2055	I AK011711 Mus musculus 8 da
gb_gss:BAH363368	- 68.50	153.81	25.47	466	I BAH363368 CH230-96D12.TJ CHOR
gb_gss:BA294485	- 68.50	152.09	31.74	551	I BA294485 2M0279P23R Mouse 10
gb_gss:BAH322213	- 68.50	151.93	32.42	560	I BAH322213 CH230-116C20.TJ CHO
gb_gss:BAH336692	- 68.50	151.67	33.49	574	I BAH336692 CH230-20I013.TV CHO
gb_gss:BAH325872	- 68.50	151.03	36.35	611	I BAH325872 CH230-18B1.TJ CHOR
gb_gss:AZ521974	- 68.50	150.82	37.37	624	I AZ521974 200PBf10 Pb MBN #21
gb_gss:AG035967	- 68.50	149.34	45.18	721	I AG035967 CPG2746B CptOWAGDNA
gb_gss:AG035967	- 68.50	149.32	45.26	722	I BE914746 G01667765F1 NCI-CGA
gb_est2:BF1122303	- 68.50	148.89	47.83	733	I BF1122303 G01755785F1 NCI-CGA
gb_gss:BAH14206	- 68.50	148.81	48.33	759	I BAH14206 CH230-209A8.TJ CHOR
gb_est2:BF033475	- 68.50	146.06	68.78	993	I BF033475 G01457219F1 NIH.MGC
gb_est1:BF031814	- 68.00	161.71	9.25	191	I BF031814 CMO-BF70306-221299-1
gb_gss:AG035967	- 68.00	155.98	19.26	334	I B1743153 kx39d03.y1 Parastro
gb_est2:BI743153	+ 68.00	152.77	29.08	457	I BI743153 kx34g11.y1 Parastro
gb_est2:BI742764	+ 68.00	152.64	29.58	463	I BI742764 kx12b11.y1 Parastro
gb_est2:BI322438	+ 68.00	152.47	30.25	471	I BI322438 kx16C06.y3 Parastro
gb_est2:BI322792	+ 68.00	152.40	30.50	474	I BG272792 WHE2237_G08_M1525A

[illegible]

gb_gss:BH340242	64.00	142.06	114.92	497	BH340242	CH230-41E22.TJ	CHORI-2	gb_gss:BH262780	64.00	137.26	212.61	794	BH262780	CH230-171E21.TJ	CHOR
gb_est2:B6726797	64.00	142.02	115.53	514	B6726797	sac027a11.y1	Gm-cl0107.G	gb_gss:BH264097	64.00	137.24	213.32	796	BH264097	CH230-91C13.TJ	CHOR
gb_est1:A1900348	64.00	141.71	120.11	514	A1900348	sc04d12.y1	Gm-cl0102.G	gb_gss:AO935402	64.00	137.06	218.26	810	AO935402	CPG23452B	CPiOWAGDNA
gb_gss:BH351381	64.00	141.71	120.11	514	BH351381	CH230-54N23.TJ	CHORI-2	gb_gss:BH337749	64.00	136.94	221.45	819	BH337749	CH230-51C2.TJ	CHORI
gb_gss:AO928051	64.00	141.67	120.73	516	AO928051	479.dif03h12.s1	Saccha	gb_gss:BH570197	64.00	136.92	221.16	821	BH570197	BOG9011TR	BOG9Bras
gb_gss:AO9202574	64.00	141.46	124.12	527	AO9202574	V5H2.mtn-3XHA/lacZ	Inf	gb_gss:BH570197	64.00	136.92	222.87	823	BH570197	BOG9011TR	BOG9Bras
gb_est2:B1621110	64.00	141.28	126.91	536	B1621110	RE01521.Sprime	RE Dros	gb_gss:BH073736	64.00	136.47	235.40	858	BH073736	RPCI-24-391E18.TJ	R
gb_est2:B1972255	64.00	141.17	128.78	542	B1972255	sag89b10.y1	Gm-cl084.C	gb_gss:BH357701	64.00	136.38	237.92	865	BH357701	CH230-6B34.TJ	CHORI
gb_est1:A1259492	64.00	141.11	129.71	545	A1259492	LP02916.Sprime	LP Dros	gb_gss:BH073674	64.00	136.36	238.64	867	BH073674	RPCI-24-391C18.TJ	R
gb_est2:B188049	64.00	141.11	129.71	545	B188049	sap84b06.y1	Gm-cl074.C	gb_gss:BH339740	64.00	136.12	246.26	888	BH339740	CH230-130I19.TV	CHOR
gb_gss:BH333605	64.00	141.10	130.03	546	BH333605	CH230-26L5.TV	CHORI-2	gb_gss:CHNS07AFV	64.00	135.56	264.63	938	CHNS07AFV	T7 end of clone	BCO
gb_est1:AW309043	64.00	141.06	130.65	548	AW309043	sf94b08.y1	Gm-cl019.G	gb_gss:CHNS06FYS	64.00	135.56	264.63	938	CHNS06FYS	T7 end of clone	BCO
gb_est2:B1587261	64.00	141.06	130.65	548	B1587261	sf94b08.y1	Gm-cl019.G	gb_hct:AK020784	64.00	133.24	286.32	996	AK020784	Mus musculus	0 day
gb_gss:BH357704	64.00	141.01	131.59	551	BH357704	CH230-163M18.TV	CHORI-	gb_est1:AW317574	63.50	144.36	85.57	352	AW317574	sg52h02.y1	Gm-cl025
gb_gss:BH3505192	64.00	140.97	132.22	553	BH3505192	CH230-192Y21.TJ	CHORI-	gb_est1:AW317574	63.50	144.36	85.57	352	AW317574	sg52h02.y1	Gm-cl025
gb_gss:BH578296	64.00	140.95	132.53	554	BH578296	rk10c10.y1	MeloIdogvne	gb_est1:AL504124	63.50	142.55	107.90	420	AL504124	A504124	Hordium vu
gb_est2:B1235763	64.00	140.82	134.74	561	B1235763	RE31684.Sprime	RE Dros	gb_est2:BM325502	63.50	142.53	108.24	421	BM325502	PIC1-45_D03	bl_A002
gb_gss:BH297578	64.00	140.82	134.74	561	BH297578	CH230-1K11.TJ	CHORI-2	gb_est2:BM325502	63.50	142.53	108.24	421	BM325502	PIC1-45_D03	bl_A002
gb_est2:B1612980	64.00	140.73	136.32	566	B1612980	RH42019.Sprime	RH Dros	gb_est1:BM184789	63.50	142.43	109.59	435	BM184789	EST320465.L	pennel
gb_gss:BH338054	64.00	140.67	137.27	569	BH338054	CH230-40P22.TV	CHORI-2	gb_est2:BM184789	63.50	142.43	109.59	435	BM184789	EST320465.L	pennel
gb_gss:BH366654	64.00	140.66	137.58	570	BH366654	CH230-112H19.TJ	CHORI-	gb_est1:BM070510	63.50	141.33	126.13	473	BM070510	sa37e10.y1	Gm-cl027
gb_est1:AH348676	64.00	140.62	138.22	572	AH348676	GM210003A11E10	Gm-r102	gb_est2:BE607645	63.50	142.07	114.70	440	BE607645	sq15b05.y1	Gm-cl046
gb_gss:BH348501	64.00	140.57	139.17	575	BH348501	CH230-42G18.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_est2:B1700119	64.00	140.48	140.76	580	B1700119	sag63d04.y1	Gm-cl082.C	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW394461	63.50	141.91	117.10	447	AW394461	sq15b05.y1	Gm-cl046
gb_gss:BH338054	64.00	140.48	140.76	580	BH338054	CH230-26FA.TV	CHORI-2	gb_est1:AW39							

gb_gss: BH286172	63.50	136.20	243.67	781	BH286172	CH230-157K8.TJ	CHORI-2	gb_est2:BF645762	63.00	136.94	221.53	644
gb_est2:BAV4030316	63.50	136.16	244.90	784	BG419313	602445984F1	NIH_MGC_14	gb_est2:BJ055073	63.00	136.93	221.98	645
gb_est1:BG190171	63.50	136.12	246.13	787	GB430076	AV403076	Bombay mori C	gb_gss: BH287018	63.00	136.89	222.89	647
gb_gss: BH361598	63.50	136.11	246.54	788	BG361598	CH230-23B6.TJ	CHORI-23	gb_est2:BF298419	63.00	136.88	223.34	648
gb_est2:BG5941798	63.50	136.09	246.95	789	BG594179	EST493467	CTS Solanum	gb_est1:AI590075	63.00	136.86	223.79	649
gb_gss: BH331917	63.50	135.93	252.31	802	BH331917	CH230-46M3.TJ	CHORI-23	gb_gss: BH230544	63.00	136.75	226.97	656
gb_est2:AL2537032	63.50	135.27	274.43	855	AL2537032	AL537032	LTT_F013_FBI	gb_gss: BH235789	63.00	136.57	232.44	668
gb_est2:CL25694	63.50	135.26	274.85	856	CL25694	C25694	Dicystostellum dis	gb_gss: BH275671	63.00	136.51	234.27	672
gb_gss: CNS06E5G	63.50	135.07	281.62	872	AL34682	T3 end of clone AROAA		gb_est1:BB331004	63.00	136.43	236.56	677
gb_gss: BH149605	63.50	134.93	286.72	884	BH149605	ENTPG19TR	Entamoeba hi	gb_est2:R1371000	63.00	136.40	237.48	679
gb_gss: BH210268	63.50	134.88	288.42	888	AZ210268	SP_0152_B2_B04_SP6E	SD	gb_gss: BH285044	63.00	136.38	237.93	680
gb_gss: BH160873	63.50	134.52	302.15	920	BH160873	ENTRO28TR	Entamoeba hi	gb_gss: BH318980	63.00	136.32	239.77	684
gb_est2:BE413179	63.50	134.13	317.77	956	BE413179	MCG014.B07R990625	ITEC	gb_gss: BH366666	63.00	136.18	244.39	694
gb_gss: CNS06NC9	63.50	133.94	325.65	974	AL406591	T3 end of clone AUOAA		gb_gss: BH321878	63.00	136.15	245.31	696
gb_gss: CNS06PI2	63.50	133.33	352.24	1034	AL409392	T3 end of clone AUOAA		gb_gss: BH264483	63.00	136.13	245.78	697
gb_est1:AI985918	63.00	145.25	76.30	286	AI985918	wn76C02.X1	NCL_CGAP_U0	gb_gss: BH324575	63.00	136.03	249.02	704
gb_est1:AV138551	63.00	145.07	78.06	291	AV138551	AV138551	Mus CGAP_U0	gb_est2:BF486181	63.00	135.96	251.35	709
gb_est1:AV177561	63.00	144.76	81.24	300	AV177561	AV177561	Yuj1 Kohara u	gb_gss: BH308704	63.00	135.88	253.68	714
gb_est1:AI164583	63.00	141.87	117.76	398	AI164583	A065P30	Hybrid aspen	gb_gss: BH299512	63.00	135.87	254.14	715
gb_est2:BI473583	63.00	141.87	117.76	398	BI473583	f39d05.y3	zebrafish	gb_gss: BH359719	63.00	135.87	254.14	715
gb_gss: AQ970982	63.00	141.84	118.15	399	AQ970982	RPC1-23-310K15.TJ	RPC1	gb_est2:BI913032	63.00	135.80	256.48	720
gb_gss: BH3311595	63.00	141.15	129.15	427	BH3311595	CH230-62I17.TJ	CHORI-2	gb_gss: BH290093	63.00	135.77	257.42	722
gb_est1:AI967452	63.00	140.66	137.55	448	AI967452	Ljlrpes02-128-d1	Ljlr	gb_gss: BH357202	63.00	135.77	257.42	722
gb_gss: BH281671	63.00	140.01	149.36	477	BH281671	CH230-166J10.TJ	CHORI-1	gb_gss: BH356800	63.00	135.76	257.88	723
gb_gss: BH275161	63.00	139.76	154.32	489	BH275161	CH230-1D12.TJ	CHORI-23	gb_est2:BJ149853	63.00	135.71	259.29	726
gb_gss: BH337579	63.00	139.66	156.39	494	BH337579	CH230-99M2.TJ	CHORI-23	gb_gss: BH297596	63.00	135.53	265.40	739
gb_gss: BH344720	63.00	139.37	162.24	508	BH344720	CH230-11N8.TJ	CHORI-23	gb_gss: BH298522	63.00	135.50	266.35	741
gb_est1:BE107781	63.00	139.19	166.02	517	BE107781	UI-R-CAO-aw-g-11-0-U0		gb_est2:BF496523	63.00	135.49	266.82	742
gb_gss: BH331574	63.00	138.96	171.10	529	BH331574	CH230-175B21.TJ	CHORI-1	gb_gss: BH265613	63.00	135.49	266.82	742
gb_gss: BH356124	63.00	138.80	174.51	537	BH356124	CH230-16P6.TJ	CHORI-23	gb_est2:BF504261	63.00	135.44	268.71	746
gb_est1:AV731639	63.00	138.74	175.79	540	AV731639	AV731639	HTF Homo sap1	gb_est2:BF504443	63.00	135.23	275.83	761
gb_gss: BH339108	63.00	138.69	177.07	543	BH339108	CH230-105P20.TJ	CHORI-1	gb_gss: BH280079	63.00	135.22	276.30	762
gb_gss: BH330113	63.00	138.66	180.08	550	BH330113	CH230-46H24.TJ	CHORI-2	gb_gss: BH297178	63.00	135.18	277.73	765
gb_est2:BE637773	63.00	138.54	180.91	551	BE637773	WHE1755-1758.L01.L01Z		gb_gss: BH288242	63.00	135.17	278.21	766
gb_gss: BH301651	63.00	138.52	180.94	552	BH301651	CH230-147P18.TJ	TJB CHORI-1	gb_gss: BH503132	63.00	135.05	282.51	775
gb_gss: BH333528	63.00	138.45	182.66	556	BH333528	CH230-26L1.TJ	CHORI-23	gb_gss: BH294884	63.00	134.98	284.91	784
gb_est2:BE426108	63.00	138.41	183.52	558	BH287013	CH230-20K62.TJ	CHORI-2	gb_est2:BJ151863	63.00	134.91	287.31	785
gb_gss: BH267878	63.00	138.39	183.96	559	BE426108	WHE320-F05.L10Z5	Whea	gb_gss: BH582066	63.00	134.90	287.79	786
gb_gss: BH279495	63.00	138.37	184.39	560	BH267878	CH230-215G12.TJ	CHORI-1	gb_gss: BH366727	63.00	134.72	294.54	800
gb_gss: BH320354	63.00	138.16	189.59	572	BH279495	CH230-128017.TJ	CHORI-1	gb_gss: BH503086	63.00	134.62	298.41	808
gb_est2:BG603011	63.00	138.12	190.46	574	BH290354	CH230-173F2.TJ	CHORI-2	gb_gss: BH473109	63.00	134.41	306.68	825
gb_gss: BH267402	63.00	138.08	191.34	576	BG603011	EST502101	Plasmodium y	gb_gss: BH527134	63.00	134.31	310.59	833
gb_gss: BH362939	63.00	138.01	193.08	580	BH267402	CH230-82K21.TJ	CHORI-2	gb_gss: BH527134	63.00	134.18	315.50	843
gb_gss: BH3319611	63.00	138.01	193.08	580	BH362939	CH230-5M5.TJ	CHORI-23	gb_gss: BH607460	63.00	134.17	315.99	844
gb_gss: BH279577	63.00	137.87	196.59	588	BH319611	CH230-119P17.TJC	CHORI-1	gb_gss: CNS0755L	63.00	134.03	321.90	856
gb_gss: BH325404	63.00	137.86	197.03	589	BH279577	CH230-71F23.TJ	CHORI-2	gb_gss: CNS075Q0	63.00	133.86	328.83	870
gb_gss: BH283769	63.00	137.84	197.47	590	BH25404	CH230-104N9.TJ	CHORI-2	gb_est2:BG493342	63.00	133.71	335.30	883
gb_gss: BH291429	63.00	137.68	201.43	599	BH283769	CH230-97K8.TJ	CHORI-23	gb_gss: BH134601	63.00	133.12	361.47	935
gb_gss: BH305818	63.00	137.68	201.43	599	BH291429	CH230-78G2.TJ	CHORI-23	gb_est2:BM472021	63.00	133.05	365.03	942
gb_gss: A2995079	63.00	137.63	202.76	602	A2995079	2M0280H1AR	Mouse 10kb	gb_gss: CNS077A6	63.00	132.16	408.88	1027
gb_gss: BH332062	63.00	137.63	202.76	602	BH332062	CH230-150C8.TJ	CHORI-2	gb_gss: CNS039640	63.00	132.06	414.11	1037
gb_gss: BH258323	63.00	137.56	204.53	606	BH258323	CH230-112J7.TJ	CHORI-2	gb_est2:BG719916	63.00	131.18	463.55	1130
gb_gss: BH47305	63.00	137.56	204.53	606	BH47305	CH230-42D23.TJ	CHORI-2	gb_gss: BH5056109	63.00	130.21	525.35	1243
gb_hlc: AK004646	63.00	137.55	204.97	607	BH283831	CH230-49M18.TJ	CHORI-2	gb_hlc: AK004646	63.00	128.43	660.07	1479
gb_est1:AA571079	63.00	137.50	206.30	610	BH318603	CH230-119P17.TJC	CHORI-1	gb_est1:AA571079	63.00	120.07	1.9e+03	3345
gb_gss: BH301207	63.00	137.50	206.30	610	BH301207	CH230-84012.TJ	CHORI-2	gb_est1:BM472021	62.50	141.14	129.34	379
gb_est1:AW518116	63.00	137.40	208.97	616	AW518116	x81B08.X1	NCL_CGAP_LY	gb_est1:BM472021	62.50	140.61	138.37	399
gb_gss: BH325404	63.00	137.38	208.97	616	BH282292	CH230-117M16.TJ	CHORI-1	gb_gss: BH313369	62.50	140.26	144.78	413
gb_gss: BH329198	63.00	137.38	209.42	617	BH29198	CH230-18J79.TJ	CHORI-2	gb_est2:BM094920	62.50	139.96	150.33	425
gb_gss: BH364749	63.00	137.36	209.86	618	BH364749	CH230-608R.TJ	CHORI-23	gb_est1:BM037416	62.50	139.92	151.26	427
gb_est2:BF295997	63.00	137.30	211.65	622	BF295997	032PB09	Pb cdNA #17	gb_est1:BE017846	62.50	139.47	157.34	440
gb_gss: BH310152	63.00	137.26	212.54	624	BH310152	CH230-17H12.TVB	CHORI-1	gb_est1:BE200666	62.50	139.47	160.16	446
gb_gss: BH338693	63.00	137.26	212.54	624	BH338693	CH230-51E5.TJ	CHORI-23	gb_est2:BM040408	62.50	139.24	164.89	456
gb_gss: BH342581	63.00	137.26	212.54	624	BH342581	CH230-18J17.TJ	CHORI-1	gb_gss: BH259114	62.50	139.18	166.32	459
gb_gss: BH393970	63.00	137.25	212.99	625	BH393970	AG-ND-174P19	TRR NC-TAM	gb_est1:BE201413	62.50	139.13	167.27	461
gb_est2:BG018576	63.00	137.20	214.33	628	BG018576	daa51C04.v1	Wellcome c	gb_gss: BH333847	62.50	139.09	168.22	463
gb_gss: BH337134	63.00	137.18	214.78	629	BH337134	CH230-89A8.TV	CHORI-23	gb_est1:BE017697	62.50	138.76	175.42	478
gb_est2:BF490990	63.00	137.15	215.68	631	BF490990	AT27637	Spime AT Dros	gb_est1:BE202130	62.50	138.57	179.77	487
gb_gss: BH327493	63.00	137.09	217.48	635	BH327493	CH230-32E24.TJ	CHORI-2	gb_est2:BF563790	62.50	138.51	181.22	490
gb_gss: BH297889	63.00	137.07	217.93	636	BH297889	CH230-84E24.TJ	CHORI-2	gb_est1:BE201425	62.50	138.30	186.09	500
gb_est2:BF506180	63.00	137.01	219.73	640	BF506180	AT08582	Spime AT Dros	gb_gss: AQ022825	62.50	138.24	187.56	503
								gb_gss: AQ024123	62.50	138.22	188.05	504

qb_est2:BM282772	+	61.50	133.01	366.82	659	BM282772	ki40d08_v1 Ascaris suum
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qb_gss:BH319724	+	61.50	132.87	373.41	668	BH319724	CH230-20E23.TJ CHORI-2
qb_gss:BH467561	-	61.50	132.87	373.41	668	BH467561	BOGEG61TR.BOGP.Brassica
qb_est1:AW713956	+	61.50	132.82	375.62	671	AW713956	EST3212942 KV3 Medicag
qb_gss:BG918770	+	61.50	132.81	376.35	672	BG918770	60281924971 NC1.CGAP.M
qb_est2:BG918770	+	61.50	132.81	376.35	672	BG918770	60281924971 NC1.CGAP.M
qb_est2:C84701	+	61.50	132.79	377.99	673	C84701	Dactyostelium discoideum
qb_est2:BM160882	+	61.50	132.75	379.30	676	BM160882	EST563405 PyBs Plasmod
qb_est1:BB638635	-	61.50	132.72	380.77	678	BB638635	BB638635 RIKEN full-length
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seq_name: qb_est2:BI813876

seq_documentation_block:			
LOCUS	BT183876	487 bp	mRNA linear EST 03-OCT-2001
DEFINITION	P8180aa19d05.y1 Plasmodium falciparum 3D7 asexual cDNA Plasmodium falciparum cDNA 5', mRNA sequence.		

ACCESSION	BI813876
VERSION	BI813876.1
	GI:15906057

KEYWORDS

SOURCE malaria parasite *P. falciparum*

ORGANISM Plasmodium falciparum

REFERENCE
1. (bacc 1 to 407)
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

REFERENCE
I (bases 1 to 487)
Tang K, Cole R, Chakrabarti D, Haywood P, Clifton S, Pa

Mangat, C. J. 1977. Chalkwaterbirds, p. 145-150. In: J. A. Baker and J. R.
 Burger (eds.), *Waterfowl and Wetlands*. Academic Press, New York.
 Marra, M., Hillier, L., Martin, J., Wylie, T., Dente, M., Theising, B.,
 Swales, Y., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I.,
 Tsagarisvilli, R., Belaygorod, L., Franklin, C., Carr, L., Grow, A.,
 Maguire, L., Richey, J., Wadkins, J., Kennedy, S., Levinso, D.,
 Waterston, R., Wilson, R., and Sibley, D.

TITLE Washu Plasmodium EST Project

JOURNAL
Unpublished (2001)

COMMENT
Contact: L. David Sibley
Wasbu Plasmodium FST Project

WASHINGTON UNIVERSITY SCHOOL OF MEDICINE
WASHINGTON UNIVERSITY ESI PROJECT

4444 Forest Park Parkway, Bo

Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu
Library was constructed by D

Library was constructed by
Washington University Genome

obtaining a clone please con

(sibley@borcim.wustl.edu), W

Seq primer: -400p from GIBCO
High quality sequence store:

FEATURES

source
1. .487

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xhoI; Library was c

High quality sequence stop: 471.

FEATURES

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1. 471
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/cdone_lib="BR0248"
/dev_stage="Adult"
/notes="Organ: breast; Vector:
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from ORESTES PCR (U. S. Lett
716 - Ludwig Institute for
into the pUC 18 vector. Rev
mRNA and cDNA amplification
stringency conditions."
124 a 118 c 122 g 107 t
BASE COUNT
ORIGIN

alignment_scores:
Quality: 78.50
Ratio: 1.744
Percent Similarity: 57.692
Length:
Gaps:
Percent Identity:

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Reagent Resource Center, ATCC
<http://www.malaria.mr4.org/mr4pages/index.html>
 Seq primer: ADF.

FEATURES

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FEATURES             Location/Qualifiers
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         /strain="17XL"
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         /clone="pYCPW42"
         /clone_lib="PyBS"
         /dev_stage="Asexual blood stages"
         /lab_host="E. coli XL-1 Blue"
         /notes="Vector: pAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/cBYJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose columns. Total RNA was
isolated using the guanidium isothiocyanate method, and
mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to
HybridAP arms directionally using EcoRI-XhoI cleaved arms.
After packaging, the phagemid vector (pAD-GAL4) was
excised from the HybridAP vector and plasmid DNA

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```

sequence.
ACCESSION      AL275743
VERSION        AL275743.1 GI:8009945
KEYWORDS       GSS; genome survey sequence.
SOURCE         Tetraodon nigroviridis.
ORGANISM       Tetraodon nigroviridis
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
               Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
               Tetraodontidae; Tetraodon.
REFERENCE      1 (bases 1 to 1055)
AUTHORS        Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
               Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
               Weissenbach,J.
TITLE          Characterization and repeat analysis of the compact genome of the
               freshwater pufferfish Tetraodon nigroviridis
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 1055)
AUTHORS        Roest-Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
               Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
               Saurin,W. and Weissenbach,J.
TITLE          Human gene number estimate provided by genome wide analysis using
               Tetraodon nigroviridis DNA sequence
JOURNAL        Unpublished
REFERENCE      3 (bases 1 to 1055)
AUTHORS        Direct Submission
TITLE          Submitted (12-APR-2000) to the EMBL/GenBank/DBDJ databases
JOURNAL        This sequence is a single read and was generated as part of a large
               scale clone-end sequencing project of the Tetraodon nigroviridis
               genome. For more information, please take a look at
               http://www.genoscope.cns.fr/Tetraodon.
FEATURES       Location/Qualifiers
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               /clone_lib="G"
               /note="Genoscope sequence ID : C0BG084BA10SPL-end :
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Quality:       78.00      Length: 109
Ratio:         1.345      Gaps: 7
Percent Similarity: 53.211 Percent Identity: 30.275
alignment_block:
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15 AlaAsnThrAsnThrThrGlnPheLeuAsnMetGly.....AsnGly 29
   ::::::::::: ::::::::::: :: ::::
692 TCACAACCGCTCCGCTCTCAGATGCCGACTCGGCGCTTGGGAG 741
29 uValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuSerAlaGluG 46
   ::::::::::: ::::::::::: :::::
742 CATCCGCTGGGAGGAGG...CGCACSSTAGGCATCCCTCCGCTWG 788
46 lVGlyMetAsp.....ArgAspLeu.....PheGlySerAla 56
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789 GGGGAAGACCTGCAGCTCAGGACCTTCGTAAACTGGGGAGCGCA 838
57 AsnIleAspGlyPhe.....ProGluValArgGluPheAsnSe 69
   ::::: ::::: :::::::::::
839 AACACGCGTGTATTAAATAGCCGCGCGCTTTGAAAGATCACATAG 888
69 rIeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnH 86
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889 C.....CCGCAGC 896
seq_name: gb_gss:CNS06FOV
seq_documentation_block:
LOCUS          CNS06FOV
DEFINITION     T3 end of clone AR0AA031H06 of library AR0AA from strain CBS 732 of
               Zygocaccharomyces rouxii, genomic survey sequence.
ACCESSION      AL396677
VERSION        AL396677.1 GI:12148934
KEYWORDS       GSS.
SOURCE         Zygocaccharomyces rouxii.
ORGANISM       Zygocaccharomyces rouxii
               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
               Saccharomycetales; Saccharomycetaceae; Zygocaccharomyces.
REFERENCE      1 (bases 1 to 982)
AUTHORS        de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B.,
               Wincker,P., Artiguenave,F. and Souciet,J.
TITLE          Genomic exploration of the hemiascomycetous yeasts: 8.
JOURNAL        Zygocaccharomyces rouxii
MEDLINE        FEBS Lett. 487 (1), 52-55 (2000)
REFERENCE      2 (bases 1 to 982)
AUTHORS        Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
               Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
               de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
               Malpertuy,A., Neueglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
               Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
               Wincker,P. and Weissenbach,J.
TITLE          Genomic exploration of the hemiascomycetous yeasts: 1. A set of
               yeast species for molecular evolution studies
JOURNAL        FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE        20584711
REFERENCE      3 (bases 1 to 982)
AUTHORS        Genoscope.
TITLE          Direct Submission
JOURNAL        Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,
               2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
               seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT        This GSS is part of a random genomic sequencing program of thirteen
               yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
               exiguus, Saccharomyces servazzii, Zygocaccharomyces rouxii,
               Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
               lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
               angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
               Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
               5 kb were prepared and both extremities were sequenced. See
               keywords for description of this sequence and for the sequence of
               the other extremity of this insert.
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               2 putative frameshift(s)"
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FEATURES
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/dev_stage="0-3 day old Ore-R males"
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
AT.121-AT.319: DH5-alpha Tona"
/notes="Organ: ADULT testes; Vector: pOTB7; Site.1: EcoRI;
Site.2: XhoI; The mRNA for the testis library was made
from testes and seminal vesicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid cDNA library."
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190 ....GCACCTAACCTGTCGGGATGATGGCTGGATGATGACTCTCTTCGT 235
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380 GGC 382
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DEFINITION      067PbF01 Pb cDNA #20, Charles Yowell and Jane Carlton Plasmodium
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ACCESSION      BF299368
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KEYWORDS
SOURCE
  organism      plasmodium berghei.
  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
  1 (bases 1 to 645)
REFERENCE
  Carlton,J.M.-R. and Dame,J.B.
  The Plasmodium vivax and P. berghei gene sequence tag projects
  Parasitol. Today 16 (10), 409 (2000)
  Contact: Dame JB
  Department of Pathobiology, College of Veterinary Medicine
  University of Florida

```

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2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611-0880, USA
Tel: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.vetmed.ufl.edu
Seq primer: M13(-20)forward.
Location/Qualifiers
1. .645
/organism="Plasmodium berghei"
/strain="ANKA clone 15cyl (clone of the ANKA 8417 HP clone
)"
/db_xref="taxon:5821"
/clone_lib="Pb cDNA #20, Charles Yowell and Jane Carlton"
/dev_stage="asynchronous blood stage"
/lab_host="Swiss white mice"
/notes="Vector: pBluescript II vector DNA, excised from
Lamda ZAP II.; Site.1: EcoRI; Site.2: XhoI; Total RNA was
extracted from asynchronous blood stage forms of the
cloned ANKA isolate of P. berghei grown in laboratory
Swiss white mice. Contaminating host white cells had
previously been removed using a novel biomagnetic bead
protocol (J. Carlton et al., manuscript in preparation).
PolyA+ RNA was extracted and reverse transcribed using an
oligo dT-XhoI primer. Second strand cDNA was prepared
using RNase H and DNA polymerase I. EcoR I adaptors were
ligated to the cDNA, and it was digested with XhoI.
Fragments were size selected, and those between 1-5 kb
ligated into EcoRI /XhoI digested vector."
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|||||:|||||:|||||:|||||:|||||:
337 .....TCTATAGACAGTTTAAATTTTATAAC 312
71 oAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnHisAspA 88
|||||:|||||:|||||:|||||:|||||:
311 CAATATATAA.....GAAGATATAAATAAGATAAACAAACAAG 271
88 laAspPheLysTyrIleLysLeuLeuIle.....AsnAsnAspGly 102
|||||:|||||:|||||:|||||:|||||:
270 CCGAT...AAAAAATATATTATTCATTATTAGTACCATCTAAAACTCAAT 224
103 PhePheSer 105
|||||:|||||:
223 TTTTATAAT 215
seq_name: gb_est2:BF293289
seq_documentation_block:
LOCUS      BF293289

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```

DEFINITION EST543194 tomato callus Lycopersicon esculentum cDNA clone
ACCESSION cLEC80117 5' end, mRNA sequence.
VERSION BI923289
KEYWORDS BI923289.1 GI:16222284
SOURCE EST.
ORGANISM tomato.
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 752)
Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai
,J., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin
,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato callus tissue (2001)
Unpublished (2001)
Contact: CUGI
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
Location/Qualifiers
1..752
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC80117"
/clone_lib="tomato callus"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRF"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Boyce Thompson Institute; sequencing: The
Institute for Genomic Research; cLEC - Cotyledons of
seedlings 7-10 days post-germination were excised, cut at
both ends and placed on MS medium with no selection. Mixed
callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
BASE COUNT 206 a 127 c 178 g 241 t
ORIGIN

alignment_scores:
Quality: 74.00 Length: 119
Ratio: 1.175 Gaps: 6
Percent Similarity: 52.941 Percent Identity: 26.050

alignment_block:
US-09-528-682-4 x BI923289 ..
Align seg 1/1 to: BI923289 from: 1 to: 752
13 ProfileAlaAsnThrAsn.....ThrTh 20
|||||.....|
343 CCGGTGCTTTCGACGAAATTTGGAAATTTCCGGAACATCGACGGCAGC 392
20 rThrGlnPheLeuAsnMet...GlyAsnGluVal..... 30
|||||.....|
393 GCGCGATTTGTCAGGTGGAGCAATATCTGTTGTTGTTAAAC 442
31 .....AlaLeuAspGlyArgTyrSerAsnTyrAlaLeu 42
|||||.....|
443 GTGGAAGGAGAGGTGCAATGGAGGATCGTTATCT.....GCATTGTC 486
43 SerAlaGluGlyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAs 59
|||||.....|
487 AATTACAGGAGGATTCAAAACAGGGATTTTGTGTTATTTGATGGACA 536
59 pGlyPheProGluValArgGluPheAsnSerLeuProAsnAsnLysAlaAs 76

```

```

|||||.....|
537 TGGAGGACCTAAAGCTGCAGAGTTTGCAGCAGACACCTTGAATAAGACA 586
|||||.....|
76 erSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLys 92
|||||.....|
587 TTATGGAT.....GAATTAGTAGAGGAGGAATGATGAAGATGTTGTGGAA 630
|||||.....|
93 TyrIleLys.....LeuLeuIleAsnAsnAspGlyPhePheSerAsnAs 107
|||||.....|
631 GTGCTGAAAATGTTTATTAAACACAGATACCGAATTCCTCAGTGAAGA 680
|||||.....|
107 nGlyGly 109
681 TTTTGGG 687
seq_name: gb_gss:BH302927
seq_documentation_block:
LOCUS BH302927 816 bp DNA linear GSS 30-NOV-2001
DEFINITION CH230-58G18.TVB CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-58G18, DNA sequence.
ACCESSION BH302927
VERSION BH302927.1 GI:17215335
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 816)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
COMMENT
Other_GSSs: CH230-58G18.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
plate: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 58 row: G column: 18
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..816
/organism="Rattus norvegicus"
/strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-58G18"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"
BASE COUNT 380 a 161 c 144 g 131 t
ORIGIN

alignment_scores:
Quality: 74.00 Length: 125
Ratio: 1.213 Gaps: 4
Percent Similarity: 48.800 Percent Identity: 24.800

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alignment_block:
US-09-528-682-4 x BH302927
Align seg 1/1 to: BH302927 from: 1 to: 816
3 pheThrValArgIleGlnAspAlaTyrGluProIleAlaAsnThrAsnTh 19
236 TTCCACCAACAGAGATACAGAGATGGAAGAGAAATCTCAGGAACAGAGA 285
19 rThrThrGlnPheLeuAsnMetGly..... 27
286 TTCCATAGAAATCATTTGACTCACTGCTCAAGATTAATGTAAAGCGGAAAA 335
28 .....AsnGluValAlaLeuAspGlyArgTyrSer 37
336 AGCTACTGTGTCACCAACATACAGGAATCCAGGACTCAATGAGAGATCA 385
38 AsnTyrAlaLeuIleSerAlaGluGlyMetAspArgAspLeuPheG1 54
386 AACCTAAGAGATAATAGGTATAGAGAGAGTGAAGACTCCCGAGCTCAAGG 435
54 ySerAlaAsnIle.....AspGlyPhePro..... 62
436 ACCAGTAAATATCTTCAACAAATCATGAGAGAACTTCCTTAACCTAA 485
63 .....GluValArgGluPheAsnSerLeuProAsnAsn 73
486 AAAAGAGATACCCATAGACATACAGAGAGCTCAGAACTCCAAATAGA 535
74 LysAlaSerSerAspThrAlaSer.....LeuAsnLysGlnHisAs 87
536 AACACCAGAAAAAGAACACCCCGCTCACATAATTTGTTGAAAAAACACCA 585
87 pAlaAspPheLysLysTyrIleLys 95
586 AACGCACAAAAATAAGATATTAA 610
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```
seq_name: gb_gss:AZ930886
seq_documentation_block:
LOCUS AZ930886 501 bp DNA linear GSS 01-APR-2001
DEFINITION 474.dhz59f11.sl Saccharomyces unisporus NRRL Y-1556 Saccharomyces
unisporus genomic clone 474.dhz59f11.sl, DNA sequence.
ACCESSION AZ930886
VERSION AZ930886.1 GI:13501796
KEYWORDS GSS.
SOURCE Saccharomyces unisporus.
ORGANISM Saccharomyces unisporus.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 501)
AUTHORS Cliften,P.F., Hillier,L.W., Fulton,L., Graves,T., Miner,T., Gish
W.R., Waterston,R.H. and Johnston,M.
TITLE Surveying Saccharomyces genomes to identify functional elements by
comparative DNA sequence analysis
JOURNAL Unpublished (2001)
COMMENT Contact: Johnston M
Department of Genetics
Washington University Medical School
Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
Tel: 314 362 2735
Fax: 314 362 7855
Email: mj@genetics.wustl.edu
Class: random plasmid subclone.
FEATURES
source
1..501
/organism="Saccharomyces unisporus"
/strain="NRRL Y-1556 (CBS 398)"
/db_xref="taxon:27294"
/clone="474.dhz59f11.sl"
/clone_lib="Saccharomyces unisporus NRRL Y-1556"
/note="Random genomic sequence"
BASE COUNT 151 a 86 c 72 g 192 t
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ORIGIN
alignment_scores:
Quality: 73.50 Length: 116
Ratio: 1.205 Gaps: 6
Percent Similarity: 52.586 Percent Identity: 28.448
alignment_block:
US-09-528-682-4 x AZ930886/rev
Align seg 1/1 to reverse of: AZ930886 from: 1 to: 501
16 AsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLe 32
501 AACAGACACACTATACAAAT...CTAAATTTAGTTCATGGTAACT... 457
32 uAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyGlyMeta 49
456 .GATAAAGATATACAAACATTAT.....G 435
49 sPAtgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArg 65
434 ATAGACGCTTATATCGAGTCCCAATCTGCAATGTACATGATGTCAAATTATA 385
66 GluPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLe 82
384 GAATAAATGGCTTACCAGATGATGATAATGAAGCAGAGAGAGGACCCA 335
82 uAsnLysGlnHisAspAlaAsp...Phe..... 90
334 CGATAGGCATCACTCTCGACATAGTTTCACCTGAATTAAGAGAGACCCAAAA 285
91 .....LysLysTyrIleLysLeuL 97
284 GCTCTGGAAGGGCCTTTTAGAATCATCACCAGCAATGATGATCAAGTTAT 235
97 euille.....AsnAsnAspGlyPhePheSerAsnAsnGlyGlyLys 110
234 AAATATGTGGTGAATAATCATGGGTATACTTCGAATAATAAAGAAAA 188
seq_name: gb_gss:AZ523935
seq_documentation_block:
LOCUS AZ523935 664 bp DNA linear GSS 07-MAY-2001
DEFINITION 225PbC02 Pb MBN #21 Plasmodium berghei genomic 3', DNA sequence.
ACCESSION AZ523935
VERSION AZ523935.1 GI:13963369
KEYWORDS GSS.
SOURCE Plasmodium berghei.
ORGANISM Plasmodium berghei.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 664)
AUTHORS Carlton,J.M.-R. and Dame,J.B.
TITLE The Plasmodium vivax and P. berghei gene sequence tag projects
JOURNAL Parasitol. Today 16 (10), 409 (2000)
COMMENT Contact: Dame JB
Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
Tel: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.vetmed.ufl.edu
Seq primer: M13(-20) forward
Class: shotgun.
location/Qualifiers
source
1..664
/organism="Plasmodium berghei"
/strain="ANKA clone 15cyl (clone of the ANKA 8417 clone)"
/db_xref="taxon:5821"
/clone_lib="Pb MBN #21"
/dev_stage="asexual blood forms"
/lab_host="Mus musculus"
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seq_name: gb_est1:AW257463
seq_documentation_block:
LOCUS      AW257463                655 bp    mRNA    linear    EST 20-DEC-1999
DEFINITION EST305600 KV2 Medicago truncatula cDNA clone KV2-9L18, mRNA
sequence.
ACCESSION  AW257463
VERSION    AW257463
KEYWORDS   EST.
SOURCE     barrel medic.
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 655)
AUTHORS   VandenBosch,K., Hurt,J., Moore,J., Beremand,P., Peng,H., Ellis,L.,
            Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
            Fraser,C.M.
TITLE     ESTs from roots of Medicago truncatula after Rhizobium inoculation
JOURNAL   Unpublished (1999)
COMMENT   Contact: VandenBosch K
            Department of Biology
            Texas A&M University
            College Station, TX 77843-3258, USA
            Tel: 409 845 7707
            Fax: 409 845 2891
            Email: kate@mail.bio.tamu.edu
            Texas A&M EST name: r1l6168e
            TIGR sequence name: MTAAT69TK
            More information is available at: . (and for clone ordering info)
            http://chryslie.tamu.edu/medicago
            Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
FEATURES   Location/Qualifiers
            1..655
                /organism="Medicago truncatula"
                /cultivar="genotype Al7"
                /db_xref="taxon:3880"
                /clone="KV2-9L18"
                /clone_lib="KV2"
                /tissue_type="Seedling roots"
                /dev_stage="2 days post-inoculation with Sinorhizobium
                meliloti"
                /lab_host="E. coli strain SOLR"
                /note="Vector: pBluescript SK -; Site.1: EcoRI; Site.2:
                XhoI; cDNA was prepared from polyA+ enriched RNA. The
                cDNA was directionally ligated into the Unizap XR vector
                from Stratagene and packaged using Gigapack III Gold
                packaging extracts. Plasmids containing cDNA inserts
                were excised from the recombinant lambda-zap phage using
                Ex-assist helper phage and propagated in SOLR cells."
BASE COUNT      220 a 138 c 109 g 188 t
ORIGIN
alignment_scores:
    Quality: 72.50      Length: 107
    Ratio: 1.394        Gaps: 5
Percent Similarity: 48.598 Percent Identity: 24.299
alignment_block:
US-09-528-682-4 x AW257463
Align seg 1/1 to: AW257463 from: 1 to: 655
18 AsnThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspG1 34
||||| : : : : : : : : : : : : : : : : : : : : : : : :
328 AATGTAATAAATCAAGTACATCAGTGTGGAAATCAAAATTAACCTAATGA 377
34 yAGTyRSerAsnThrAlaLeuIleSerAlaGluGlyGlyMetAspArgA 51
: : : : : : : : : : : : : : : : : : : : : : : :
378 CAATGAGGCCCAATACATCTCTCCCTGCATGCAAAAC.....ATTCAAA 421

```

```

51 sPlLeuPheGlySerAlaAsnIleAspGly..... 60
: : : : : : : : : : : : : : : : : :
422 ATGCAATTTTCATCTGCAAAATTTTCAAGGCCAAATCAAGGTCTCAACAGCA 471
61 .....PheProGluValIArgGluPheAs 68
472 ATAGACATGACTTTTGATTGGTAAGTCAATTTCCA..... 504
68 nSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLysG 85
505 .....CCCAATGATGGTGTCTTTTCAGTGACCAAGCA..... 534
85 InHisAspAlaAspPheLysLysTyrIleLysLeuLeuIleAsnAsnAsp 101
||| |||||: : : : : : : : : : : :
535 .....AAACCATATATACACCAACCAATAATAAAC..... 561
102 GlyPhePheSerAsnAsnGly 108
|||: : : : : : : : : : : :
562 ...TTCTTAACAACAATGGA 579
seq_name: gb_est2:BG647231
seq_documentation_block:
LOCUS      BG647231                736 bp    mRNA    linear    EST 24-APR-2001
DEFINITION EST508850 HOGA Medicago truncatula cDNA clone PHOGA-16E21 5' end,
mRNA sequence.
ACCESSION  BG647231
VERSION    BG647231.1 GI:13782343
KEYWORDS   EST.
SOURCE     barrel medic.
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 736)
AUTHORS   Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,
            Utterback,T., Cho,J. and Fraser,C.M.
TITLE     ESTs from roots of Medicago truncatula treated with
            oligogalacturonides of DP 6-20
JOURNAL   Unpublished (2001)
COMMENT   Contact: Michael G. Hahn
            Complex Carbohydrate Research Center
            University of Georgia
            220 Riverbend Road, Athens, GA 30602-4712, USA
            Tel: 706-542-4457
            Fax: 706-542-4412
            Email: hahn@ccrc.uga.edu
            G390837e TIGR sequence name: MTMBW35TK More information is
            available at: www.medicago.org
            Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
FEATURES   Location/Qualifiers
            1..736
                /organism="Medicago truncatula"
                /cultivar="Al7"
                /db_xref="taxon:3880"
                /clone="PHOGA-16E21"
                /clone_lib="HOGA"
                /tissue_type="3 day old seedling roots"
                /dev_stage="24 hours after treatment in the dark at 26 C
                with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
                presence of 100 ug/ml Gentamicin"
                /lab_host="XL0LR"
                /note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:
                XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
                was directionally ligated into the Unizap XR vector from
                Stratagene and packaged using Gigapack III Gold packaging
                extracts. Plasmids containing cDNA inserts were excised
                from the recombinant lambda-zap phage using Ex-assist
                helper phage and propagated in SOLR cells."
BASE COUNT      245 a 157 c 123 g 211 t
ORIGIN

```



```

alignment_scores:
  Quality: 72.50      Length: 107
  Ratio: 1.394      Gaps: 5
  Percent Similarity: 48.598      Percent Identity: 24.299

alignment_block:
  US-09-528-682-4 x BG647231 ..

  Align seq 1/1 to: BG647231 from: 1 to: 736

18 AsnThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspG1 34
  |||:::  :::::|||||:::  :::
328 AATGTAATAATCAAGTACATCATCTTCCTGCCATGCAAAAC.....ATTCAA 421
34 YAGTYrSerAsnTYrAlaLeuLeuSerAlaGluGlyMetAspArgA 51
  :::  :::::||||  |||  :::  :::::
378 CAATGAGGCCCAATACATCTTCCTGCCATGCAAAAC.....ATTCAA 421
51 spLeuPheGlySerAlaAsnIleAspGly..... 60
422 ATGCAATTTCTATCTGCAAAATTTACAGGCCCAATCAAGGTCTCAACAGCA 471
61 .....PheProGluValArgGluPheAs 68
472 ATAGACATGACTTTGATGTTGTAAGTCATTTCCA..... 504
68 nSerLeuProAsnLysAlaSerSerAspThrAlaSerLeuAsnLysG 85
  |||:::  :::  |||||  |||
505 .....CCCAATGATGGTGTCTTTCAGTGACCAAGCA..... 534
85 lnHisAlaAspPhePheLysLysTYrIleLysLeuLeuIleAsnAsnAsp 101
  |||  |||||:::  :::::|||||
535 .....AAACCATATATACACCAATAATAAAC..... 561

102 GlyPhePheSerAsnAsnGly 108
  |||:::  :::::|||||
562 ...TTCTAAACAACAATGGA 579

seq_name: gb_gss:BH486660

seq_documentation_block:
  LOCUS BH486660
  DEFINITION BOHKF67R BOHK Brassica oleracea genomic clone BOHKF67, DNA
  ACCESSION BH486660.1 GI:17694764
  VERSION BH486660
  KEYWORDS GSS.
  SOURCE Brassica oleracea.
  ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
  REFERENCE 1 (bases 1 to 773)
  AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL Unpublished (2001)
  COMMENT Other_GSSs: BOHKF67TF
  Contact: Chris Town
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA.
  Tel: 301-838-3523
  Fax: 301-838-0208
  Email: cdtown@tigr.org
  DNA is from a doubled haploid provided by Tom Osborn.
  Seq primer: TR
  Class: sheared ends.
  FEATURES
    source
    1..773
    /organism="Brassica oleracea"
    /strain="T01000DH3"
    /db_xref="taxon:3712"

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/clone="BOHKF67"
/clone_lib="BOHK"
/note="Vector: pHS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHS1 using BstXI linkers"
BASE COUNT 222 a 147 c 207 g 197 t
ORIGIN

alignment_scores:
  Quality: 72.50      Length: 59
  Ratio: 2.071      Gaps: 2
  Percent Similarity: 59.322      Percent Identity: 35.593

alignment_block:
  US-09-528-682-4 x BH486660 ..

  Align seq 1/1 to: BH486660 from: 1 to: 773

9 AspAlaTYrGluProIle.....AlaAsnThrAsnThrThrThrGlnPh 23
  |||:::  ::|||:::  |||||  |||
383 GATCTGGTACACCTGTAACACAGCTAATACAATGAGGAGCCCCAAGC 432
23 eLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgTYrSerAsnTYrA 40
  :::::  ::|||  |||||  :::::
433 CATAAGCTTGGAAATATTTCCTTGTAGATGGATCTTGACGCTCTCTG 482
40 laLeuIleSerAlaGluGlyGlyMetAspArgAspLeuPheGlySerAla 56
  ||  ::|||:::  |||  |||  |||:::  |||
483 CTACTTTAGTGGATGCGGATGGCGTGGATGGATGGATGGATGGATGGCA 532
57 AsnIleAspGly.....PhePro 62
  :::::  |||  |||||
533 CAGCTTATGGGACACAGGAATTTCCCT 559

seq_name: gb_gss:BH552001

seq_documentation_block:
  LOCUS BH552001
  DEFINITION BOHMW73TF BOHM Brassica oleracea genomic clone BOHMW73, DNA
  ACCESSION BH552001
  VERSION BH552001.1 GI:17803781
  KEYWORDS GSS.
  SOURCE Brassica oleracea.
  ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
  REFERENCE 1 (bases 1 to 801)
  AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL Unpublished (2001)
  COMMENT Other_GSSs: BOHMW73TR
  Contact: Chris Town
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA.
  Tel: 301-838-3523
  Fax: 301-838-0208
  Email: cdtown@tigr.org
  DNA is from a doubled haploid provided by Tom Osborn.
  Seq primer: TF
  Class: sheared ends.
  FEATURES
    source
    1..801
    /organism="Brassica oleracea"
    /strain="T01000DH3"
    /db_xref="taxon:3712"
    /clone="BOHMW73"
    /clone_lib="BOHM"
    /note="Vector: pHS1; Site_1: BstXI; 2-3 kb sheared
    genomic DNA inserted into pHS1 using BstXI linkers"
BASE COUNT 202 a 212 c 158 g 229 t
ORIGIN

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```

alignment_scores:
  Quality: 72.50      Length: 59
  Ratio: 2.071        Gaps: 2
  Percent Similarity: 59.322  Percent Identity: 35.593

alignment_block:
US-09-528-682-4 x BH552001/rev ..
Align seg 1/1 to reverse of: BH552001 from: 1 to: 801

9 AspAlaTyrGluProIle.....AlaAsnThrAsnThrThrThrGlnPh 23
||||| :|||||: ||||||| |||
453 GATGGGTACACACCTGTACACAGCTAATAACAAATGAGGAGCCCAAGC 404

23 eLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgTyrSerAsnTyrA 40
:|||||: ||||||| :|||||: |||
403 CATAAGCTTGGGAATAATTGCTTGTAGATGGATCTTGGAGCTTCTCG 354

40 LaLeuIleSerAlaGluGlyGlyMetAspArgAspLeuPheGlySerAla 56
|| :|||||: ||| ||| ||| ||| |||
353 CTAACCTTATAGTGGATCGGATGGGCTGGATGGATGGATGGGAATGCA 304

57 AsnIleAspGly.....PhePro 62
:||||| ||| ||||||
303 CAGCTTATGGGACAAAGGAATTTCCT 277

seq_name: gb_est2:BF032307

seq_documentation_block:
LOCUS BF032307 1733 bp mRNA linear EST 20-OCT-2000
DEFINITION 601452770F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856649 5',
mRNA sequence.
ACCESSION BF032307
VERSION BF032307.1 GI:10740019
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1733)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@email.nih.gov
Tissue procurement: DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9585 row: k column: 18.
Location/Qualifiers
1. .1733
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3856649"
/clone_lib="NIH_MGC_66"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT 451 a 444 c 399 g 439 t
ORIGIN

alignment_scores:
  Quality: 72.50      Length: 91

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```

Ratio: 1.343      Gaps: 5
Percent Similarity: 59.341  Percent Identity: 31.868

alignment_block:
US-09-528-682-4 x BF032307 ..
Align seg 1/1 to: BF032307 from: 1 to: 1733

31 AlaLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyG1 47
||||| :|||||: ||||||| |||
873 GCATTACGGAACAGGTTTCCT...TACAGTCTCCAAACCCGCAAGCGGGC 919

47 yMetAspArgAspLeuPheGlySerAlaAsn..... 57
:|||||: ||||||| :|||||: |||
920 ACTT.....ATTTCGGCTCTGGAACGGCTTTTAAACCCCTTCCT 960

58 .....IleAspGlyPheProGluValArgGluPheAsnSer 69
:|||||: ||| |||
961 TTGTTTAAAGGCCTCTTAAGCATTAACCATCTTGGGATTTTTC..... 1004

70 LeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnHi 86
||| :|||||: ||||||| |||
1005 CTTTTTCCACAAATCCACAGCACACAGGACCTTTTCGGAACACA 1054

86 sAspAlaAspPheLysLysTyrIleLysLeuLeuIleAsnAsn.....A 101
:||||| ||| |||
1055 GGGTAAATCCCCCAAGAAAGTAGACGCCCTTTTATACCAAGGTGGTTG 1104

101 spGlyPhePheSerAsnAsnGly 108
:|||||: |||
1105 CAAACTTCTTTCAACTACCGGT 1127

seq_name: gb_est1:AV916505

seq_documentation_block:
LOCUS AV916505 620 bp mRNA linear EST 18-JAN-2002
DEFINITION AV916505 K. Sato unpublished cDNA library, cv. Haruna NiJo
germination shoots Hordeum vulgare subsp. vulgare cDNA clone
bags17105 5', mRNA sequence.
ACCESSION AV916505
VERSION AV916505.1 GI:18212282
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 620)
AUTHORS Sato,K., Saisho,D. and Takeda,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .620
/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Haruna NiJo"
/db_xref="taxon:112509"
/clone="bags17105"
/clone_lib="K. Sato unpublished cDNA library, cv. Haruna
NiJo germination shoots"
/tissue_type="shoots"
/dev_stage="germination"
BASE COUNT 146 a 172 c 153 g 149 t
ORIGIN

alignment_scores:

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Quality: 72.00 Length: 121
Ratio: 1.309 Gaps: 4
Percent Similarity: 45.455 Percent Identity: 23.967

alignment_block:

US-09-528-682-4 x AV916505 ..

Align seg 1/1 to: AV916505 from: 1 to: 620

```

13 ProileAlaAsnThrAsnThr.....ThrGlnPheLeuAsnMetG1 27
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
45 CCGTAGTCAACCTCTCTGCTGCGTTTGGAACTAGTCTCTAGCTGTGG 94
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
27 YAsnGluValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerA 44
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
95 TGGTGATGTGCTGCTGATACATCCACCAAGAATTTCAACCAATACATG 144
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
44 laGlu...GlyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAsp 59
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
145 CTGCGTTTAGCTACACTAACCAAGATCTTATCGCATCCCTGGAACCTG... 191
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
60 GlyPheProgluValArgGluPheAsnSerLeuProAsnAsnLysAlaSe 76
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
192 .....AACCAAGAGGAGA 205
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
76 rSerAspThrAlaSer..... 81
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
206 CAGCCTCAGCGATCTCTATTACCATTTTGTGGAGAGTCAGCACAGCTG 255
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
81 ..... 81
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
256 TTGGGGCGGAGCTGACCCACAGCTTCTCGAGCAACGAGACAGCCTCACC 305
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
82 LeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysLeuIle 98
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
306 TTGGGCACCTCAGCATACCTTAGACCCGCTCACCCTCGTGAAGCTCGCAT 355
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
98 eAsnAsnAspGly 102
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
356 CAACAACCTCTGGC 368
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

seq_name: gb_estl:AV916629

seq_documentation_block:

LOCUS AV916629 633 bp mRNA linear EST 18-JAN-2002
DEFINITION AV916629 K. Sato unpublished cDNA library, cv. Haruna NiJo
germination shoots Hordeum vulgare subsp. vulgare cDNA clone
bags19b07 5', mRNA sequence.

ACCESSION AV916629

VERSION AV916629

KEYWORDS EST.

SOURCE AV916629.1 GI:18212406

ORGANISM Hordeum vulgare subsp. vulgare.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

; Triticeae; Hordeum.

1 (bases 1 to 633)

Sato, K., Saisho, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadasu Shin-i

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshinigenes.nig.ac.jp.

Location/Qualifiers

1..633

/organism="Hordeum vulgare subsp. vulgare"

/cultivar="Haruna NiJo"

/db_xref="taxon:112509"

/clone="bags19b07"

FEATURES

source

/clone_lib="K. Sato unpublished cDNA library, cv. Haruna
NiJo germination shoots"
/tissue_type="shoots"
/dev_stage="germination"
BASE COUNT 157 a 180 c 150 g 145 t 1 others
ORIGIN

alignment_scores:

Quality: 72.00 Length: 121
Ratio: 1.309 Gaps: 4
Percent Similarity: 45.455 Percent Identity: 23.967

alignment_block:

US-09-528-682-4 x AV916629 ..

Align seg 1/1 to: AV916629 from: 1 to: 633

```

13 ProileAlaAsnThrAsnThr.....ThrGlnPheLeuAsnMetG1 27
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
147 CCGTAGTCAACCTCTCTGCTGCGTTTGGAACTAGTCTCTAGCTGTGG 196
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
27 YAsnGluValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerA 44
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
197 TGGTGATGTGCTGCTGATACATCCACCAAGAATTTCAACCAATACATG 246
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
44 laGlu...GlyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAsp 59
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
247 CTGCGTTTAGCTACACTAACCAAGATCTTATCGCATCCCTGGAACCTG... 293
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
60 GlyPheProgluValArgGluPheAsnSerLeuProAsnAsnLysAlaSe 76
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
294 .....AACCAAGAGGAGA 307
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
76 rSerAspThrAlaSer..... 81
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
308 CAGCCTCAGCGATCTCTATTACCATTTTGTGGAGAGTCAGCACAGCTG 357
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
81 ..... 81
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
358 TTGGGGCGGAGCTGACCCACAGCTTCTCGAGCAACGAGACAGCCTCACC 407
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
82 LeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysLeuIle 98
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
408 TTGGGCACCTCAGCATACCTTAGACCCGCTCACCCTCGTGAAGCTCGCAT 457
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
98 eAsnAsnAspGly 102
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
458 CAACAACCTCTGGC 470
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

seq_name: gb_estl:AV917534

seq_documentation_block:

LOCUS AV917534 715 bp mRNA linear EST 18-JAN-2002
DEFINITION AV917534 K. Sato unpublished cDNA library, cv. Haruna NiJo
germination shoots Hordeum vulgare subsp. vulgare cDNA clone
bags10f08 3', mRNA sequence.

ACCESSION AV917534

VERSION AV917534

KEYWORDS EST.

SOURCE AV917534.1 GI:18213311

ORGANISM Hordeum vulgare subsp. vulgare.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

; Triticeae; Hordeum.

1 (bases 1 to 715)

Sato, K., Saisho, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

13 proIleAlaAsnThrAsnT

13 proIleAlaAsnThrAsnThrThr.....ThrGlnpheLeuAsnMetGI 27


```

seq_documentation_block:
LOCUS      AZ006675                      624 bp    DNA        linear    GSS 25-FEB-2000
DEFINITION RPCI-23-31511.TJ RPCI-23 Mus musculus genomic clone RPCI-23-31511,
            DNA sequence.
ACCESSION  AZ006675
VERSION    AZ006675.1 GI:7082059
KEYWORDS   GSS.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 624)
AUTHORS    Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Aklnret
            ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
            and Fraser,C.M.
TITLE      Mouse BAC End Sequences from Library RPCI-23
JOURNAL    Unpublished (1999)
COMMENT    Other_GSSs: RPCI-23-31511.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact pletier de Jong
            (pletier@jeong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tcdb/bac_ends/mouse/bac_end_intro.html
            Plate: 315 row: I column: 1
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source           1..624
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-31511"
                     /clone_lib="RPCI-23"
                     /sex="Female"
                     /lab_host="DH10B"
                     /note="Organ: Kidney/Brain; Vector: pBACE3.6; Site:1;
                     EcoRI; Site:2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and partially digested
                     with a combination of EcoRI and EcoRI Methylase. Size
                     selected DNA was cloned into the pBACE3.6 vector at the
                     EcoRI sites. The ligation products were transformed into
                     DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT  299 a 113 c 108 g 104 t
ORIGIN
alignment_scores:
    Quality: 71.50          Length: 107
    Ratio: 1.172           Gaps: 6
    Percent Similarity: 57.009 Percent Identity: 31.776
alignment_block:
US-09-528-682-4 x AZ006675
Align seg 1/1 to: AZ006675 from: 1 to: 624
      6  ArgIlleGlnAspAlaTyrGluProIleAlaAsnThrAsnThrThr.. 21
      143 AGAATCTCAGAGCGGAGAGATACCATAGAAAACACATTGACACAAATGCAA 192
      22 .....GlnPheLeuAsnMetGly...AsnGluVala 31
      193 AGAAATGTAAATGCAAAAGATTCTTCCACCAAAACATCCAGGAATCC 242

```

```

31 laLeuAspGlyArgTyrSerAsnTyrAlaLeuLeuSerAlaGluGlyGly 47
    ||| ||| ::||| ||| ||| |||
243 AGGACAAATGAGAAGACCAAACTTAAGGATAATAAGTATAGAAGGAGT 292
48 MetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluVa 64
    ||| ::||| ||| ::||| ||| |||
293 AAAGATTCCCAACTTAAGGGACCACTAAATATC.....TTCAACAATA 336
64 laIrgGlu.....PheAsnSerLeuProAsnAsnLysAlaSerSerAspT 79
    ||| ||| ::||| ||| ::||| |||
337 TATAGAGAAAACCTTCCTACCTTAAAAAAGAGATGCCCATAAACATA 386
79 hrAlaSerLeu...AsnLysGlnHisAspAlaAspPheLysLysTyrIle 94
    || ||||| ||| ::||| ||| |||
387 CAAGAAGCCTACAGAACTCCAAATAGATTGTACCAGTAAAGAAATTC... 433
95 LysLeuLeuIleAsnAsnAsp 101
    ||||| ::||| |||
434 ...CTCCTGTGCACATAATAAT 451
seq_name: gb_est2:BE366639
seq_documentation_block:
LOCUS      BE366639                      666 bp    mRNA        linear    EST 20-JUL-2000
DEFINITION P11_35_D02.g1_A002 Pathogen induced 1 (P11) Sorghum bicolor cDNA,
            mRNA sequence.
ACCESSION  BE366639
VERSION    BE366639.1 GI:9308196
KEYWORDS   EST.
SOURCE     sorghum.
ORGANISM   Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE  1 (bases 1 to 666)
AUTHORS    Cordonnier-Pratt,M.-M., Gingle,A., Dean,R., Sudman,M. and Pratt
            ,L.H.
TITLE      An EST database from Sorghum: pathogen-induced plants
JOURNAL    Unpublished (2000)
COMMENT    Contact: Cordonnier-Pratt MM
            Department of Botany
            The University of Georgia
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 542 1805
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: PolyTMix
            High quality sequence start: 12
            High quality sequence stop: 666
            POLYA-No. Location/Qualifiers
            1..666
            /organism="Sorghum bicolor"
            /db_xref="taxon:4558"
            /clone_lib="Pathogen induced 1 (P11)"
            /note="Organ: Anthracnose-infected leaves from
            two-week-old sorghum plants 48 hr after inoculation;
            Vector: pBluescript II from Lambda Zap II; Site:1: XhoI;
            Site:2: EcoRI; Two-week-old sorghum plants (BRX 623
            cultivar) were infected with pathogen (isolate FRM421 of
            Colletotrichum graminicola, which is a sorghum isolate).
            RNA was prepared from infected leaves harvested from 45
            seedlings 48 hours after inoculation. Note: young
            seedlings (2 weeks old) exhibit juvenile resistant
            reaction, which is an incompatible interaction. As they
            grow older (4 weeks or older), plants resume susceptibility
            to anthracnose disease. The library was made from poly-A
            RNA in the cloning vector lambda Zap II. Clones to be
            sequenced were prepared by mass excision. WARNING: While
            most or all ESTs are expected to derive from the host

```


clone	UUGC1M0179K18 F, DNA sequence.
Accession	AZ408211
Version	AZ408211.1 GI:10532224
Keywords	GSS.
Source	house mouse.
Organism	Mus musculus
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Reference	1 (bases 1 to 567)
Authors	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0179 row: K column: 18
 Seq primer: CGTTGTAAACACGACGGCCAGT
 Class: plasmid ends

```

FEATURES
source
1. .567
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0179K18"
/clone_lib="Mouse 10kb plasmid uugc1m library"
/sex="Male"

```

/note="Vector: pWD42nv; Purified genomic DNA from *M. musculus* C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

138 a 92 c 115 g 222 t

BASE COUNT
 ORIGIN

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alignment_scores:      Quality: 71.00      Length: 105
                        Ratio:   1.092     Gaps:    2
                        Percent Similarity: 61.905   Percent Identity: 20.952

alignment_block:
US-09-528-682-4 x AZ408211/rev ..

Align seg 1/1 to reverse of: AZ408211 from: 1 to: 567

      8 GlnAspAlaTyrGluProIleAalaAsnThrAsnThrThrThrGlnPheLeu 24
|||| :|||:|||:|||:: |||:|||:|||:::
:
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69 rLeuPro 71
   ::::|
211 TGTTCCTCC 217

seq_name: gb_gss:BH350007

seq_documentation_block:
LOCUS      BH350007              749 bp      DNA      linear      GSS 03-DEC-2001
DEFINITION CH230-198K12.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone.
            CH230-198K12, DNA sequence.
ACCESSION  BH350007
VERSION    BH350007.1  GI:17280741
KEYWORDS   GSS.
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 749)
AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
            ,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
            Jong,P. and Fraser,C.M.
TITLE     Rat BAC End Sequences from Library CHORI-230 EcoRI segment
COMMENT   Other_GSSs: CH230-198K12.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@email.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/orering\_information.htm). BAC end
            page: http://www.tigr.org/tldb/bac\_ends/rat/bac\_end\_intro.html
            Plate: 198 row: K column: 12
            Seq primer: SP6
            Class: BAC ends.

FEATURES             Location/Qualifiers
     source           1..749
                     /organism="Rattus norvegicus"
                     /strain="BN/SNHsd/MCW"
                     /db_xref="taxon:10116"
                     /clone="CH230-198K12"
                     /clone_lib="CHORI-230 Segment 1"
                     /sex="Female"
                     /cell_type="Brain"
                     /note="vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                     CHORI-230 Rat (BN/SNHsd/MCW) BAC library produced by
                     Pieter de Jong"
BASE COUNT          360 a 137 c 139 g 113 t
ORIGIN

alignment_scores:
  Quality: 70.50      Length: 126
  Ratio: 1.102       Gaps: 5
  Percent Similarity: 50.794  Percent Identity: 24.603

alignment_block:
us-09-528-682-4 x BH350007  ..
Align seg 1/1 to: BH350007 from: 1 to: 749

3 PheThrValArgIleGlnAspAlaTy rGluProIleAlaAsnThrAsnTh 19
325 TTCCACCAAGACAGATACAGAGATGGAAGAGAGAGATCTCAGGACGAGA 374
19 rThrThrGlnPheLeuAsnMetGly..... 27

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   ::::|
375 TTCCATAGAAATCATTGACTCAACTGCTCAAAGATAAATTTAAAGCAGAAAA 424
28 .....AsnGluValAlaLeuAspGlyArgTy rSer 37
   ::::|
425 AGCTACTGGTCCAAAACATACAGGAAATCCAGGACTCAATGAGAAGATCA 474
38 AsnTy rAlaLeuIleSerAlaGluGlyGlyMetAspArgAspLeuPheG1 54
   ::::|
475 ACCTAAGATATAGTATAGAGAGAGAGTGAAGACTCCAGCTCAAGG 524
54 ySerAlaAsnIle.....AspGlyPheProGlu.... 63
   ::::|
525 ACCAGTAAATATCTTCAACAAAATCATAGAAGAAACTTCCTCAACGTAA 574
64 .....ValArgGluPheAsnSerLeuProAsnAsn 73
   ::::|
575 AAAAGAGTTACCCATAGCAGCATACAAGAGCCCTACAGAACTCCAAATAGA 624
74 LysAlaSerSerAspThrAlaSer.....LeuAsnLysGlnHisAs 87
   ::::|
625 TTGGACCAAAAGAAACACCTCCGTCACATATTTGTCAAAACACCCAAA 674
87 pAlaAspPheLysLys....Ty rIleLys 95
   ::::|
675 CGCACAAATAAGAAAGAAATATTTAAAG 702

seq_name: gb_est2:BG603389

seq_documentation_block:
LOCUS      BG603389              360 bp      mRNA      linear      EST 14-AUG-2001
DEFINITION EST502479 Plasmodium yoelii sporozoite cDNA Plasmodium yoelii CDNA
            clone PYCDR11, mRNA sequence.
ACCESSION  BG603389
VERSION    BG603389.1  GI:15153403
KEYWORDS   EST.
SOURCE     Plasmodium yoelii.
ORGANISM   Plasmodium yoelii
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE  1 (bases 1 to 360)
AUTHORS   Kappe,S.H.I., Gardner,M.J., Brown,S.M., Ross,J., Matuschewski,K.,
            Ribeiro,J.M., Adams,J.H., Quackenbush,J., Cho,J., Carucci,D.J.,
            Hoffman,S.L. and Nussenzweig,V.
            Exploring the transcriptome of the malaria sporozoite stage
            Proc. Natl. Acad. Sci. U. S. A. 98 (17), 9895-9900 (2001)
            21396555
            Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org
            Request for clones, please contact: Stefan Kappe,
            kappes01@popmail.med.nyu.edu Michael Heidelberger Division,
            Department of Pathology New York University School of Medicine.

FEATURES             Location/Qualifiers
     source           1..360
                     /organism="Plasmodium yoelii"
                     /strain="17XNL"
                     /db_xref="taxon:5861"
                     /clone="PYCDR11"
                     /clone_lib="Plasmodium yoelii sporozoite cDNA"
                     /dev_stage="sporozoites from salivary gland"
                     /lab_host="E. coli TOP10"
                     /note="Vector: pCR4; TA cloning; Plasmodium yoelii
                     sporozoite cDNA library from salivary gland sporozoites 14
                     days post-infection"
BASE COUNT          75 a 71 c 63 g 151 t
ORIGIN

alignment_scores:

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38 AsnTyrAlaLeuIleSerAlaGluGlyMetAspArgAspLeuPheG1 54
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202 AACCTAAGGATAATAGGTATAGAGAGAGTGAAGACTCCCGAGTCAAGG 251

54 ySerAlaAsnIle.....AspGlyPheProGluVal. 64
| :||| :||| :||| :||| :||| :||| :||| :||| :|||
252 ACCAGTAATATCTTCAACAAAATCATAGAGAAAACCTCCCTAACCTAA 301

65 .....ArgGluPheAsnSerLeuProAsnAsnLysAlaSer 76
| :||| :||| :||| :||| :||| :||| :||| :||| :|||
302 AAAGAGATACCATAGGATACAGAGAGCTTACAGAACTCCAAATAGGT 351

77 SerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLys 92
| :||| :||| :||| :||| :||| :||| :||| :||| :|||
352 GGACCAGAAAGAAACACCTCCCGTCACATTAATAGTCAAAACCCCAAG 399

seq_name: gb_gss:BH260164

seq_documentation_block:
LOCUS BH260164 607 bp DNA linear GSS 30-NOV-2001
DEFINITION CH230-90E16_TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-90E16, DNA sequence.
ACCESSION BH260164
VERSION BH260164.1 GI:17164239
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 607)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Gear,K., Shvartsbeyn
A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
TITLE Rat BAC End Sequences from Library CHORI-230 EcoRI segment
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: CH230-90E16.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 90 row: E column: 16
Seq primer: T7
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..607
/organism="Rattus norvegicus"
/strain="BN/SsNhsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-90E16"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/notes="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SsNhsd/MCW) BAC library produced by
Pieter de Jong"
BASE COUNT 270 a 125 c 111 g 101 t
ORIGIN

alignment_scores:
Quality: 70.00 Length: 138
Ratio: 1.029 Gaps: 4

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Percent similarity: 49.275 Percent identity: 22.464
alignment_block:
US-09-528-682-4 x BH260164 ..
Align seg 1/1 to: BH260164 from: 1 to: 607

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52 TTCCACCAACAGATACAGAGATGGAAGAGAGATCTCAGAGCAGAGA 101

19 rThrThrGlnPheLeuAsnMetGly..... 27
| :||| :||| :||| :||| :||| :||| :||| :||| :|||
102 TTCACAGAAAATCATTTGACTTAATGTCAAAAGATAATGTAAGCAGAAAA 151

28 .....AsnGluValAlaLeuAspGlyArgTyrSer 37
| :||| :||| :||| :||| :||| :||| :||| :||| :|||
152 AGTACTGTGTCACAAACATACAGAAATCCAGGACTCAATGAGAAGATCA 201

38 AsnTyrAlaLeuIleSerAlaGluGlyMetAspArgAspLeuPheG1 54
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
202 AACCTAAGGATAATAGGTATAGAGAGAGTGAAGACTCCCGAGTCAAGG 251

54 ySerAlaAsnIle.....AspGlyPhePro..... 62
| :||| :||| :||| :||| :||| :||| :||| :||| :|||
252 ACCAGTAATATCTTCAACAAAATCATAGAGAAAACCTCCCTAACCTAA 301

63 .....GluValArgGluPheAsnSerLeuProAsn... 72
| :||| :||| :||| :||| :||| :||| :||| :||| :|||
302 AAAGAGATACCATAGATACAGAGAGCTTACAGAACTCCAAATAGAGA 351

73 .....AsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnHisAs 87
| :||| :||| :||| :||| :||| :||| :||| :||| :|||
352 TTGACCAGAAAGAAACACCTCCCGTCACATAATAGTCAAAACACCAA 401

87 palAspPheLysLysTyrIleLysLeuLeuIleAsnAsnAspGlyPheP 104
| :||| :||| :||| :||| :||| :||| :||| :||| :|||
402 CGCACAAAATAAAGAAAGATATTAAAGCAGTAAGGCAAAAGGTCAAG 451

104 heSerAsnAsnGly 108.
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452 TAACATATAAAGGG 465

seq_name: gb_est2:BI887904

seq_documentation_block:
LOCUS BI887904 608 bp mRNA linear EST 12-OCT-2001
DEFINITION ZF637-1-002159 zebrafish shield stage whole embryo cDNA library
MPMGp637_danio rerio cDNA clone MPMGP637_F0410 5',
mRNA sequence.
ACCESSION BI887904
VERSION BI887904.1 GI:16095175
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 608)
AUTHORS Clark,M., Aanstad,P., Hennig,S., Johnson,S.L. and Lehrach,H.
TITLE EST sequencing of a zebrafish shield stage cDNA library normalised
by oligonucleotide fingerprinting
JOURNAL Unpublished (2001)
COMMENT Contact: Hennig S
Laboratory 123, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Innestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
Email: hennig@molgen.mpg.de
5' EST sequencing of clones from a zebrafish shield stage library,
normalised from 55,000 starting clones by oligonucleotide
fingerprinting

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OM of: US-09-528-682-4 to: Issued_Patents_NA:* out_format : pfs
Date: Jun 18, 2002 7:52 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=framet-p2n.model -DEV=xlp
-O=/cgn2_1/USPTO.spool/US09528682/runat.18062002_082443_7827/app_query.fasta_1.689
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPEXT=6.000 -GAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -DELOP=6.000 -DELOP=7.000 -XGAPOP=10.000
-XGAPEXT=0.500 -DELOP=6.000 -DELOP=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cgi -LIST=1000 -DOCALLIGN=200
-THR_SCORE=pcpt -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09528682.@CGN1_1_96 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-528-682-4

Query length: 110

Database: Issued_Patents_NA.*

Database sequences: 383533

Database length: 122816752

Search time (sec): 143.210000

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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-200-232-3	+	67.00	141.76	3.30	1541
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-434-008A-5	+	66.50	130.93	13.24	3630
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-312-157-5	+	66.50	130.93	13.24	3630
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-038-682-3	+	66.00	126.21	24.27	4937
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-530-198-3	+	66.00	126.21	24.27	4937
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-469-880-3	+	66.00	126.21	24.27	4937
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-728-470-3	+	66.00	126.21	24.27	4937
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-617-697-3	+	66.00	126.21	24.27	4937
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-719-641-3	+	66.00	126.21	24.27	4937
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-469-880-6	+	66.00	119.14	60.10	9323
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-466-109-7	+	64.50	143.16	2.76	756
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-118-469A-4	+	64.50	136.63	6.38	1361
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-056-556-203	+	64.50	136.63	6.38	1361
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-460-739-1	+	64.50	122.43	39.37	4875
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-478-370-1	+	63.00	114.54	108.33	6973
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-968-685A-9	+	63.00	111.05	169.45	9542
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-330-330-3	+	63.00	110.18	189.55	10322
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-469-667-15	+	62.50	133.57	9.44	1121
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-224-110-15	+	62.50	133.57	9.44	1121
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-224-110-15	+	62.50	133.57	9.44	1121
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-946-914-1	+	62.50	133.40	9.65	1138
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-302-812-3	+	62.00	117.93	70.19	4069
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-511-477-3	+	62.00	120.67	49.38	2828
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-357-071-1	+	61.50	107.58	264.46	9171
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-038-682-5	+	61.50	107.58	264.46	9171
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-530-198-5	+	61.50	107.58	264.46	9171
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-728-470-5	+	61.50	107.58	264.46	9171
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-617-697-5	+	61.50	107.58	264.46	9171
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-07-972-791-6	-	61.00	117.44	74.67	3361
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-239-052-1	+	60.50	133.09	10.03	732
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-136-442-2	+	60.50	128.88	17.22	1069
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-858-007A-8	+	60.50	127.63	20.21	1196
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-609-049A-27	+	60.50	108.25	242.73	6831
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-170-996-27	+	60.50	108.25	242.73	6831
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-305-641-3	-	60.00	133.89	9.06	606
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-998-416-256	-	60.00	133.13	11.36	710
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; Patent No. 5863777
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 5863777el Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,057
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9607991.8
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmie, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31458-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:

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; INFORMATION FOR SEQ ID NO: 1:
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; STRANDEDNESS: single
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; Patent No. 6066778
; GENERAL INFORMATION:
; APPLICANT: Ginsburg, David
; APPLICANT: Cui, Jisong
; TITLE OF INVENTION: Compositions And Methods For Screening
; TITLE OF INVENTION: Compounds For Anticoagulant Activity
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,111
; FILING DATE: 06-NOV-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: UM-02536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,322
; FILING DATE: 24-OCT-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: P38,615
; REFERENCE/DOCKET NUMBER: 8600-0151.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2745 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
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29 uValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluG 46
   : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| :
2323 .ATGAGTCTTGATGGAGAAAAAATTCGTCAGCTCTACACGCAACAT 2371

46 lGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePro 62
   : : : : : : : : : : : : : : : : : : : : : : : :
2372 CAGTGTTCACCTAGTACATAAGACAGAACAAAT..... 2403

63 GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
   : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2404 .....CAGCATTTCAATGACATAACCAAGTCGTAGGCAGTAGTGACGA 2447

79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysTyrIleLysL 96
   : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| :
2448 AGATGCCCTTTCCCAAGCCCAATCATTAATTTCAATAGAAACTACCAA 2497

96 euLeuIleAsnAsnAspGlyPhePheSerAsnAsn 107
   : : : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2498 TACTTTAAATTAATGATAAGCGTCATACAAATCAAC 2532

seq_name: /cgn2_6/p/odata/2/ina/5A_COMB.seq:US-08-328-322-4

seq_documentation_block:
; Sequence 4, Application US/08328322
; Patent No. 5723436
; GENERAL INFORMATION:
; APPLICANT: Huang, Laiqiang
; APPLICANT: Cyert, Martha S.
; TITLE OF INVENTION: Calcineurin Interacting Protein Composit
; TITLE OF INVENTION: and Methods

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; Patent No. 5663060
; JOURNAL: Genomics
; VOLUME: 16
; PAGES: 374-379
; DATE: 1993
; RELEVANT RESIDUES IN SEQ ID NO: 7: FROM 1 TO 7476
; US-08-212-133A-7

alignment_scores:
  Quality: 71.50      Length: 140
  Ratio: 0.993       Gaps: 5
  Percent Similarity: 51.429  Percent Identity: 21.429

alignment_block:
US-09-528-682-4 x US-08-212-133A-7 ..
Align seg 1/1 to: US-08-212-133A-7 from: 1 to: 7493

4 ThrValArgIleGlnAspAlaTyrGluProIle...AlaAsnThrAsnTh 19
3543 ACAACAGACTTGCAAGATGCCATATTAAGGTCAATAGTGAGATTCAAGA 3592
19 rThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgT 36
3593 AGTAACAGCTTTGATTCATGATGGAACACACTTTTAGGCCAAATAATTCTACAT 3642
36 yr.....SerAsnTyrAlaLeuIleSerAlaGluGlyGlyMetAspArg 50
3643 ATTCGAGACTAACCATATGCTAAATAGAACTACCTCAACAAAATAATAA 3692
51 AspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgGluPh 67
3693 GACATATTTCTAGAAAAGATCAAGATCCTTATCCACAAGATGAGAGAA 3742
67 eAsnSerLeuProAsnAsn.....PhelystyIle..... 73
3743 TACATCATGCGCATTTTCCAGATGTTCTTCTGTCAGAAATCTTCAAAAT 3792
74 .....LysAlaSerSerAspThrAlaSerLeuAsnLysGlnHisAspAla 88
3793 GGTAAAAAGACCAGTGAATAATTCCTTCAACTCGAGCAAGATGATTTA 3842
89 Asp.....LysLeuLeuIleAsnAspGlyPhePhePhePhePhePhe 94
3843 AGTCCAAAGCAATTAGTATATTATATGTTTAAATAATATGTAATAATCA 3892
95 .....LysLeuLeuIleAsnAspGlyPhePhePhePhePhePhePhe 104
3893 AAGTTTCTTGTCAGAGAAAAATAAAGTCACAGTACAGACAGATGATTTA 3942
104 heSerAsnAspGlyLys 110
3943 CAAGAACAATAGGACTTAAA 3962

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-474-503-5
seq_documentation_block:
; Sequence 5, Application US/08474503
; Patent No. 5744446
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,503
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pratt, John S.
; REGISTRATION NUMBER: 29,476
; REFERENCE/DOCKET NUMBER: EMU106CIP(3)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6500
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7493 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: repeat_unit
; LOCATION: 1..407
; OTHER INFORMATION: /rpt_type="terminal"
; OTHER INFORMATION: /note="5'UTR"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7471..7476
; OTHER INFORMATION: /function="PolyA_signal"
; FEATURE:
; NAME/KEY: repeat_unit
; LOCATION: 7368..7493
; OTHER INFORMATION: /rpt_type="terminal"
; OTHER INFORMATION: /note="3'UTR"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 408..7367
; OTHER INFORMATION: /product="Coagulation Factor VIII"
; PUBLICATION INFORMATION:
; AUTHORS: Elder, F.
; AUTHORS: Lakich, D.
; AUTHORS: Gitschier, J.
; TITLE: Sequence of the Murine Factor VIII cDNA.
; Patent No. 5744446
; JOURNAL: Genomics
; VOLUME: 16
; PAGES: 374-379
; DATE: 1993
; RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 7476
; US-08-474-503-5
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alignment_scores:
  Quality: 71.50      Length: 140
  Ratio: 0.993       Gaps: 5
  Percent Similarity: 51.429  Percent Identity: 21.429

alignment_block:
US-09-528-682-4 x US-08-474-503-5 ..
Align seg 1/1 to: US-08-474-503-5 from: 1 to: 7493

4 ThrValArgIleGlnAspAlaTyrGluProIle...AlaAsnThrAsnTh 19
3543 ACAACAGACTTGCAAGATGCCATATTAAGGTCAATAGTGAGATTCAAGA 3592
19 rThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgT 36
3593 AGTAAAAAGACCAGTGAATAATTCCTTCAACTCGAGCAAGATGATTTA 3942
104 heSerAsnAspGlyLys 110
3943 CAAGAACAATAGGACTTAAA 3962
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; TELEPHONE: 703-684-5600
; TELEFAX: 703-836-5288
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3300 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Caulobacter crescentus
; STRAIN: CB 15
; US-08-194-290-6

alignment_scores:
    Quality: 71.00      Length: 112
    Ratio: 1.164       Gaps: 5
    Percent Similarity: 54.464      Percent Identity: 28.571

alignment_block:
US-09-528-682-4 x US-08-194-290-6 ..

Align seg 1/1 to: US-08-194-290-6 from: 1 to: 3300

1 AspTyrPheThrValArgIleGlnAspAlaTyrGluProIleAlaAsnTh 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
608 GACTACCTGACCGCCTTCGTGGCG.....GCCAACAC 639

17 rAsn...ThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuA 33
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
640 GCCGTTCCAGCGCGCTGCCGACATCGATCTGGCGTCACAGCGCGCTGA 689

33 spGlyArgTyrSerAspTyrAlaLeuIleSerAlaGluGly..... 47
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
690 TCGCCACCATCTGAAACCGCGCCACCGGTGTCGGCATCGTGTACGCG 739

48 .....MetAspArgAspLeuPhe...GlySerAlaAsnIle 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
740 ACCGCCACGCGCGCATGATCAACGACCTGTCCGACGCGCCTGTCCGAC 789

58 eAspGlyPheProGluValArgGluPheAsnSerLeuProAsnAsnLys 75
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
790 CGACACACGCGGCTGGCGTGAACCTGTTCACCGCCTATCCGTCGTGGCG 839

75 laSerSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLys 91
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
840 TGTCGGTTTCGACCTCTCGCTGACCAACCGCGCACACACC..... 880

92 LysTyrIleLysLeuLeuIleAsnAsnAspGlyPhe 103
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881 .....CTGACGGGACCGCGCCCAACACGACACGTTTC 910

seq_name: /cqn_2.6/ptodata/2/ina/5B_COMB.seq:US-08-614-377A-6

seq_documentation_block:
; Sequence 6, Application US/08614377A
; Patent No. 5976864
; GENERAL INFORMATION:
; APPLICANT: Smit, John
; APPLICANT: Bingie, Wade H.
; APPLICANT: No. 5976864ellini, John F.
; TITLE OF INVENTION: EXPRESSION AND SECRETION OF
; TITLE OF INVENTION: HETEROLOGOUS
; TITLE OF INVENTION: POLYPEPTIDES FROM CAULOBACTER
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson PC
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/614,377A
; FILING DATE: 12-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/194,290
; FILING DATE: 09-FEB-1994
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/895,367
; FILING DATE: 09-JUNE-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34053
; REFERENCE/DOCKET NUMBER: 08106/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3300 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Caulobacter crescentus
; STRAIN: CB 15
; US-08-614-377A-6

alignment_scores:
    Quality: 71.00      Length: 112
    Ratio: 1.164       Gaps: 5
    Percent Similarity: 54.464      Percent Identity: 28.571

alignment_block:
US-09-528-682-4 x US-08-614-377A-6 ..

Align seg 1/1 to: US-08-614-377A-6 from: 1 to: 3300

1 AspTyrPheThrValArgIleGlnAspAlaTyrGluProIleAlaAsnTh 17
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608 GACTACCTGACCGCCTTCGTGGCG.....GCCAACAC 639

17 rAsn...ThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuA 33
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
640 GCCGTTCCAGCGCGCTGCCGACATCGATCTGGCGTCACAGCGCGCTGA 689

33 spGlyArgTyrSerAspTyrAlaLeuIleSerAlaGluGly..... 47
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
690 TCGCCACCATCTGAAACCGCGCCACCGGTGTCGGCATCGTGTACGCG 739

48 .....MetAspArgAspLeuPhe...GlySerAlaAsnIle 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
740 ACCGCCACGCGCGCATGATCAACGACCTGTCCGACGCGCCTGTCCGAC 789

58 eAspGlyPheProGluValArgGluPheAsnSerLeuProAsnAsnLys 75
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
790 CGACACACGCGGCTGGCGTGAACCTGTTCACCGCCTATCCGTCGTGGCG 839

75 laSerSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLys 91
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
840 TGTCGGTTTCGACCTCTCGCTGACCAACCGCGCACACACC..... 880

92 LysTyrIleLysLeuLeuIleAsnAsnAspGlyPhe 103
::: |||||:|||||
881 .....CTGACGGGACCGCGCCCAACACGACACGTTTC 910

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/ INFORMATION FOR SEQUENCING:
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/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 3280 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/   MOLECULE TYPE: DNA (genomic)
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/ FEATURE:
/   NAME/KEY: CDS
/   LOCATION: 57..3114
/   US-08-729-767-6

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Align seg 1/1 to reverse of: US-09-163-833-3 from: 1 to: 594

US-08-729-767-6


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32 LeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyMe 48
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
498 CTGGATGGCTCTACCGGCTGATGTTCTCATAGATCATGAGGAGCCA 449
48 tAspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGlu.... 63
:||||: ||| ||| :|||:||||:
448 GGACAAG.....TGTGGCAGAGCG.....GCTTACCCCATGGCA 414
64 ..ValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspThr 79
||| :||| ||||| ||||| ||||| ||||| ||||| |||||
413 CAGTGTACACAGCAGCGGCTTGGGAAACACTGAGGGCAGCTCGGATGTA 364
80 AlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysLe 96
:||||: ||||| ||||| ||||| ||||| ||||| ||||| :|||
363 TCGAGCAACAGCAGCAAGTAGACACTGAGGTGGAAGAAGGGGTTGTCGT 314
96 uLeuIleAsn 99
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313 CCGCCTCAAT 304

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seq_name: /cgn2_6/ptodata/2/1na/6B_COMB.seq:US-09-163-833-1

seq_documentation_block:

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; Sequence 1, Application US/09163833
; Patent No. 6268135
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: No. 6268135el Phospholipase Molecule and Uses Therefor
; FILE REFERENCE: mni-059
; CURRENT APPLICATION NUMBER: US/09/163.833
; CURRENT FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 912
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(645)
US-09-163-833-1

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alignment_scores:
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  Ratio: 1.448        Gaps: 3
  Percent Similarity: 68.571  Percent Identity: 30.000

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alignment_block:

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US-09-528-682-4 x US-09-163-833-1/rev ..
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32 LeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyMe 48
||||| ||||| ||||| ||||| ||||| ||||| |||||
549 CTGGATGGCTCTACCGGCTGATGTTCTCATAGATCATGAGGAGCCA 500
48 tAspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGlu.... 63
:||||: ||| ||| :|||:||||:
499 GGACAAG.....TGTGGCAGAGCG.....GCTTACCCCATGGCA 465
64 ..ValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspThr 79
||| :||| ||||| ||||| ||||| ||||| ||||| |||||
464 CAGTGTACACAGCAGCGGCTTGGGAAACACTGAGGGCAGCTCGGATGTA 415
80 AlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysLe 96
:||||: ||||| ||||| ||||| ||||| ||||| ||||| :|||
414 TCGAGCAACAGCAGCAAGTAGACACTGAGGTGGAAGAAGGGGTTGTCGT 365
96 uLeuIleAsn 99
: |||||
364 CCGCCTCAAT 355

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seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-258-188-1

seq_documentation_block:

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; Sequence 1, Application US/08258188
; Patent No. 5475098
; GENERAL INFORMATION:
; APPLICANT: HALL, Robert H.
; TITLE OF INVENTION: A NEW AND DISTINCTIVE DNA SEQUENCE OF E.
; TITLE OF INVENTION: coli O157:H7 AND ITS USE FOR THE RAPID, SENSITIVE AND
; TITLE OF INVENTION: SPECIFIC DETECTION OF O157:H7 AND OTHER ENTEROHEMORRHAGIC
; TITLE OF INVENTION: E. coli
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,188
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 15280206, DHHSE135940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2278 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (plasmid)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..2275
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2278
; OTHER INFORMATION: /product= "Peptide encoded by the
; OTHER INFORMATION: hlyA gene"
; OTHER INFORMATION: /standard_name= "Nucleic acid sequence of hlyA
; OTHER INFORMATION: gene"
US-08-258-188-1

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alignment_block:

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US-09-528-682-4 x US-08-258-188-1 ..
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23 PheLeuAsn.....MetGlyAsnGluValAlaLeuAspGlyArgTyrSe 37
:||||| ||||| ||||| ||||| ||||| ||||| |||||
1745 TATCTGAATGGTGGTTTGGTAATGATATTTATGTTATGGGCAAACTA 1794
37 rAsnTyrAlaLeuIleSerAlaGluGlyGlyMet...AspArgAspLeup 53
:||||| ||||| ||||| ||||| ||||| ||||| |||||

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; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,232
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 2200.023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1541 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1541
US-08-200-232-3

alignment_scores:
    Quality: 67.00      Length: 96
    Ratio: 1.117        Gaps: 2
Percent Similarity: 62.500 Percent Identity: 22.917

alignment_block:
US-09-528-682-4 x US-08-200-232-3 ..

Align seg 1/1 to: US-08-200-232-3 from: 1 to: 1541

11 TyrGIUProIleAlaAsnThrAsnThrThrGlnPheLeuAsnMetGl 27
|||||::||:: :: ||::||:: ::::: ::::: ::
1210 TACAACCACTCATTAAGATCAATAACGTCAAAATCTCATAAAATAA 1259
27 yASnGluValAlaLeuASpGIyArgTyrSerASnTyRAlaLeuIleSeRA 44
:::::::::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||::
1260 AGAACATGTTTAGTGCAAGGGCGGAACATTGATATATATTAGTCGGAG 1309
44 laGlUGlycylMetASpArgASpLeUPheGlyserAlaAsnIleASpGly 60
:::::||::: :::: ||| :||:: ||:: ||:: ||:: ||:: ||::
1310 TGCAAGGCCT...AGTTATGACAATATTTCTGCAAGCAACCAATCTG 1356
61 PhePrOGluValArGLUpHeASnSerLeUPrOASnASnLysAlaSerSe 77
::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||::
1357 CAAGAAGCAATTCAAAGAGCGCCGTAGCCCTTTATACAAACAACACGCCAT 1406
77 rASpThrAlaserLeuASnLysGlnHisASpAlaAspPheLysLysTyri 94
|||||::||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||::
1407 GGATATTGTGTGGTGGCAAGGACCATACCAGATGACATTAAGCA...T 1453
94 leLysLeuIleASnASnASpGlyPhePheSerASn 106
::: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||::
1454 GCGGGATGCGCTATCGCAATCAAGCATGGTGAATAAC 1491

seq_name: /cgm2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US95-02219-3

seq_documentation_block:
; Sequence 3, Application PC/TUS9502219
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Blaser, Martin J.
; TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
; TITLE OF INVENTION: AND RELATED METHODS
```



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;
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02219
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 2200.023
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1541 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1541
; PCT-US95-02219-3

alignment_scores:
  Quality: 67.00      Length: 96
  Ratio: 1.117      Gaps: 2
  Percent Similarity: 62.500      Percent Identity: 22.917

alignment_block:
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1210 TACAACCACTCATTAAGATCAATAACGCTCAAAATCTCACTAAAAATAA 1259
27 yAsnGluValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSera 44
|||||:|||||:  ::  |||:|||||:  ::|||:  ::
1260 AGAACATGTTTGTAGTGAAGGCGCAACATTGATTATAATTAGTGGGAG 1309
44 laGluGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGly 60
|||||:|||||:  ::  |||:|||||:  ::|||:  ::
1310 TGCAAGGCGCT...AGTTATGACAATATTTCTGCAAGCAACACCAATCTG 1356
61 PheProGluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSe 77
|||||:|||||:  ::  |||:|||||:  ::|||:  ::
1357 CAAGACGAATTCAAGAGCGCGCTAGCCCTTTATACACCAACACCGCAT 1406
77 rAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrI 94
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1407 GGATATTTGTGTGGTGGCAAGGAAGCAATACCGATGACATTAAACA...T 1453
94 leLysLeuLeuIleAsnAsnAspGlyPhePheSerAsn 106
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seq_documentation_block:
; Sequence 3, Application PC/TUS9502219A
; GENERAL INFORMATION:
; APPLICANT: Cover, Timothy L.
; APPLICANT: Tummuru, Murali KR
; APPLICANT: Cao, Ping
; APPLICANT: Thompson, Stuart A.
; APPLICANT: Blaser, Martin J.
; TITLE OF INVENTION: VACUOLATING TOXIN-DEFICIENT H. PYLORI
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG P.C.
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02219A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 2200.023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1541 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1541
; PCT-US95-02219A-3

alignment_scores:
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  Ratio: 1.117      Gaps: 2
  Percent Similarity: 62.500      Percent Identity: 22.917

alignment_block:
US-09-528-682-4 x PCT-US95-02219A-3

Align seg 1/1 to: PCT-US95-02219A-3 from: 1 to: 1541

11 TyrGluProIleAlaAsnThrAsnThrThrThrGlnPheLeuAsnMetG1 27
|||||:|||||:  ::  |||:|||||:  ::|||:  ::
1210 TACAACCACTCATTAAGATCAATAACGCTCAAAATCTCACTAAAAATAA 1259
27 yAsnGluValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSera 44
|||||:|||||:  ::  |||:|||||:  ::|||:  ::
1260 AGAACATGTTTGTAGTGAAGGCGCAACATTGATTATAATTAGTGGGAG 1309
44 laGluGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGly 60
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1310 TGCAAGGCGCT...AGTTATGACAATATTTCTGCAAGCAACACCAATCTG 1356
61 PheProGluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSe 77
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77 rAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyxI 94
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94 leLysLeuLeuIleAsnAsnAspGlyPhePheSerAsn 106
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-434-000A-5

seq_documentation_block:

; Sequence 5, Application US/08434000A

; Patent No. 6046037

; GENERAL INFORMATION:

; APPLICANT: ANDREW C. HIATT, JULIAN

; APPLICANT: K.-C. MA, THOMAS LEHNER

; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION

; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; SUITE: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/434,000A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below: 1

; APPLICATION NUMBER: 08/367,395

; FILING DATE: 12/30/94

; ATTORNEY/AGENT INFORMATION:

; NAME: Guise, Jeffrey W.

; REGISTRATION NUMBER: 34,613

; REFERENCE/DOCKET NUMBER: 212/127

; TELEPHONE: (619) 552-8400

; TELEFAX: (619) 552-0159

; TELEX: 67-3510

; SEQUENCE LISTING

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3630 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; DESCRIPTION: Bovine Polyimmunoglobulin Receptor

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 152...2425

US-08-434-000A-5

alignment_scores:

Quality: 66.50 Length: 65

Ratio: 1.797 Gaps: 3

Percent Similarity: 56.923 Percent Identity: 33.846

alignment_block:

US-09-528-682-4 x US-08-434-000A-5 ..

Align seg 1/1 to: US-08-434-000A-5 from: 1 to: 3630

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 254 TCAGTCTCCATCAAGTCTACTACCGCCACCTCGTCAACGGCACAC 303
 19 rThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgT 36
 ::::: ||| ::::: ||| ::::: |||
 304 GCGCAAGTACTGTCGCGCAGGAGCCAG.....GGCCGCT 341
 36 ySerAsnTyraLeuIleSerAlaGluGlyGlyMetAspArgAspLeu 52
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 342 GCACG.....ACCTCATCTCTCGGAGGCTACGTCTCCGACGACTAC 385
 53 PheGlySerAlaAsnIleAspGlyPheProGluValArgGluPhe 67
 ::::: ||| ::::: ||| ::::: |||
 386 GTGGGAGAGCCCACTCCCACTTCCCGAGAGCGGCGACGTTT 430
 seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-312-157-5

seq_documentation_block:

; Sequence 5, Application US/09312157

; Patent No. 6303341

; GENERAL INFORMATION:

; APPLICANT: ANDREW C. HIATT, JULIAN

; APPLICANT: K.-C. MA, THOMAS LEHNER

; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION

; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; SUITE: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/312,157

; FILING DATE: 14-May-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/434,000

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Guise, Jeffrey W.

; REGISTRATION NUMBER: 34,613

; REFERENCE/DOCKET NUMBER: 212/127

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 552-8400

; TELEFAX: (619) 552-0159

; TELEX: 67-351

; SEQUENCE LISTING

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3630 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; DESCRIPTION: Bovine Polyimmunoglobulin Receptor

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 152...2425

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-312-157-5

alignment_scores:


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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-469-880-3

alignment_scores:
  Quality: 66.00 Length: 95
  Ratio: 1.179 Gaps: 3
  Percent Similarity: 58.947 Percent Identity: 25.263

alignment_block:
US-09-528-682-4 x US-08-469-880-3 ..

Align seg 1/1 to: US-08-469-880-3 from: 1 to: 4937

15 AlaAsnThrAsnThrThrThrGlnPheLeuAsnMetGlyAsnGluValAl 31
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3439 GCCAACCTAACTATTAAACCAAGAAATTCGAATTCACAGACCTAAG 3488

31 aLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGly 48
::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3489 TATTTACAGT.....TTCAATAAAGCAGAGATTACAGCCAAAGATGGTA 3532

48 etAspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluVal 64
||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
3533 GAGATTTAACATATGCGACAGCTAATGACGGTAACAGCGTGCCGAGGCC 3582

65 Arg.....GluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
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3583 AAACAGCTAACTTTTAAACAATGTTAAAGATTCAAAAATCTCTGCTGAC.. 3630

79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96
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96 euLeuIleAsnAsnAspGlyPhePheSerAsnAsn 107
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seq_documentation_block:
; Sequence 3, Application US/08469880
; Patent No. 5876733
; GENERAL INFORMATION:
; APPLICANT: Barenkamp, Stephen J.
; TITLE OF INVENTION: High Molecular Weight Surface Proteins
; TITLE OF INVENTION: of No. 5876733-Typeable Haemophilus
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shoemaker and Mattare, Ltd.
; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202-0286
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,880
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9205704.1
; FILING DATE: 16-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/02166
; FILING DATE: 16-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,832
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Berkstresser, Jerry W
; REGISTRATION NUMBER: 22,651
; REFERENCE/DOCKET NUMBER: 1038-516 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 415-0810
; TELEFAX: (703) 415-0813
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4937 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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15 AlaAsnThrAsnThrThrThrGlnPheLeuAsnMetGlyAsnGluValAl 31
||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
3439 GCCAACCTAACTATTAAACCAAGAAATTGAAATTGACAGACCTAAG 3488

31 aLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGly 48
::::::::::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
3489 TATTTTCAGGT.....TTCAATAAAGCAGAGATTACAGCCAAAGATGGTA 3532

48 etAspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluVal 64
||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
3533 GAGATTTAACCTATTGCGACAGCTAATGACGGTAACAGCGTGCCGAAGCC 3582

65 Arg.....GluPheAsnSerLeuProAsnAsnLysAlaSerAspTh 79
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3583 AAACAGCTAACTTTTAAACAATGTTAAAGATTCAAAAATCTCTGCTGAC.. 3630

79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96
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seq_documentation_block:
; Sequence 3, Application US/08469880
; Patent No. 5876733
; GENERAL INFORMATION:
; APPLICANT: Barenkamp, Stephen J.
; TITLE OF INVENTION: High Molecular Weight Surface Proteins
; TITLE OF INVENTION: of No. 5876733-Typeable Haemophilus
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shoemaker and Mattare, Ltd.
; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202-0286
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,880
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9205704.1
; FILING DATE: 16-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/02166
; FILING DATE: 16-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,832
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Berkstresser, Jerry W
; REGISTRATION NUMBER: 22,651
; REFERENCE/DOCKET NUMBER: 1038-516 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 415-0810
; TELEFAX: (703) 415-0813
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4937 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-469-880-3

alignment_scores:
Quality: 66.00 Length: 95
Ratio: 1.179 Gaps: 3
Percent Similarity: 58.947 Percent Identity: 25.263

alignment_block:
US-09-528-682-4 x US-08-469-880-3 ..

Align seg 1/1 to: US-08-469-880-3 from: 1 to: 4937

15 AlaAsnThrAsnThrThrThrGlnPheLeuAsnMetGlyAsnGluValAl 31
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3439 GCCAACCTAACTATTAAACCAAGAAATTGAAATTGACAGACCTAAG 3488

31 aLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGly 48
::::::::::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
3489 TATTTTCAGGT.....TTCAATAAAGCAGAGATTACAGCCAAAGATGGTA 3532

48 etAspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluVal 64
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3533 GAGATTTAACCTATTGCGACAGCTAATGACGGTAACAGCGTGCCGAAGCC 3582

65 Arg.....GluPheAsnSerLeuProAsnAsnLysAlaSerAspTh 79
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3583 AAACAGCTAACTTTTAAACAATGTTAAAGATTCAAAAATCTCTGCTGAC.. 3630

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-469-880-3

seq_documentation_block:
; Sequence 3, Application US/08469880
; Patent No. 5876733
; GENERAL INFORMATION:
; APPLICANT: Barenkamp, Stephen J.
; TITLE OF INVENTION: High Molecular Weight Surface Proteins
; TITLE OF INVENTION: of No. 5876733-Typeable Haemophilus
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shoemaker and Mattare, Ltd.
; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202-0286
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,880
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9205704.1
; FILING DATE: 16-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/02166
; FILING DATE: 16-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,832
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Berkstresser, Jerry W
; REGISTRATION NUMBER: 22,651
; REFERENCE/DOCKET NUMBER: 1038-516 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 415-0810
; TELEFAX: (703) 415-0813
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4937 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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;
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shoemaker and Mattare, Ltd.
; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
; STREET: Bldg. 1
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202-0286
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/719,641
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,832
; FILING DATE: 16-SEP-1994
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; APPLICATION NUMBER: US PCT/US93/02166
; FILING DATE: 16-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9205704.1
; FILING DATE: 16-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Berkstresser, Jerry W
; REGISTRATION NUMBER: 22,651
; REFERENCE/DOCKET NUMBER: 1038-625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 415-0810
; TELEFAX: (703) 415-0813
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4937 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-719-641-3

alignment_scores:
  Quality: 66.00 Length: 95
  Ratio: 1.179 Gaps: 3
  Percent Similarity: 58.947 Percent Identity: 25.263

alignment_block:
  US-09-528-682-4 x US-08-719-641-3 ..
  Align seg 1/1 to: US-08-719-641-3 from: 1 to: 4937
  15 AlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluValal 31
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  3439 GCCAACCTTAACCTATTAACCAAGAAATTTGAAATTCAGAGAACCTAAG 3488
  31 aLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGly 48
  :|||: |||: |||: |||: |||: |||:
  3489 TATTTCAGGT.....TTCAATAAAGCAGAGATTACAGCCAAAGATGGTA 3532
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  3533 GAGATTTTAACTATTTGGCAACAGTAAATGACGGTAAACAGCGGTGCCGAGGCC 3582
  65 Arg.....GluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
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  3583 AAACAGTAACTTTTAAACAATGTTAAAGATTCAAAAATCTCTGCTGAC... 3630
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96 eLeuIleAsnAsnAspGlyPhePheSerAsnAsn 107
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seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-038-682-6

seq_documentation_block:
; Sequence 6, Application US/08038682
; Patent No. 5549897
; GENERAL INFORMATION:
; APPLICANT: BARENKAMP, STEPHEN J
; APPLICANT: ST. GEME III, JOSEPH W
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
; TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shoemaker and Mattare, Ltd
; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
; STREET: Bldg. 1
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202-0286
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/038,682
; FILING DATE: 16-MAR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BERKSTRESSER, JERRY W
; REGISTRATION NUMBER: 22,651
; REFERENCE/DOCKET NUMBER: 1038-293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 415-0810
; TELEFAX: (703) 415-0813
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9323 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-038-682-6

alignment_scores:
  Quality: 66.00 Length: 95
  Ratio: 1.179 Gaps: 3
  Percent Similarity: 58.947 Percent Identity: 25.263

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  US-09-528-682-4 x US-08-038-682-6 ..
  Align seg 1/1 to: US-08-038-682-6 from: 1 to: 9323
  15 AlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluValal 31
  ||||| :|||: |||||: |||||: |||||: |||||:
  3879 GCCAACCTTAACCTATTAACCAAGAAATTTGAAATTCAGAGAACCTAAG 3928
  31 aLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGly 48
  :|||: |||: |||: |||: |||: |||:
  3929 TATTTCAGGT.....TTCAATAAAGCAGAGATTACAGCCAAAGATGGTA 3972
  48 eAspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluVal 64
  ||| :|||: |||: |||: |||: |||:
  3973 GAGATTTTAACTATTTGGCAACAGTAAATGACGGTAAACAGCGGTGCCGAGGCC 4022
  65 Arg.....GluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
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[illegible]


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; APPLICATION NUMBER: US PCT/US93/02166
; FILING DATE: 16-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9205704.1
; FILING DATE: 16-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Berkstresser, Jerry W
; REGISTRATION NUMBER: 22,651
; REFERENCE/DOCKET NUMBER: 1038-633
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 415-0810
; TELEFAX: (703) 415-0813
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9323 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-728-470-6

alignment_scores:
    Quality: 66.00      Length: 95
    Ratio: 1.179        Gaps: 3
    Percent Similarity: 58.947    Percent Identity: 25.263

alignment_block:
US-09-528-682-4 x US-08-728-470-6 ..

Align seg 1/1 to: US-08-728-470-6 from: 1 to: 9323

15 AlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluValAl 31
||||| ::| ||||| ::| ||||| ::| ||||| ::| ||||| ::|
3879 GCCACCTTAACATTAAACCAAGAAATTGAATTCACAGAACCTAAG 3928

31 aLeuaspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyM 48
:::::|||| ||| ||| |||||::::: |||
3929 TATTTCAGT.....TTCAATAAAGCAGAGATTACAGCCAAAGATGGTA 3972

48 etAspArgAspLeuPheGlySerAlaAsnIleaspGlyPheProGluVal 64
||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
3973 GAGATTTAACATTATGGCAACAGTAATGACGGTAACAGCGGTGCGGAAGCC 4022

65 Arg.....GluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
::| |||||::| ::| ::| ::| ::| ::| ::| ::| ::|
4023 AAACAGTAACATTTAACAATGTTAAAGATTCAAAATCTCTGCTGAC.. 4070

79 rAlaSerLeuAsnLysGlnHisAspAlaaspPheLysTyrIleLysL 96
||||| ::| ::| ::| ::| ::| ::| ::| ::|
4071 .....GGTCACAATGTGACATAATAATAGCAAAAGTGAAA 4104

96 euLeuIleAsnAsnAspGlyPhePheSerAsnAsn 107
::| ::| ::| ||| |||||::|
4105 CATCTAGCAGCAATGCGGACGCTGAAAGCAATAGC 4139

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-617-697-6

seq_documentation_block:
; Sequence 6, Application US/08617697
; Patent No. 5977336
; GENERAL INFORMATION:
; APPLICANT: Barenkamp, Stephen J
; TITLE OF INVENTION: High Molecular Weight Surface Proteins
; DATE OF INVENTION: of No. 5977336-Typeable Haemophilus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shoemaker and Mattare, Ltd.
; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.

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; APPLICANT: Barenkamp, Stephen J
; TITLE OF INVENTION: High Molecular Weight Surface Proteins
; TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shoemaker and Mattare, Ltd.
; STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202-0286
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/719,641
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,832
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/02166
; FILING DATE: 16-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9205704.1
; FILING DATE: 16-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Berkstresser, Jerry W
; REGISTRATION NUMBER: 22,651
; REFERENCE/DOCKET NUMBER: 1038-625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 415-0810
; TELEFAX: (703) 415-0813
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9323 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-719-641-6

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alignment_scores:
  Quality: 66.00      Length: 95
  Ratio: 1.179      Gaps: 3
  Percent Similarity: 58.947      Percent Identity: 25.263

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alignment_block:

US-09-528-682-4 x US-08-719-641-6 ..

Align seg 1/1 to: US-08-719-641-6 from: 1 to: 9323

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15 AlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluValAl 31
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
3879 GCCAACCACTATTAAACCAAGAAATGAAATTCAGACGAGACCTAAG 3928

31 aLeuAspGlyArgTyrSerAsnTyrAlaLeuLeuSerAlaGluGlyGlyM 48
: : : : : : : : : : : : : : : : : : : : : : : : : : :
3929 TATTTTCAGT.....TTCATAAGCAGAGATTACAGCCAAAGATGGTA 3972

48 etAspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluVal 64
||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
3973 GAGATTTAACTATTGGCAACAGTAATCACGCTAACACGCGTCGGAAGCC 4022

65 Arg.....GluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
: : : : : : : : : : : : : : : : : : : : : : : : : : :
4023 AAAACAGTAACATTTTAAACAATGTTAAAGATTCACAAATCTCTGTGAC.. 4070

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79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96
|||: : : : : : : : : : : : : : : : : : : : : : : : : : :
4071 .....GGTCACAATGTGACACTAAATAGCAAAAGTCAAAA 4104

96 euLeuIleAsnAsnAspGlyPhePheSerAsnAsn 107
: : : : : : : : : : : : : : : : : : : : : : : : : : :
4105 CATCTAGCAGCAATGGCGACGCTGAAAGCAATAGC 4139

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-148-680-1

seq_documentation_block:
; Sequence 1, Application US/09148680
; Patent No. 6255561
; GENERAL INFORMATION:
; APPLICANT: Kossmann, Jens
; APPLICANT: Willmitzer, Lothar
; APPLICANT: Emmermann, Michael
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING
; TITLE OF INVENTION: ENZYMES FROM MAIZE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/148,680
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/01141
; FILING DATE: 06-MAR-97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 196 08 918.2
; FILING DATE: 07-MAR-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: GFB-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1993 base pairs
; TYPE: nucleotide
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: zea mays
; TISSUE TYPE: Blattgewebe
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1675
; US-09-148-680-1

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alignment_scores:
  Quality: 65.50      Length: 124
  Ratio: 1.129      Gaps: 6
  Percent Similarity: 46.774      Percent Identity: 26.613

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alignment_block:


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US-09-528-682-4 x US-09-148-680-1
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|||||: |||||:|||||:
634 TTCACGATAGAAATCGGTGATGCTATATAAATGGTGGCAGTCCGTTTGGGAA 683
12 uProIleAlaAsnThrAsnThrThrThrGlnPheLeuAsn.....25
|||||: :|||: |||||:
684 TCCACTGCAACAAGGTTCTCTACTGGATTGTTCTTAGAGCCAAATGGAT 733
26 .....MetGlyAsnGlu.....29
:|||||:
734 TTTATCAGGCGCAATGAACACAGACAGACAGGCTCAGCTTGCTACATACGCT 783
30 .....ValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuI1 42
:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
784 GACCATATACAGATTGGATTAGCTGCAATTTGAAGGACTATATAGTTAT 833
42 eSerAlaGluGlyGlyMetAspArgAspLeuPheGlySerAlaAsnIleA 59
|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
834 ATCTCATAGTGGAGAGCTAGAAAA.....GGATCT.....864
59 spGlyPheProGluValArgGluPheAsnSerLeuProAsnAsnLysAla 75
|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
865 .....GAAATTCGCACCTTCGATGGCTCACCAGTTGGCTATGCT 903
76 SerSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAsp_PheLysL 92
|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
904 TCATCCCTATAGAAACAATAAATACTAGCCTCTGCTCATGACAATGAAAC 953
92 ystYrIleLysLeuLeuIle 98
|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
954 ACTATTGTATATTATGATC 973
seq_name: /cgn2_6/ptodata/2/1na/5B_COMB.seq:US-09-528-760A-3
seq_documentation_block:
; Sequence 3, Application US/08752760A
; Patent No. 5877011
; GENERAL INFORMATION:
; APPLICANT: Armentano, Donna
; APPLICANT: Gregory, Richard J.
; APPLICANT: Smith, Alan E.
; TITLE OF INVENTION: CHIMERIC ADENOVIRAL VECTORS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,760A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seide, Rochelle K
; REGISTRATION NUMBER: 32,300
; REFERENCE/DOCKET NUMBER: A31385
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-705-5000
; TELEFAX: 212-705-5020
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TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1552 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-752-760A-3
alignment_scores:
Quality: 65.00 Length: 77
Ratio: 1.275 Gaps: 3
Percent Similarity: 66.234 Percent Identity: 24.675
alignment_block:
US-09-528-682-4 x US-08-752-760A-3
Align seg 1/1 to: US-08-752-760A-3 from: 1 to: 1552
27 GlyAsnGluValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSe 43
|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
69 GGAGGTTCCGTTTGTGCTCCCGGTATATGCTCTACGGA.....110
43 rAlaGluGlyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspG 60
|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
111 .....GGCAGAAACACGATTCGTTACTCGGAGCTGGCTCCGTT....149
60 lyPheProGluValArgGluPheAsnSerLeuProAsnAsnLysAlaSer 76
|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
150 .....GTACGACACCACTCGCTGCTACTTGGTGACAAACAGTCG 188
77 SerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTy 93
|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
189 GCGGACATCGCTTCCCTGAACATATCAAAAC.....GACCACAGCAACTT 232
93 rIleLysLeuLeuIleAsnAsnAspGlyPhe 103
|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
233 CTGACACCGGTGGTGCAGAACACGATTC 263
seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-08-822-322-7
seq_documentation_block:
; Sequence 7, Application US/08822322
; Patent No. 6037158
; GENERAL INFORMATION:
; APPLICANT: Hummel, Werner, Riebel, Bettina
; TITLE OF INVENTION: Alcohol dehydrogenase and its use for
; enzymatic production of chiral hydroxy compounds
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,322
; FILING DATE: 21-March-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 196 10 984
; FILING DATE: 21-March-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6037158man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1076
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; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,469A
; FILING DATE: 08-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/099,757
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: YU-102CIP
; TELEPHONE: (212) 596-9090
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1361 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..1359
; US-08-118-469A-4

alignment_scores:
  Quality: 64.50      Length: 98
  Ratio: 1.316      Gaps: 3
  Percent Similarity: 50.000      Percent Identity: 23.469

alignment_block:
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Align seg 1/1 to: US-08-118-469A-4 from: 1 to: 1361

24 LeuAsnMetGlyAsnGluValAlaLeuAspGlyArgTyrSerAsnTyr.. 39
||||| |||||
244 CTAATTTCTAAGAACAATAGGCTTAAGATTCGTTAAGTAATTTGA 293
39 .....

294 AGCAAAAAAATGACGACATTAATAAATCCAAAGACTTTAAAGG 343
40 .....AlaLeuIleSerAlaGluGlyMetAspArgAspLeuPhe 53
||||| |||||
344 ATTTACAAACTTTAAGAAATTCAAAATTTAATGCTTAAGACTTGGAT 393
54 GlySerAlaAsnTleAspGlyPheProGluValArgGluPheAsnSerLe 70
||||| |||||
394 CAGTCGAGTAAT .....GATTTGAAAATTT 419
70 uProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnHis 87
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420 AGACAATTTCTGAGTCTTGCAAGAAGCTTCTTCA .....AAGCAC 460
87 spAlaAspPheLysLysTyrIleLysLeuLeuIleAsnAsnAsp 101
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; : : : : : ||| ||| ||| : : : : :
461 ATATTGGCAAGTCAAGATACGGTAAAGCTTTGCTGAAAAATGAT 504
seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-909-119-4

seq_documentation_block:
; Sequence 4, Application US/08909119
; Patent No. 5807685
; GENERAL INFORMATION:
; APPLICANT: Flavell, Richard A.
; APPLICANT: Fikrig, Erol
; APPLICANT: Lam, Tuan T.
; APPLICANT: Kantor, Fred S.
; APPLICANT: Barthold, Stephen W.
; TITLE OF INVENTION: NOVEL B. BURGENDORFERI POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,119
; FILING DATE: 11-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/118,469
; FILING DATE: 08-SEP-1993
; APPLICATION NUMBER: US 08/099,757
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: YU-102CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9090
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1361 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..1359
; US-08-909-119-4

alignment_scores:
  Quality: 64.50      Length: 98
  Ratio: 1.316      Gaps: 3
  Percent Similarity: 50.000      Percent Identity: 23.469

alignment_block:
  US-09-528-682-4 x US-08-909-119-4 ..

Align seg 1/1 to: US-08-909-119-4 from: 1 to: 1361

24 LeuAsnMetGlyAsnGluValAlaLeuAspGlyArgTyrSerAsnTyr.. 39
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244 CTAATTTCTAAGAACAATAGGCTTAAGATTCGTTAAGTAATTTGA 293
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39 .....
294 AAGCAAAAAAATGACCAGACATTAAAAAATCCAAAGACTTTAAAAAGG 343
40 .....AlaLeuIleSerAlaGluGlyGlyMetAspArgAspLeuPhe 53
344 ATTTACAAACTTTAAGAAATTCAAAAATTTAATGCCTAAAGACTTGAT 393
54 GlySerAlaAsnIleAspGlyPheProGluValArgGluPheAsnSerLe 70
394 CAGTCGAGTAAT.....GATTTGAAATTT 419
70 uProAsnAsnLysAlaSerAspThrAlaSerLeuAsnLysGlnHisa 87
420 AGACAATTCAGCTTTGCAAGAAGCTTCTTCA.....AAGCACA 460
87 spAlaAspPheLysLysTyrIleLysLeuLeuIleAsnAsnAsp 101
461 ATATTGGCAAGTCAAGATACGGTAAAGCTTTGCTGAAAAATGAT 504
seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-056-556-203

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seq_documentation_block:
; Sequence 203, Application US/09056556
; Patent No. 6350456
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,556
; FILING DATE: 07-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.457
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 203:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2852 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-056-556-203

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alignment_scores:
  Quality: 64.50      Length: 126
  Ratio: 1.057      Gaps: 8
Percent Similarity: 48.413 Percent Identity: 26.984

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771 GTCAACACGCGGTACTGTAACAGCGCAACTACAACACCGCGCTTGCCAA 820
32 euAspGlyArgTyrSerAsnTyrAlaLeuIleSerAla..... 44
821 ACTCCGCGCAATGCAACACCGCGCCTTCATTACTGCAACTTCAACAAC 870
45 .....GluGlyGlyMetAspArgAspLeuPheGlySerAlaAs 57
871 GGCTTCTTGTGGCGCGGACCAAGGCTCATTTTCGGGAGC..... 915
57 nileAspGlyPheProGluValArgGluPheAsnSerLeuPro..... 71
916 ....CCCGGCTTC.....TTCAAACTCGACCAAGTGCGCCGT 946
72 .....AsnAsnLysAlaSerSerAspThrAlaSerLeuAsn 83
947 CGTCGGGATTCTTCAACAGCGGTAGCGCGTCCGCGCTTCCTCGAAC 996
84 LysGlnHisAspAlaAspPheLysLysTyrIleLysLeuLeuIleAsnAs 100
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-460-739-1
seq_documentation_block:
; Sequence 1, Application US/08460739
; Patent No. 5698416
; GENERAL INFORMATION:
; APPLICANT: Wolf, Marcia K.
; APPLICANT: Cassels, Frederick J.
; APPLICANT: Bell, Brian A.
; TITLE OF INVENTION: Improved Methods for Production of
; TITLE OF INVENTION: Antigens Under Control of Tempature-Regulated Promotors
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glenna Hendricks
; STREET: 9669 A Main Street
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,739
; FILING DATE: 20-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna M.
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: wolf2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4875 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown

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TREATM


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; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: DNA for CS6 protein
; US-08-460-739-1

alignment_scores:
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  Ratio: 1.240        Gaps: 2
Percent Similarity: 51.485 Percent Identity: 20.792

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US-09-528-682-4 x US-08-460-739-1 ..
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1 AsptYrPhrValArgIleGlnAspAlaTyrGluProIleAlaAsnTh 17
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2831 AATTATTTCATGCGGTGGCGTAATCTTTTGAATTTAACCAAAACAA 2880
17 rAsnThrThrThrGlnPheLeuAsn..... 25
  ::::|||
2881 CGATGAAAAAACATCGGAAGAACTACACTTATCTAGAAAAAAGTTTTT 2930
26 .....MetGlyAsnGluValAlaLeuAspGly 34
  ::::::::::: ||::::::::: ::::||
2931 ATGATAAAAGCTAACTAGTCGTTGGTGAAGTTATACGAATTCAAAT 2980
35 ArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyGlyMetAspArgAs 51
  ::::::::::: ||::::::::: ::::||
2981 GTTTATAATACTACTCTTTTACTGCTGTTTCTCAGTTTCTACAGATACAGA 3030
51 PleuPheGlySerAlaAsnIleAspGlyPheProGluValArgGluPheA 68
  ::::::: ||::::::::: ||:::::::::
3031 TATGTATACGCCAAGTGAATCGATTATACACACAGAAAT..... 3070
68 snSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLys 84
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3071 .....CATGGAGTGGCTGATTACAGACTCTCAGATTATTGTCAGG 3109
85 Gln 85
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3110 CAA 3112

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-709-912-19

seq_documentation_block:
; Sequence 19, Application US/08709912
; Patent No. 5759840
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of xylanase to improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,912
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; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Olsen Mr., Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1039.2000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-2400
; TELEFAX: (212) 758-2982
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: pYbc
; POSITION IN GENOME:
; UNITS: bp
; US-08-709-912-19

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440 GTGACGTAATGTTGGCGTTCGAACCACTCGCGCGCTTAGATTGCTAAC 391
21 ThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgTyrSe 37
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390 ACTCCAATACTAGTAAAGGTGGTCGATCGCATCGATGGAAGG..... 346
37 rAsnTyrAlaLeuIleSerAlaGluGly..... 46
  ::::::::::: ||::::::::: |||
345 .....TCGGTTGTATCTTTGGTGGTGTAGATGTATAGGTACCACCA 303
47 ..GlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGly...Phe 61
  ::::::::::: ||::::::::: |||
302 TCGCTTTTGACTGTGCCCTTTGTAGTTCCAGTCG.....GACGGTAGGTTTC 257
62 ProGluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAs 78
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256 CCGAAGAGTCGACGACGTAATATTCAATCAGTGGCGAAGCGGTCCAGCCA 207
78 pThrAlaSerLeuAsnLysGlnHis 86
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206 TACAGTGTACAGGTAAACCGTTACCAT 182
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OM of: US-09-528-682-4 to: Pending_Patents_NA_Main: * out_format : pfs

Date: Jun 18, 2002 9:44 PM

About: Results were produced by the GenCore software, version 4.5,
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-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPEXT=4.500 -CGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPEXT=6.000 -FGAPEXT=7.000 -XGAPOP=10.000
-XGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
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-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pfs -NORW=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09528682.@CGN1_18511 -NCPU=6 -ICPU=3 -LONGLOG
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Search information block:

Query: US-09-528-682-4

Query length: 110

Database: Pending_Patents_NA_Main: *

Database sequences: 21979536

Database length: -2067452561

Search time (sec): 7363.740000

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/cgn2_6/ptodata/2/pna/US096B_COMB.seq:US-09-620-392-64418 -	71.50	134.49	485.01		
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/cgn2_6/ptodata/2/pna/US0917_COMB.seq:US-09-172-376-3257 -	70.00	152.66	47.17		
/cgn2_6/ptodata/2/pna/US096C_COMB.seq:US-09-654-617-135238 +	70.00	151.98	51.49		
/cgn2_6/ptodata/2/pna/US096E_COMB.seq:US-09-684-016-135238 +	70.00	151.98	51.49		
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/cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-305-638-18 -	70.00	137.64	323.79	26	
/cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-305-638-12 -	70.00	135.68	416.56	32	
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/cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-305-638-11 -	70.00	134.67	474.48	40	
/cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-305-638-10 -	70.00	133.32	564.02	35	
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/cgn2_6/ptodata/2/pna/US095B_COMB.seq:US-09-528-859-196 +	70.00	103.07	2.7e+04		

[illegible]

[illegible]

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/cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-371-1468-117862 +	63.50	143.97	143.92	
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/cgn2_6/ptodata/2/pna/US096E_COMB.seq:US-09-684-016-5354 +	63.50	135.82	409.39	64
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/cgn2_6/ptodata/2/pna/US095B_COMB.seq:US-09-533-559-4762 -	63.50	131.09	750.75	10
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/cgn2_6/ptodata/2/pna/US06031_COMB.seq:US-60-316-362-2019 -	63.50	129.25	950.14	12
/cgn2_6/ptodata/2/pna/US06011_COMB.seq:US-60-316-362-1019 -	63.50	127.30	1.2e+03	15
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/cgn2_6/ptodata/2/pna/US096C_COMB.seq:US-09-654-617-263015 +	63.50	125.89	1.5e+03	
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/cgn2_6/ptodata/2/pna/US088_COMB.seq:US-08-827-356-2779 +	63.50	114.25	6.5e+03	
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/cgn2_6/ptodata/2/pna/US099B_COMB.seq:US-09-933-524A-2740 -	63.00	139.92	241.93	
/cgn2_6/ptodata/2/pna/US099B_COMB.seq:US-09-933-524A-2740 -	63.00	139.92	241.93	
/cgn2_6/ptodata/2/pna/US099B_COMB.seq:US-09-933-524A-2740 -	63.00	139.92	241.93	
/cgn2_6/ptodata/2/pna/US099B_COMB.seq:US-09-933-524A-2740 -	63.00	139.92	241.93	
/cgn2_6/ptodata/2/pna/US099B_COMB.seq:US-09-933-524A-2740 -	63.00	139.92	241.93	
/cgn2_6/ptodata/2/pna/US099B_COMB.seq:US-09-933-524A-2740 -	63.00			


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/cgn2_6/ptodata/2/pna/US6019_COMB.seq:US-60-197-873-35742 + 63.00 137.86 315.05 4
/cgn2_6/ptodata/2/pna/US096C_COMB.seq:US-09-654-617-414275 - 63.00 137.73 320.17
/cgn2_6/ptodata/2/pna/US096D_COMB.seq:US-09-669-817A-5845 - 63.00 137.73 320.17
/cgn2_6/ptodata/2/pna/US096E_COMB.seq:US-09-684-016-414275 - 63.00 137.73 320.17
/cgn2_6/ptodata/2/pna/US095A_COMB.seq:US-09-521-640-261379 + 63.00 137.30 338.24
/cgn2_6/ptodata/2/pna/US095B_COMB.seq:US-09-537-8294 + 63.00 136.87 357.38
/cgn2_6/ptodata/2/pna/US0919_COMB.seq:US-60-191-637-8294 + 63.00 136.82 360.01
/cgn2_6/ptodata/2/pna/US0916_COMB.seq:US-60-167-217-8366 + 63.00 135.98 400.76
/cgn2_6/ptodata/2/pna/US0917_COMB.seq:US-60-172-363-18826 - 63.00 135.54 424.18
/cgn2_6/ptodata/2/pna/US100_COMB.seq:US-10-020-338-18894 + 63.00 134.91 459.80
/cgn2_6/ptodata/2/pna/US095C_COMB.seq:US-09-540-236-1431 + 63.00 133.60 544.16
/cgn2_6/ptodata/2/pna/US100_COMB.seq:US-10-029-386-22831 + 63.00 133.60 544.16

seq_name: /cgn2_6/ptodata/2/pna/US094_COMB.seq:US-09-404-520-11975

seq_documentation_block:
; Sequence 11975, Application US/09404520
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Ghodssi, Azita
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: McIninch, James
; APPLICANT: Timberlake, William E.
; APPLICANT: Yu, Jaehyuk
; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-10(15498)A
; CURRENT APPLICATION NUMBER: US/09/404,520
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 44345
; SEQ ID NO 11975
; LENGTH: 3159
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-09-404-520-11975

alignment_scores:
Quality: 83.50 Length: 86
Ratio: 1.670 Gaps: 1
Percent Similarity: 58.140 Percent Identity: 26.744

alignment_block:
US-09-528-682-4 x US-09-404-520-11975 ..
Align seg 1/1 to: US-09-404-520-11975 from: 1 to: 3159

6 ArgileGlnAspAlaTyrGluProIleAlaAsnThrThrThrG1 22
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1951 AGAGTCCCAAGCGGTATGAGCCCTGTCTTCCCATACACCACTTCCA 2000
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2001 AATCCTGGCGCTGCAGATACCTCTGGAATGCCGCCATCGTTGAACA 2050
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
39 yrAlaLeu.....IleSerAlaGluGly 46
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2051 CTGCGTCCCTCAGACACGCAAGATAGACGTCACTTCTCGCCTCTCCC 2100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
47 GlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProG1 63
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2101 GTGTGTTTCATTGGCCCTCCCAACAAAGCTCGAAGACGAGTTCGCCGA 2150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 uValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrA 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2151 AATCCGGATGACGGAGACTACAGCAGTCAATATGCCITAGCGGACACA 2200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 laSerLeu 82
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2201 CAATATC 2208

seq_name: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:US-09-540-236-152

seq_documentation_block:
; Sequence 152, Application US/09540236
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; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CA
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 152
; LENGTH: 1596
; TYPE: DNA
; ORGANISM: M. catarrhalis
US-09-540-236-152

alignment_scores:
Quality: 81.00 Length: 101
Ratio: 1.397 Gaps: 6
Percent Similarity: 57.426 Percent Identity: 30.693

alignment_block:
US-09-528-682-4 x US-09-540-236-152 ..
Align seg 1/1 to: US-09-540-236-152 from: 1 to: 1596

10 AlaTyrGluProIleAlaAsnThrThrThrThrGlnPheLeu...As 25
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
973 GCCTATCATCCACAAGTCTGACAATACGCTGGCGCAATATTTGCCAAA 1022
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
25 nMetGlyAsn.....GluValAlaLeuAspGlyArgTyrSerAsnT 39
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1023 TTTGGGTAAACCCAACTTAGAATTGCCGAACCGAAAAATACGCACATG 1072
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
39 yrAlaLeuIleSerAlaGluGly.....GlyMetAsp 49
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1073 TAACCTTTTCTTTAGCGGTGCTGGAAGCGCTGTACATGGCGAAGAT 1122
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
50 ArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgG1 66
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1123 CGCATTTTGATTAAATAGT.....CCTGATGTTAAAC 1154
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 uPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuA 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1155 ATACGACCTAAAACTGAATGATGCTTTTGGAGTTACCGAAAAATTAA 1204
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 snLysGlnHisAspAla...AspPheLysLysTyrIleLysLeuLeuIle 98
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1205 AT.....GATGCAATGACTCGGGCAATATATGATGATTAAATGTC 1245
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
99 Asn 99
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1246 AAT 1248

seq_name: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:US-60-128-476-1482

seq_documentation_block:
; Sequence 1482, Application US/60128476
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA
; FILE REFERENCE: 107196.139
; CURRENT APPLICATION NUMBER: US/60/128,476
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 5002
; SEQ ID NO 1482
; LENGTH: 1596
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
US-60-128-476-1482

alignment_scores:
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; LENGTH: 65792
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte template ID No: 31
; PUBLICATION INFORMATION:
US-60-140-121-31

alignment_scores:
    Quality:      81.00      Length:     101
    Ratio:        1.397      Gaps:         6
    Percent Similarity: 57.426   Percent Identity: 30.693

alignment_block:
US-09-528-682-4 x US-60-140-121-31 ..
Align seg 1/1 to: US-60-140-121-31 from: 1 to: 65792

10 AlaTyrGluProIleAlaAsnThrAsnThrThrThrGlnPheLeu...As 25
|||||::||| :: |||||:: |||||:: |||||:: ||
45471 GCCTATCATCCAACAAGCTGCACAAATACGTGGCGGAATTATTACAAA 45520
|||||::||| :: |||||:: |||||:: |||||:: ||

45521 TTTGGGTAACCAACCTTAGAATTGCCGAACCGAAAAATACGCATG 45570
|||||::||| :: |||||:: |||||:: |||||:: ||

39 yrAlaLeuIleSerAlaGluGly.....GlyMetasp 49
|||||::||| :: |||||:: |||||:: |||||:: ||
45571 TAACCTTTTTCTTAGTGCGTCGTGAAGATCTGTACAAACGGCAGAAT 45620
|||||::||| :: |||||:: |||||:: |||||:: ||

50 ArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgGl 66
|||||::||| :: |||||:: |||||:: |||||:: ||
45621 CGCATTTTGATTAGT.....CCTGATGTTAAAC 45652
|||||::||| :: |||||:: |||||:: |||||:: ||

66 uPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuA 83
|||||::||| :: |||||:: |||||:: |||||:: ||
45653 ATACGACCCTAAAGCCCTGAATGAGTCTTTGAGGTTACCGAAAAATAA 45702
|||||::||| :: |||||:: |||||:: |||||:: ||

83 snLysGlnHisAspAla....AspPheLysLysTyrlleLysLeuIle 98
|||||::||| :: |||||:: |||||:: |||||:: ||
45703 AT.....GATCGGATGACTCGGGCAAATATGATGTTAATTATGTC 45743
|||||::||| :: |||||:: |||||:: |||||:: ||

99 Asn 99
|||
45744 AAT 45746

seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-304-517A-268958

seq_documentation_block:
; Sequence 268958, Application US/09304517A
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)B
; CURRENT APPLICATION NUMBER: US/09/304,517A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 268958
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Glycine max
US-09-304-517A-268958

alignment_scores:
    Quality:      79.50      Length:     92
    Ratio:        1.656      Gaps:         2
    Percent Similarity: 52.174   Percent Identity: 27.174

alignment_block:
US-09-528-682-4 x US-09-985-678-268958 ..
Align seg 1/1 to: US-09-985-678-268958 from: 1 to: 321

20 ThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgTy 36
|||||::||| :: |||||:: |||||:: |||||:: ||
26 ACCCACAGATTTAAGAGCATGGTGGTGGAGTTAGCAGTGGTGGTGCTCA 75
|||||::||| :: |||||:: |||||:: |||||:: ||

36 rSerAsnTyrrAlaLeuIleSerAlaGluGlyGlyMetaspArgAspLeuP 53
|||||::||| :: |||||:: |||||:: |||||:: ||
76 AAGTTCCTTGGTTATCTTTTGGCAGTGGAGAGGCCCTGCCCAAAAC 125
|||||::||| :: |||||:: |||||:: |||||:: ||

53 heGlySerAlaAsnIleAspGlyPheProGluValArgGluPheAsnSer 69
|||||::||| :: |||||:: |||||:: |||||:: ||
126 CGGCAACAACAATGCCCCAGCCCAACCTGAAGTGCAGGCTGTAAATAAT 175
|||||::||| :: |||||:: |||||:: |||||:: ||

70 LeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsn..... 83
|||||::||| :: |||||:: |||||:: |||||:: ||
176 GCGCTCTCTCAAAAGCATCTCTCTCTACTATAAACAAATAGACCTACAA 225
|||||::||| :: |||||:: |||||:: |||||:: ||

84 .....LysGlnHisAspAlaAspPheLysLysTyrlleLysL 96
|||||::||| :: |||||:: |||||:: |||||:: ||
226 GGCTGCTGGTATAAACAGTCATTCTACTGATGGCCAG..... 262
|||||::||| :: |||||:: |||||:: |||||:: ||

96 euLeuIleAsnAsnAspGlyPhePhe 104
|||||::||| :: |||||:: |||||:: |||||:: ||
263 .....AACACGGCTACTTTC 277
|||||::||| :: |||||:: |||||:: |||||:: ||

seq_name: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:US-09-985-678-268958

seq_documentation_block:
; Sequence 268958, Application US/09985678
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 16517.255/38-21(15097)F
; CURRENT APPLICATION NUMBER: US/09/985,678
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 09/304,517
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 295529
; SEQ ID NO 268958
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Glycine max
US-09-985-678-268958

alignment_scores:
    Quality:      79.50      Length:     92
    Ratio:        1.656      Gaps:         2
    Percent Similarity: 52.174   Percent Identity: 27.174

alignment_block:
US-09-528-682-4 x US-09-985-678-268958 ..
Align seg 1/1 to: US-09-985-678-268958 from: 1 to: 321

20 ThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgTy 36
|||||::||| :: |||||:: |||||:: |||||:: ||
26 ACCCACAGATTTAAGAGCATGGTGGTGGAGTTAGCAGTGGTGGTGCTCA 75
|||||::||| :: |||||:: |||||:: |||||:: ||

36 rSerAsnTyrrAlaLeuIleSerAlaGluGlyGlyMetaspArgAspLeuP 53
|||||::||| :: |||||:: |||||:: |||||:: ||
76 AAGTTCCTTGGTTATCTTTTGGCAGTGGAGAGGCCCTGCCCAAAAC 125
|||||::||| :: |||||:: |||||:: |||||:: ||

53 heGlySerAlaAsnIleAspGlyPheProGluValArgGluPheAsnSer 69
|||||::||| :: |||||:: |||||:: |||||:: ||
126 CGGCAACAACAATGCCCCAGCCCAACCTGAAGTGCAGGCTGTAAATAAT 175
|||||::||| :: |||||:: |||||:: |||||:: ||

70 LeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsn..... 83
|||||::||| :: |||||:: |||||:: |||||:: ||
```



```

CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/068.139
FILING DATE: HERewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0008-2 P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 1118 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: genomic DNA
IMMEDIATE SOURCE:
CLONE: MCAlc071
US-60-068-139-71

alignment_scores:
Quality: 78.00 Length: 116
Ratio: 1.300 Gaps: 6
Percent Similarity: 51.724 Percent Identity: 29.310

alignment_block:
US-09-528-682-4 x US-60-068-139-71/rev ..
Align seg 1/1 to reverse of: US-60-068-139-71 from: 1 to: 1118

5 ValArgIleGlnAspAlaTyrGluProIleAla.....AsnThrAs 18
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
705 GTTACGACTCGTGATGCACTAAATATGATTGCTAAATTCGTCACAAACCAA 656

18 nThrThrThrGlnPheLeuAsnMetGly.....AsnGluValAlaLeuA 33
||||| ||| ||| ||| ||| ||| ||| ||| ||| :|||
655 CCAACACAGCGCTGTTAGTCATGGTTATTAAACCTGTTGAATCA 606

33 sPGLyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyMetAsp 49
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
605 TTGGT...TATGATAATTTTGTAAATTTGCTGCTGATGCTGCGGTGAT 559

50 ArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgGl 66
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
558 GCAATTTTGATG.....GTGGAT.....541

66 uPheAsnSerLeuProAsnAlaSerSerAspThrAlaSerLeuA 83
||||| ||| :||| :||| :||| :||| :||| :||| :||| :|||
540 .....TTACGCCCAACAGACAGATGCTATGCAAAATCACTGA 501

83 snLyGlnHisAspAlaAspPheLysTyrIle.....94
:||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
500 CCGAGGTACCGATCATCCATGAATCAAAATTTTTCGTGCGCAACACC 451

95 .....LysLeuLeuIleAsnAsnAspGlyPhe 103
:||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
450 ACAAATCATAGTCGCGGTACCAAGGTTATCGAAACACTGTAGTGGGTTT 403

seq_name: /cgn2_6/ptodata/2/pna/US6008_COMB.seq:US-60-082-116-250
seq_documentation_block:
Sequence 250, Application US/60082116
GENERAL INFORMATION:
APPLICANT: LAGACE, ROBERT E.
APPLICANT: CORLEY, NEIL C.
APPLICANT: RUSSO, FRANK D.
APPLICANT: HANN, AMY L.
APPLICANT: HEATH, JOE D.
APPLICANT: FINNEY, GREGORY L.
APPLICANT: BROOKS, JACQUELINE
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 385
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/082.116
FILING DATE: HERewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0008-3 P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 250:
SEQUENCE CHARACTERISTICS:
LENGTH: 8860 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: genomic DNA
IMMEDIATE SOURCE:
CLONE: MCAlc250
US-60-082-116-250

alignment_scores:
Quality: 78.00 Length: 116
Ratio: 1.300 Gaps: 6
Percent Similarity: 51.724 Percent Identity: 29.310

alignment_block:
US-09-528-682-4 x US-60-082-116-250 ..
Align seg 1/1 to: US-60-082-116-250 from: 1 to: 8860

5 ValArgIleGlnAspAlaTyrGluProIleAla.....AsnThrAs 18
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
8032 GTTACGACTCGTGATGCACTAAATATGATTGCTAAATTCGTCACAAACCAA 8081

18 nThrThrThrGlnPheLeuAsnMetGly.....AsnGluValAlaLeuA 33
||||| ||| ||| ||| ||| ||| ||| ||| ||| :|||
8082 CCAACACAGCGCTGTTAGTCATGGTTATTAAACCTGTTGAATCA 8131

33 sPGLyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyMetAsp 49
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
8132 TTGGT...TATGATAATTTTGTAAATTTGCTGCTGATGCTGCGGTGAT 8178

50 ArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgGl 66
```


[illegible]

; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9496
; LENGTH: 2619
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2619)
US-09-815-242-9496

alignment_scores:
Quality: 77.00 Length: 94
Ratio: 1.481 Gaps: 5
Percent Similarity: 55.319 Percent Identity: 29.787

alignment_block:
US-09-528-682-4 x US-09-815-242-9496/rev ..

Align seg 1/1 to reverse of: US-09-815-242-9496 from: 1 to: 2619

14 IleAlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluVa 30
2028 GTTGCCCAACATGAGTACCACCAAGATTC.....AATAGAGT 1991

30 lAlaLeuAspGlyArgTyrSerAsnTyr...AlaLeuIleSerAlaGluG 46
1990 AGTCACCGATAGTCAGCAGACAGAACTTCCTGCCGTATTTCTCACCAAG 1941

46 lyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePro 62
1940 AGGCCATAGCTCCCATTTCTTTAGCAGTGTCAATATC..... 1903

63 GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
1902CGTTTCAAC..... 1894

79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96
1893TGCTTAACITCAAGAGCTTCCAGATTTT.....TTCGTTGACT 1854

96 euLeuIleAsnAsnAspGlyPhePheSerAsn 106
1853 TGCTGTTCATCGCAGCAATTTCTTCAGCAGT 1822

seq_name: /cgn2_6/ptodata/2/pna/US100_COMB.seq:US-10-072-851-9496

seq_documentation_block:
; Sequence 9496, Application US/10072851
; GENERAL INFORMATION:
; APPLICANT: Carr, Grant J.
; APPLICANT: Xu, H. Howard
; APPLICANT: Foulkes, J. Gordon
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Roemer, Terry

; APPLICANT: Jiang, Bo
; APPLICANT: Boosey, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: ELITRA.028A
; CURRENT APPLICATION NUMBER: US/10/072,851
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9496
; LENGTH: 2619
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2619)
US-10-072-851-9496

alignment_scores:
Quality: 77.00 Length: 94
Ratio: 1.481 Gaps: 5
Percent Similarity: 55.319 Percent Identity: 29.787

alignment_block:

US-09-528-682-4 x US-10-072-851-9496/rev ..

Align seg 1/1 to reverse of: US-10-072-851-9496 from: 1 to: 2619

14 IleAlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluVa 30
2028 GTTGCCCAACATGAGTACCACCAAGATTC.....AATAGAGT 1991

30 lAlaLeuAspGlyArgTyrSerAsnTyr...AlaLeuIleSerAlaGluG 46
1990 AGTCACCGATAGTCAGCAGACAGAACTTCCTGCCGTATTTCTCACCAAG 1941

46 lyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePro 62
1940 AGGCCATAGCTCCCATTTCTTTAGCAGTGTCAATATC..... 1903

63 GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
1902CGTTTCAAC..... 1894

79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96
1893TGCTTAACITCAAGAGCTTCCAGATTTT.....TTCGTTGACT 1854

96 euLeuIleAsnAsnAspGlyPhePheSerAsn 106
1853 TGCTGTTCATCGCAGCAATTTCTTCAGCAGT 1822

seq_name: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:US-60-068-175-457

seq_documentation_block:
; Sequence 457, Application US/60068175
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert E.
; APPLICANT: Corley, Neil C.
; APPLICANT: Russo, Frank D.
; APPLICANT: Hann, Amy L.
; APPLICANT: Heath, Joe D.
; APPLICANT: Finney, Gregory L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
; TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
; NUMBER OF SEQUENCES: 1175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE


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; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/068,175
; FILING DATE: HERewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PM-0009-2 P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-416
; INFORMATION FOR SEQ ID NO: 457:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4720 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: genomic DNA
; IMMEDIATE SOURCE:
; CLONE: SPN2c459
; US-60-068-175-457

alignment_scores:
  Quality: 77.00 Length: 94
  Ratio: 1.481 Gaps: 5
  Percent Similarity: 55.319 Percent Identity: 29.787

alignment_block:
US-09-528-682-4 x US-60-068-175-457 ..
Align seg 1/1 to: US-60-068-175-457 from: 1 to: 4720
14 lIeAlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluVa 30
   ::::: ::::: ::::: ::::: :::::
2169 GTTCCACACATGATGACGACCAACCAAGTTC.....AATAGACT 2206
30 lAlaLeuaspGlyArgTySerAsnTyr...AlaLeuIleSerAlaGluG 46
   ::::: ::::: ::::: ::::: :::::
2207 AGTCACCGATAGTCACGACACGACGAACTTCCTGCCGTATTTTCACCAAG 2256
46 lYgLYmetAspArgAspLeuPheGlySerAlaAsnIleaspGlyPhePro 62
   ::::: ::::: ::::: ::::: :::::
2257 AGGGCATAGCTCCCATCTCTTTAGCAGTGCAATATC..... 2294
63 GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
   ::::: :::::
2295 .....CGTTTCAAC..... 2303
79 rAlaSerLeuAsnLysGlnHisAspAlaaspPheLysTyrIleLysL 96
   ::::: :::::
2304 ...TGCTTAATCAAGAGAGCTTCCAGATTTT.....TTCGTTGACT 2343
96 euleuIleAsnAsnAspGlyPhePheSerAsn 106
   ::::: :::::
2344 TGCTGTTCAATCGCAGCGCAATCTTCAGCAGT 2375

seq_name: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:US-09-620-392-23849

seq_documentation_block:
; Sequence 23849, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalic, David K.
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; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 23849
; LENGTH: 17891
; TYPE: DNA
; ORGANISM: Oryza sativa
; US-09-620-392-23849

alignment_scores:
  Quality: 77.00 Length: 111
  Ratio: 1.481 Gaps: 5
  Percent Similarity: 46.847 Percent Identity: 28.829

alignment_block:
US-09-528-682-4 x US-09-620-392-23849/rev ..
Align seg 1/1 to reverse of: US-09-620-392-23849 from: 1 to: 17891
46 GlyGlyMetAspArgAspLeuPheGlySerAlaAsnIleaspGlyPhePr 62
   ::::: ::::: ::::: ::::: :::::
5124 GGTTCCTACCTAGGAATCTTGCTGGTGACAAGGTACACCGTGCCTCC 5075
62 oGluValArgGluPhe...AsnSerLeuProAsnAsnLysAlaSerSera 78
   ::::: ::::: ::::: ::::: :::::
5074 AGAGGTTGTAGAGTTCTATCAAAAGTCTCATGAAGCGTGAAGCAAGAAG 5025
78 spThAlaSerLeu.AsnLysGlnHis..... 86
   ::::: ::::: ::::: ::::: :::::
5024 ACACAACTTCTCTGGGATCAACAACATCAAGTCTCTCTGATGAGAGAAGC 4975
86 ..... 86
4974 AACATGATTGGAGAGATTGAGAAATAGATCAACATTCCTCTTAGCTGAAG 4925
87 .....AspAlaAspPheLysLysTyrIle..... 94
   ::::: ::::: ::::: :::::
4924 TTATTCAAGATGATGCTACCTTTTCAGAAATATATACTACTGAATTCCTTT 4875
95 ...LysLeuIleAsnAsnasp..... 101
   ::::: ::::: ::::: :::::
4874 AGTCCACTGCTAATTCAGGTAGATTATTATGAGGACTTACTTTTATATA 4825
102 .....GlyPhePheSerAsnAsnGlyGly 109
   ::::: ::::: ::::: :::::
4824 AAAAAATGGATTGTGTTTCAGGTCAAGTGGA 4794

seq_name: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:US-09-702-134-8854

seq_documentation_block:
; Sequence 8854, Application US/09702134
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Plant Genome Sequence and Uses thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 8854
; LENGTH: 17891
; TYPE: DNA
; ORGANISM: Oryza sativa
; US-09-702-134-8854
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alignment_scores:
  Quality: 77.00      Length: 111
  Ratio: 1.481       Gaps: 5
  Percent Similarity: 46.847   Percent Identity: 28.829

alignment_block:
US-09-528-682-4 x US-09-702-134-8854/rev ..
Align seg 1/1 to reverse of: US-09-702-134-8854 from: 1 to: 17891

46 GlyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePr 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5124 GGTTCCTACTAGGAATCTTCTGGTGGTGACAAAGGTACACCGTCTCC 5075

62 oGluValAlaGluPhe...AsnSerLeuProAsnAsnLysAlaSerSera 78
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5074 AGAGGTTGTAGAGTCTATCAAAAGTCTCATGAAGCGTGAAGCAAGAGG 5025

78 spThrAlaSerLeu.AsnLysGlnHis..... 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5024 ACACAACCTTCTGGGATCAACAACATCAAGTCTCTGATGTGAGAAGC 4975

86 ..... 86
4974 AACATGATTGGAGATTGAGATAGATCAACATTCCTCTTAGCTGTAA 4925

87 .....AspAlaAspPheLysLysTyrIle..... 94
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4924 TTATTCAGATGATGCTACCTTTTCAGAAATATATACTACTGAATTCCTTT 4875

95 ...LysLeuLeuIleAsnAsnAsp..... 101
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4874 AGTCCACTGCTAATTCAGGTAGATATTATGAGGAGCTTACTTTTATATA 4825

102 .....GlyPhePheSerAsnAsnGlyGly 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4824 AAAAAATGGATTGTTTCAGGTCAAAGTGA 4794

seq_name: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:US-09-815-264-81462

seq_documentation_block:
; Sequence 81462, Application US/09815264
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Koshi, Jeffrey M.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51237)G
; CURRENT APPLICATION NUMBER: US/09/815,264
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/702,134
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 109669
; SEQ ID NO 81462
; LENGTH: 17891
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-815-264-81462

alignment_scores:
  Quality: 77.00      Length: 111
  Ratio: 1.481       Gaps: 5
  Percent Similarity: 46.847   Percent Identity: 28.829
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alignment_block:
US-09-528-682-4 x US-09-815-264-81462/rev ..
Align seg 1/1 to reverse of: US-09-815-264-81462 from: 1 to: 17891

46 GlyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePr 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5124 GGTTCCTACTAGGAATCTTCTGGTGGTGACAAAGGTACACCGTCTCC 5075

62 oGluValAlaGluPhe...AsnSerLeuProAsnAsnLysAlaSerSera 78
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5074 AGAGGTTGTAGAGTCTATCAAAAGTCTCATGAAGCGTGAAGCAAGAGG 5025

78 spThrAlaSerLeu.AsnLysGlnHis..... 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5024 ACACAACCTTCTGGGATCAACAACATCAAGTCTCTGATGTGAGAAGC 4975

86 ..... 86
4974 AACATGATTGGAGATTGAGATAGATCAACATTCCTCTTAGCTGTAA 4925

87 .....AspAlaAspPheLysLysTyrIle..... 94
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4924 TTATTCAGATGATGCTACCTTTTCAGAAATATATACTACTGAATTCCTTT 4875

95 ...LysLeuLeuIleAsnAsnAsp..... 101
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4874 AGTCCACTGCTAATTCAGGTAGATATTATGAGGAGCTTACTTTTATATA 4825

102 .....GlyPhePheSerAsnAsnGlyGly 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4824 AAAAAATGGATTGTTTCAGGTCAAAGTGA 4794

seq_name: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US97-06635-1

seq_documentation_block:
; Sequence 1, Application PC/TUS9706635
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: Novel Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/06635
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9607991.8
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31458-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2619 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
PCT-US97-06635A-1

alignment_scores:
  Quality: 76.00      Length: 94
  Ratio: 1.490       Gaps: 5
  Percent Similarity: 54.255      Percent Identity: 30.851

alignment_block:
US-09-528-682-4 x PCT-US97-06635A-1/rev ..

Align seg 1/1 to reverse of: PCT-US97-06635A-1 from: 1 to: 2619
14 IleAlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluVa 30
  :::::::::: ::::::::::::::::::::|
2028 GTTCCCAACATGATGATCACCACCAAAAGTTC.....AATAGAGT 1991
30 lAlaLeuAspGlyArgTyrSerAsn...TyrAlaLeuIleSerAlaGluG 46
  :::::::::: ::::::::::|
1990 AGTCACCGATAGTCACGACACGAACTGCCGTTCCTGATTTCTCACCAGAG 1941
46 lYglyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePro 62
  ||| ::| ::::::::::::::::::::|
1940 AGGCGATAGTCCCATTTCTTTAGCAGTGTCATATC.....1903
63 GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
  ::::::::::|
1902 .....CGTTTCAAC.....1894
79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96
  ::::::::::|
1893 ....TGTCTTAACCTCAAGAGCTTCCAGATTTT.....TTCGTTGACT 1854
96 euLeuIleAsnAsnAspGlyPhePheSerAsn 106
  ::::::::::|
1853 TGCTGTTCATCGCACGCAATTTCTTCAGCAGT 1822

seq_name: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US97-06635A-1

seq_documentation_block:
; Sequence 1, Application PC/TUS9706635A
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: Novel Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/06635A
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9607991.8
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31458-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478

; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2619 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
PCT-US97-06635A-1

alignment_scores:
  Quality: 76.00      Length: 94
  Ratio: 1.490       Gaps: 5
  Percent Similarity: 54.255      Percent Identity: 30.851

alignment_block:
US-09-528-682-4 x PCT-US97-06635A-1/rev ..

Align seg 1/1 to reverse of: PCT-US97-06635A-1 from: 1 to: 2619
14 IleAlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluVa 30
  :::::::::: ::::::::::::::::::::|
2028 GTTCCCAACATGATGATCACCACCAAAAGTTC.....AATAGAGT 1991
30 lAlaLeuAspGlyArgTyrSerAsn...TyrAlaLeuIleSerAlaGluG 46
  :::::::::: ::::::::::|
1990 AGTCACCGATAGTCACGACACGAACTGCCGTTCCTGATTTCTCACCAGAG 1941
46 lYglyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePro 62
  ||| ::| ::::::::::::::::::::|
1940 AGGCGATAGTCCCATTTCTTTAGCAGTGTCATATC.....1903
63 GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
  ::::::::::|
1902 .....CGTTTCAAC.....1894
79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96
  ::::::::::|
1893 ....TGTCTTAACCTCAAGAGCTTCCAGATTTT.....TTCGTTGACT 1854
96 euLeuIleAsnAsnAspGlyPhePheSerAsn 106
  ::::::::::|
1853 TGCTGTTCATCGCACGCAATTTCTTCAGCAGT 1822

seq_name: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:PCT-US97-06635A-1

seq_documentation_block:
; Sequence 1, Application US/09006730
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: Novel Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,730
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,057
; FILING DATE: 18-APR-1997
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; APPLICATION NUMBER: 9607991.8
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31458-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2619 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-006-730-1

alignment_scores:
  Quality: 76.00      Length: 94
  Ratio: 1.490       Gaps: 5
  Percent Similarity: 54.255      Percent Identity: 30.851

alignment_block:
US-09-528-682-4 x US-09-006-730-1/rev ..
Align seg 1/1 to reverse of: US-09-006-730-1 from: 1 to: 2619

14 IleAlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluVa 30
   :||||| :||||| :||||| :||||| :||||| :||||| :|||||
2028 GTTGCCAAATGAGTACCAACCAAGTTC.....AATAGAT 1991

30 lAlaLeuAspGlyArgTyrSerAsn...TyrAlaLeuSerAlaGluG 46
   :||: :||: :||: :||: :||: :||: :||: :||:
1990 AGTCACCGATAGTCACGACACGAAGTCCCTGCGGTATTTCTCACCGAAG 1941

46 lYgLYMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePro 62
   ||| :||: :||: :||: :||: :||: :||: :||:
1940 AGGCGGATAGTCCCATTTCTTACGAGTGTCAATATC.....1903

63 GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
   :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1902 .....CGTTTCAAC.....1894

79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96
   :||||| :||: :||: :||: :||: :||: :||: :||:
1893 ....TGCTTTAACTTCAAGAGCTTCCAGATTTT.....FTCGTTGACT 1854

96 euLeuIleAsnAsnAspGlyPhePheSerAsn 106
   :||||| :||: :||: :||: :||: :||: :||: :||:
1853 TGCTGTTCAATCGCAGCAATCTTCAGCAGT 1822

seq_name: /cgn2_6/ptodata/2/pna/US6036_COMB.seq:US-60-360-207-18907

seq_documentation_block:
; Sequence 18907, Application US/60360207
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/60/360,207
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 18907
; LENGTH: 6413
; TYPE: DNA
; ORGANISM: HUMAN
US-60-360-207-18907

alignment_scores:
  Quality: 76.00      Length: 106
  Ratio: 1.169       Gaps: 4
  Percent Similarity: 61.321      Percent Identity: 25.472

alignment_block:
US-09-528-682-4 x US-60-360-207-18907 ..
Align seg 1/1 to: US-60-360-207-18907 from: 1 to: 6413

1 AspTyrPheThrValArgIleGlnAspAlaTyrGluProIleAlaAsnTh 17
   :||||| :||: :||: :||: :||: :||: :||: :||:
2058 GATTATGCAATGAGGACTCATATGAGATTTATGAACCTCTCGCACCTAC 2107

17 rAsnThrThrThrGlnPheLeu.....AsnMetGlyAsnGluValAlaL 32
   :||: :||: :||: :||: :||: :||: :||: :||:
2108 ATCCATGACAACCTCGGAGAATTCATGATTCCTTACAAAATGAATTTGGCA 2157

32 euAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyMet 48
   :||||| :||: :||: :||: :||: :||: :||: :||:
2158 TAGACACGAAGATGATGATTACCACTACTTACTGGCGTCATCATTAGGA 2207

49 AspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValAr 65
   :||||| :||: :||: :||: :||: :||: :||: :||:
2208 ATTAGGTCA...TTCAAAACTCATCATTTGAAT.....CCAGAGGAAAA 2248

65 gGluPheAsnSerLeuPro.....AsnAsnLysAlaSerSerAspTh 79
   :||||| :||: :||: :||: :||: :||: :||: :||:
2249 TGAGTTCAATCTCACTGCTCTCGCTCTCGGAGAACAGCTCTGAGTTTCATAT 2298

79 hrAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLys 95
   :||: :||: :||: :||: :||: :||: :||: :||:
2299 CTCCAAGCACAGACAGAGTTGTGTGACTCAAACCTCTTCACGAATCCTTAGT 2348

96 LeuLeuIleAsnAsnAsp 101
   :||||| :||: :||: :||: :||: :||: :||: :||:
2349 AAAATCATCAATAATAAC 2366

seq_name: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:US-09-847-513A-1

seq_documentation_block:
; Sequence 1, Application US/09847513A
; GENERAL INFORMATION:
; APPLICANT: MBARI
; APPLICANT: DeLong, Edward
; APPLICANT: Beja, Oged
; TITLE OF INVENTION: Light-driven energy generation using proteorhodopsin
; FILE REFERENCE: MBA-101
; CURRENT APPLICATION NUMBER: US/09/847,513A
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 60/201,602
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 105184
; TYPE: DNA
; ORGANISM: Naturally occurring gamma proteobacterium
; FEATURE:
; NAME/KEY: gene
; LOCATION: (50866)..(51615)
; OTHER INFORMATION: Proteorhodopsin gene sequence.
; NAME/KEY: misc.feature
; LOCATION: (1593)..(2807)
; OTHER INFORMATION: Predicted threonine dehydratase. Contains 'n' at position 275
; AUTHORS: Beja, O., Aravind, L., Koonin, E.V., Suzuki, M.T., Hadd, A., Nguyen, L.P.,
; AUTHORS: Jovanovich, S.B., Gates, C.M., Feldman, R.A., DeLong, E.F.
; TITLE: Bacterial rhodopsin: evidence for a new type of phototrophy in the sea
; JOURNAL: Science
; VOLUME: 289
; ISSUE: 5486
; PAGES: 1902-1906
; DATE: 2000-09-15
```


;
; DATABASE ACCESSION NUMBER: AF279106
; DATABASE ENTRY DATE: 2000-06-15
; RELVANT RESIDUES: (50866)..(51615)
US-09-847-513A-1

alignment_scores:
Quality: 76.00 Length: 74
Ratio: 1.727 Gaps: 3
Percent Similarity: 59.459 Percent Identity: 33.784

alignment_block:

US-09-528-682-4 x US-09-847-513A-1 ..

Align seg 1/1 to: US-09-847-513A-1 from: 1 to: 105184

26 MetGlyAsnGluValAlaLeuAspGlyArgTyr.....SerAsnTy 39

|||||: : : : : |||||
58167 ATGGGTGATCCTATTACA.....GGAAGGTATCTGCAGATTCTGGAGT 58210

39 rAlaLeuIleSerAlaGluGlyMetAspArgAspLeuPheGlySera 56

|||||: : : : : |||||
58211 AAAGTTCATTCTTCATGATGGGAATGATGAAGATAAATTCATGATTA 58260

56 laAsnIleAspGlyPheProGluValArgGluPheAsnSerLeuProAsn 72

|||||: : : : : |||||
58261 TGAATACCTGCTGATATGCTATATTTACAGATTAAATAATGTTTCT 58310

73 AsnAlaSerSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAs 89

|||||: : : : : |||||
58311 AATAAG...AATACAGAAAGCATTTATGAAATCCCTCATGAAGCAGA 58357

89 pPheLysLysTyrIleLysLeu 96

|||: ||| |||||: : : : : |||||

58358 CCTTCTTAAAGCCATTAAAGTA 58379

seq_name: /cgn2_6/ptodata/2/pna/US091_COMB.seq:US-09-134-000-1761

seq_documentation_block:

; Sequence 1761, Application US/09134000A

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS

; FILE REFERENCE: GTC-005

; CURRENT APPLICATION NUMBER: US/09/134,000A

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 6810

; SEQ ID NO 1761

; LENGTH: 2061

; TYPE: DNA

; ORGANISM: Enterococcus faecalis

US-09-134-000-1761

alignment_scores:
Quality: 75.50 Length: 102
Ratio: 1.280 Gaps: 2
Percent Similarity: 57.843 Percent Identity: 21.569

alignment_block:

US-09-528-682-4 x US-09-134-000-1761 ..

Align seg 1/1 to: US-09-134-000-1761 from: 1 to: 2061

18 AsnThrThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspG1 34

|||||: |||||: |||||: |||||: |||||
478 AGTACATTTACTTCAAGTCTCAATTTAGGACACAGAGGATCTAAAGTGG 527

34 yArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyGlyMetAspArga 51

|||||: |||||: |||||: |||||: |||||
528 AGAAGTATATCAAAAGTCCCAATTTTGTGATGCAACAGTAAACAAACATTTA 577

51 sPLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgGluPhe 67

|||||: |||||: |||||: |||||: |||||
578 ATTTTGTGAATAGTGTCTCTAGATGG..... 606

68 AsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLy 84

|||||: |||||: |||||: |||||: |||||
607 ...AAAATGAGAATGTAAGAAATAGATGAAAGTAAACTACTAGAAAA 653

84 s.....GlnHisAspAlaAspPheLysL 92

|||||: |||||: |||||: |||||: |||||
654 GCCTAAATGCTTAAGGAAGAGAAATAATTTGAAAAAATAGAAAAA 703

92 yTyrIleLysLeuLeuIleAsnAsnAspGlyPhePheSerAsnAsnGly 108

|||||: |||||: |||||: |||||: |||||
704 AATATATAGATAAGGTAGTTGATGATAATCCATCTCGCACAGGACGGA 753

109 GlyLys 110

|||||

754 GCAAAA 759

seq_name: /cgn2_6/ptodata/2/pna/US096A_COMB.seq:US-09-614-221A-288

seq_documentation_block:

; Sequence 288, Application US/09614221A

; GENERAL INFORMATION:

; APPLICANT: Yu, Jaehyuk

; APPLICANT: Kishore, Ganesh M.

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED

; FILE REFERENCE: 16516.075

; CURRENT APPLICATION NUMBER: US/09/614,221A

; CURRENT FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/142,981

; NUMBER OF SEQ ID NOS: 626

; SEQ ID NO 288

; LENGTH: 2748

; TYPE: DNA

; ORGANISM: Saccharomyces cerevisiae

US-09-614-221A-288

alignment_scores:
Quality: 74.50 Length: 95
Ratio: 1.330 Gaps: 2
Percent Similarity: 58.947 Percent Identity: 26.316

alignment_block:

US-09-528-682-4 x US-09-614-221A-288 ..

Align seg 1/1 to: US-09-614-221A-288 from: 1 to: 2748

13 ProIleAlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnG1 29

|||||: |||||: |||||: |||||: |||||
2275 CCGAGTCAGAACGTTAATTCACACACTCTATTTTGCAGTCTTTAAAC... 2322

29 uValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluG 46

|||||: |||||: |||||: |||||: |||||
2323 .ATCAGTCTTGTATGGGAGAAAAAATCGTGCCAGTCTACACGCAACAT 2371

46 lyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePro 62

|||||: |||||: |||||: |||||: |||||
2372 CAGTGTTCCTCTAGTACAAATAGACAGAACAAAT..... 2403

63 GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79

|||||: |||||: |||||: |||||: |||||
2404CAGCATTTCAATGACATAAACAGATGCTAGCAGTACTAGCGA 2447

79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96

|||||: |||||: |||||: |||||: |||||
2448 AGATGCCTTTCCCAAGCAATCATTAATTTTCAATAAGAAACTACCAA 2497


```

96 euLeuIleAsnAsnAspGlyPhePheSerAsnAsn 107
:||||| |||||: : : : : : : : : :
2498 TACTTAAATTAATGATAACGTCATACAATCAAAAC 2532
seq_name: /cgn2_6/ptodata/2/pna/US090_COMB.seq:US-09-012-031-312

seq_documentation_block:
; Sequence 312, Application US/09012031A
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; FILE REFERENCE: 1107.73251
; CURRENT APPLICATION NUMBER: US/09/012,031A
; EARLIER FILING DATE: 1998-01-22
; EARLIER FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 317
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 666448
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-012-031-312

alignment_scores:
Quality: 74.50 Length: 95
Ratio: 1.330 Gaps: 2
Percent Similarity: 58.947 Percent Identity: 26.316

alignment_block:
US-09-528-682-4 x US-09-012-031B-312 ..
Align seg 1/1 to: US-09-012-031B-312 from: 1 to: 666448
13 ProIleAlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnG1 29
||| |||||: |||||: ||| :|||: |||
481149 CCGAGTGAGACGTTAATTACACACTCTCTATTTGCGAGTCTTAAAC... 481196
29 uValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluG 46
:||||| |||||: |||||: ||| :|||: |||
481197 .ATGAGCTTGTATGGGAGAAAAAATCGCCAGCTACACGCAACAT 481245
46 lyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePro 62
: ||| : ||| : ||| : ||| : ||| : |||
481246 CAGTGTACCTAGTACATAAGACAGACAACAT..... 481277
63 GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
:||||| |||||: |||||: ||| :|||: |||||
481278 .....CAGCATTTCAATGACATAACACAGATGCTAGGAGTAGTGACGA 481321
79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96
:||||| |||||: |||||: ||| :|||: |||||
481322 AGATGCCCTTCCCAAGCAATCATTAATTTCAATAAGAAACTACCAA 481371
96 euLeuIleAsnAsnAspGlyPhePheSerAsnAsn 107
:||||| |||||: |||||: ||| :|||: |||||
481372 TACTTAAATTAATGATAACGTCATACAATCAAAAC 481406
seq_name: /cgn2_6/ptodata/2/pna/US090_COMB.seq:US-09-012-031C-312

seq_documentation_block:
; Sequence 312, Application US/09012031C
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; FILE REFERENCE: 1107.73251
; CURRENT APPLICATION NUMBER: US/09/012,031C
; EARLIER FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/035,917
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 666448
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-012-031C-312

alignment_scores:
Quality: 74.50 Length: 95
Ratio: 1.330 Gaps: 2
Percent Similarity: 58.947 Percent Identity: 26.316

alignment_block:
US-09-528-682-4 x US-09-012-031-312 ..
Align seg 1/1 to: US-09-012-031-312 from: 1 to: 666448
13 ProIleAlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnG1 29
||| |||||: |||||: ||| :|||: |||
481149 CCGAGTGAGACGTTAATTACACACTCTCTATTTGCGAGTCTTAAAC... 481196
29 uValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluG 46
:||||| |||||: |||||: ||| :|||: |||
481197 .ATGAGCTTGTATGGGAGAAAAAATCGCCAGCTACACGCAACAT 481245
46 lyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePro 62
: ||| : ||| : ||| : ||| : ||| : |||
481246 CAGTGTACCTAGTACATAAGACAGACAACAT..... 481277
63 GluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspTh 79
:||||| |||||: |||||: ||| :|||: |||||
481278 .....CAGCATTTCAATGACATAACACAGATGCTAGGAGTAGTGACGA 481321
79 rAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysL 96
:||||| |||||: |||||: ||| :|||: |||||
481322 AGATGCCCTTCCCAAGCAATCATTAATTTCAATAAGAAACTACCAA 481371
96 euLeuIleAsnAspGlyPhePheSerAsnAsn 107
:||||| |||||: |||||: ||| :|||: |||||
481372 TACTTAAATTAATGATAACGTCATACAATCAAAAC 481406
seq_name: /cgn2_6/ptodata/2/pna/US090_COMB.seq:US-09-012-031B-312

seq_documentation_block:
; Sequence 312, Application US/09012031B
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Characterization of the Yeast
; FILE REFERENCE: 1107.73251

```



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seq_name: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:US-09-702-134-19444

seq_documentation_block:
; Sequence 19447, Application US/09702134
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Plant Genome Sequence and Uses Thereof
; FILE REFERENCE: 38-21(51237)F
; CURRENT APPLICATION NUMBER: US/09/702,134
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 52202
; SEQ ID NO 19447
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-702-134-19447

alignment_scores:
Quality: 74.00 Length: 79
Ratio: 1.542 Gaps: 5
Percent Similarity: 60.759 Percent Identity: 34.177

alignment_block:
US-09-528-682-4 x US-09-702-134-19447 ..

Align seg 1/1 to: US-09-702-134-19447 from: 1 to: 684

10 AlaTyrGluProile...AlaAsnThrAsnThrThrGlnPheLeuAs 25
||||| ||||| : : : : : : : : : : : : : : : : : :
166 GCTTTGCACCTATAGACTCAGAGTCAGATCAGTAGCAAAATTCTCGC 215

25 nMetGlyAsnGluValAlaLeu.....AspGlyArgTyrSerAsnTyr 40
||||| : : : : : ||| ||||| |||
216 CATGTATCTCCCTGCTGCTCTCTCAGCCATGCGACCTACAGC...TACA 262

40 laLeuIleSerAlaGluGlyGlyMetAspArgAspLeuPheGlySerAla 56
: : : : : ||||| ||||| : : : : : : : : : : : : : : : :
263 GRGCCACCACAGCTTCAGCTGGGAACCAAGACTCTTCAGGCATGTC 312

57 AsnIle.....AspGlyPheProGluValArgGluPheAsnSe 69
::: ||||| ||||| : : : : :
313 CCAGTGTCCTCCGGTCGACGCGCGTGACGACGATCCGG..... 351

69 rLeuProAsnAsnLysAlaSerSerAspThrAlaSer 81
: : : : : : : : : : : : : : : : : :
352 .TTCCCTCACGGCTGCAATCCAGCAACACATCATCA 387

seq_name: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:US-09-815-264-73323

seq_documentation_block:
; Sequence 73323, Application US/09815264
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Cao, Yongwei
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Koshi, Jeffrey M.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Genomic Plant Sequences And Uses Thereof
; FILE REFERENCE: 38-21(51237)G
; CURRENT APPLICATION NUMBER: US/09/815,264
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
```

```
; PRIOR APPLICATION NUMBER: US 09/702,134
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 109669
; SEQ ID NO 73323
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-815-264-73323

alignment_scores:
    Quality:      74.00      Length:      79
    Ratio:        1.542     Gaps:       5
Percent Similarity: 60.759   Percent Identity: 34.177

alignment_block:
US-09-528-682-4 x US-09-815-264-73323 ..

Align seg 1/1 to: US-09-815-264-73323 from: 1 to: 684

10 AlatyrGluProIle...AlaAsnThrAsnThrThrThrGlnPheLeuAs 25
||||| ||||| : : : : : : : : : : : : : : : : : :
166 GCTTTTGCACCTATAGACTCAGAGATCAGGATGAGTAGCAAAATTCTCGC 215
||||| : : : : : : : : : : : : : : : : : :

25 nMetGlyAsnGluValAlaLeu.....AspGlyArgTyrSerAsnTyrA 40
||||| : : : : : : : : : : : : : : : : : :
216 CATGTATCTCCGCTTGCTCTCCTCAGCCATGGCACCTACAGC...TACA 262
||||| : : : : : : : : : : : : : : : : : :

40 laLeuIleSerAlaGluGlyGlyMetAspArgAspLeuPheGlySerAla 56
:: : : : : : : : : : : : : : : : : : : : : :
263 GTGCCACCACAGCTTCAGGCTGGGAAGAACCAAGACTTCTTCAGGCATTGC 312
||||| : : : : : : : : : : : : : : : : : :

57 AsnIle.....AspGlyPheProGluValArgGluPheAsnSe 69
:: : : : : : : : : : : : : : : : : : : : : :
313 CCAGTGTCCCGTCGAGCGAGCGGTGGACCAGAGATCCGG..... 351

69 rLeuProAsnAsnLysAlaSerSerAspThrAlaSer 81
:: : : : : : : : : : : : : : : : : : : : : :
352 .TTCCCTCAGGCGCTGCAATCCAGCAACACATCATCA 387

seq_name: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:US-09-739-449-4641

seq_documentation_block:
; Sequence 4641, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 4641
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-4641

alignment_scores:
    Quality:      74.00      Length:      108
    Ratio:        1.138     Gaps:       5
Percent Similarity: 60.185   Percent Identity: 25.000

alignment_block:
US-09-528-682-4 x US-09-739-449-4641 ..

Align seg 1/1 to: US-09-739-449-4641 from: 1 to: 1071

5 ValArgIleGln...AspAlaTyrGluProIleAlaAsnThrAsnThrTh 20
||||| : : : : : : : : : : : : : : : : : :

```



```

493 GTCCGCTCGAGCTCGATCAATATAAGCGCATCCCAACACCGATTCGCT 542
20 rThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgTyr 37
|||||: : : : : : : : : : : : : : : : : : : : : : : : : :
543 GACGCGC.....CTCTCCAAACCGCGCGCTTTCGACGACCGCTGG 583
37 erAsnTyrAlaLeuIleSerAlaGluGlyMetAspArgLeuPhe 53
: : : : : : : : : : : : : : : : : : : : : : : : : :
584 CC.....TCCGTTTATGACAGCTCCATCGCCTGCAATATACACGCTC 627
54 GlySerAlaAsnIleAspGlyPheProGluValArgGlu....PheAsnSe 69
: : : : : : : : : : : : : : : : : : : : : : : : : :
628 GTCTTCTCGATATCGATCACTTCAAGCGAATCAACGATACGTTCCGCCA 677
69 rLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnH 86
: : : : : : : : : : : : : : : : : : : : : : : : : :
678 TCCGGTTCGGCGACAAAGATTCTCGCCACCGTCGCTCGCTC..... 717
86 isAspAlaAspPheLysLysTyrIleLysLeuLeuIleAsnAsnAspGly 102
|||||: : : : : : : : : : : : : : : : : : : : : : : : : :
718 TCCGGTTCGGCGACAAAGATTCTCGCCACCGTCGCTCGCTC..... 717
86 isAspAlaAspPheLysLysTyrIleLysLeuLeuIleAsnAsnAspGly 102
|||||: : : : : : : : : : : : : : : : : : : : : : : : : :
718 TCCGGTTCGGCGACAAAGATTCTCGCCACCGTCGCTCGCTC..... 717
103 PhePheSerAsnAsnGlyLys 110
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
745 TTCTGTTCCCGGAAGCGCGCGGAG 768

```

seq_name: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:US-09-803-110-4641

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seq_documentation_block:
; Sequence 4641, Application US/09803110
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)D
; CURRENT APPLICATION NUMBER: US/09/803,110
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/739,449
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: US 60/168,139
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 4641
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-803-110-4641

```

```

alignment_scores:
  Quality: 74.00      Length: 108
  Ratio: 1.138        Gaps: 5
  Percent Similarity: 60.185  Percent Identity: 25.000

```

```

alignment_block:
US-09-528-682-4 x US-09-803-110-4641
..
Align seg 1/1 to: US-09-803-110-4641 from: 1 to: 1071

```

```

5 ValArgIleGln...AspAlaTyrGluProIleAlaAsnThrAsnThrH 20
|||||: : : : : : : : : : : : : : : : : : : : : : : : : :
493 GTCCGCTCGAGCTCGATCAATATAAGCGCATCCCAACACCGATTCGCT 542
20 rThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgTyr 37
|||||: : : : : : : : : : : : : : : : : : : : : : : : : :
543 GACGCGC.....CTCTCCAAACCGCGCGCTTTCGACGACCGCTGG 583
37 erAsnTyrAlaLeuIleSerAlaGluGlyMetAspArgLeuPhe 53
: : : : : : : : : : : : : : : : : : : : : : : : : :
584 CC.....TCCGTTTATGACAGCTCCATCGCCTGCAATATACACGCTC 627

```

```

54 GlySerAlaAsnIleAspGlyPheProGluValArgGlu....PheAsnSe 69
: : : : : : : : : : : : : : : : : : : : : : : : : :
628 GTCTTCTCGATATCGATCACTTCAAGCGAATCAACGATACGTTCCGCCA 677
69 rLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnH 86
: : : : : : : : : : : : : : : : : : : : : : : : : :
678 TCCGGTTCGGCGACAAAGATTCTCGCCACCGTCGCTCGCTC..... 717
86 isAspAlaAspPheLysLysTyrIleLysLeuLeuIleAsnAsnAspGly 102
|||||: : : : : : : : : : : : : : : : : : : : : : : : : :
718 TCCGGTTCGGCGACAAAGATTCTCGCCACCGTCGCTCGCTC..... 717
103 PhePheSerAsnAsnGlyLys 110
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
745 TTCTGTTCCCGGAAGCGCGCGGAG 768

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seq_name: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:US-09-620-392-59882

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seq_documentation_block:
; Sequence 59882, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 59882
; LENGTH: 6118
; TYPE: DNA
; ORGANISM: Oryza sativa
; OTHER INFORMATION: unsure at all n locations
US-09-620-392-59882

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alignment_scores:
  Quality: 74.00      Length: 79
  Ratio: 1.542        Gaps: 5
  Percent Similarity: 60.759  Percent Identity: 34.177

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```

alignment_block:
US-09-528-682-4 x US-09-620-392-59882
..
Align seg 1/1 to: US-09-620-392-59882 from: 1 to: 6118

```

```

10 AlaTyrGluProIle...AlaAsnThrAsnThrThrThrGlnPheLeuAs 25
|||||: : : : : : : : : : : : : : : : : : : : : : : : : :
4966 GCTTTTCACCTATAGAGTCAGAGATCAGGATGAGTAGAGTAATAATTCCTCCG 5015
25 nMetGlyAsnGluValAlaLeu.....AspGlyArgTyrSerAsnTyrA 40
||| : : : : : : : : : : : : : : : : : : : : : : : : : :
5016 CATGTATCTCTGCTGCTCTCTCTCCAGCCATGGCAGCTACAGC...TACA 5062
40 laLeuIleSerAlaGluGlyGlyMetAspArgLeuPheGlySerAla 56
: : : : : : : : : : : : : : : : : : : : : : : : : :
5063 GTCCACACACAGCTTCAGGCTGGGAAGACCAAGACTTCTTCAGGCATGTC 5112
57 AsnIle.....AspGlyPheProGluValArgGluPheAsnSe 69
: : : : : : : : : : : : : : : : : : : : : : : : : :
5113 CCAGTGTCCCGGTGCAGCGAGCGTGGACGACGATCCGG..... 5151
69 rLeuProAsnAsnLysAlaSerSerAspThrAlaSer 81
|||||: : : : : : : : : : : : : : : : : : : : : : : : : :
5152 .TTCCCTCACGGCTGCAATCCAGCAACACATCATCA 5187

```

seq_name: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:US-60-168-139-2269

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seq_documentation_block:
; Sequence 2269, Application US/60168139
; GENERAL INFORMATION:

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; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(15490)A
; CURRENT APPLICATION NUMBER: US/60/168,139
; CURRENT FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 3432
; SEQ ID NO 2269
; LENGTH: 8630
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
US-60-168-139-2269

alignment_scores:
  Quality: 74.00      Length: 108
  Ratio: 1.138      Gaps: 5
  Percent Similarity: 60.185      Percent Identity: 25.000

alignment_block:
US-09-528-682-4 x US-60-168-139-2269/rev ..

Align seg 1/1 to reverse of: US-60-168-139-2269 from: 1 to: 8630

5 ValArgileGln...AspAlaTyrgluProileAlaAsnThrAsnThrTh 20
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5487 GTGGCCTCGAGTCGATGATATAGCGCATCGCCACACCGATTGCT 5438
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 rThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgTyrS 37
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5437 GACGGCGC.....CTCTCCACCGCGCGCTTCGACGACCGCTGG 5397
|||||:|||||:|||||:|||||:|||||:|||||:
37 erAsnTyAlaLeuIleSerAlaGluGlyMetAspArgAspLeuPhe 53
|||||:|||||:|||||:|||||:|||||:|||||:
5396 CC.....TCCGTTATGACAGCTCCATCGCCCTGCAATATACACGCTC 5353
|||||:|||||:|||||:|||||:|||||:
54 GlySerAlaAsnIleAspGlyPheProGluValArgGlu...PheAsnSe 69
|||||:|||||:|||||:|||||:|||||:|||||:
5352 GTCCTTCTGGATATCGATCATCTTCAAGCGAATCAACGATAGCTTCGGCCA 5303
|||||:|||||:|||||:|||||:|||||:
69 rLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnH 86
|||||:|||||:|||||:|||||:|||||:
5302 TCCGGTCGGCGACAGAATTCGCGCACCGTCGCTCCGTC..... 5263
|||||:|||||:|||||:|||||:|||||:
86 isAspAlaAspPheLysLysTyrIleLysLeuLeuIleAsnAspGly 102
|||||:|||||:|||||:|||||:|||||:
5262 .....ATCCGCGCCCAATGTCCGCAAGGATGTT 5236
|||||:|||||:|||||:|||||:
103 PhePheSerAsnAsnGlyGlyLys 110
|||:|||||:|||||:|||||:
5235 TTCGTTGCCCGAAGCGCGCGGAG 5212
|||||:|||||:|||||:|||||:

seq_name: /cgn2_6/ptodata/2/pna/US095A_COMB.seq:us-09-514-000-377

seq_documentation_block:
; Sequence 377, Application US/09514000
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)B
; CURRENT APPLICATION NUMBER: US/09/514,000
; CURRENT FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 15034
; SEQ ID NO 377
; LENGTH: 40451
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
US-09-514-000-377

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```

alignment_scores:
  Quality: 74.00      Length: 108
  Ratio: 1.138      Gaps: 5
  Percent Similarity: 60.185      Percent Identity: 25.000

alignment_block:
US-09-528-682-4 x US-09-514-000-377/rev ..

Align seg 1/1 to reverse of: US-09-514-000-377 from: 1 to: 40451

5 ValArgileGln...AspAlaTyrgluProileAlaAsnThrAsnThrTh 20
|||||:|||||:|||||:|||||:|||||:|||||:
30983 GTGGCCTCGAGTCGATGATATAGCGCATCGCCACACCGATTGCT 30934
|||||:|||||:|||||:|||||:|||||:
20 rThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgTyrS 37
|||||:|||||:|||||:|||||:|||||:
30933 GACGGCGC.....CTCTCCACCGCGCGCTTCGACGACCGCTGG 30893
|||||:|||||:|||||:|||||:
37 erAsnTyAlaLeuIleSerAlaGluGlyMetAspArgAspLeuPhe 53
|||||:|||||:|||||:|||||:
30892 CC.....TCCGTTATGACAGCTCCATCGCCCTGCAATATACACGCTC 30849
|||||:|||||:|||||:|||||:
54 GlySerAlaAsnIleAspGlyPheProGluValArgGlu...PheAsnSe 69
|||||:|||||:|||||:|||||:
30848 GTCCTTCTGGATATCGATCATCTTCAAGCGAATCAACGATAGCTTCGGCCA 30799
|||||:|||||:|||||:|||||:
69 rLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnH 86
|||||:|||||:|||||:|||||:
30798 TCCGGTCGGCGACAGAATTCGCGCACCGTCGCTCCGTC..... 30759
|||||:|||||:|||||:|||||:
86 isAspAlaAspPheLysLysTyrIleLysLeuLeuIleAsnAsnAspGly 102
|||||:|||||:|||||:|||||:
30758 .....ATCCGCGCCCAATGTCCGCAAGGATGTT 30732
|||||:|||||:|||||:|||||:
103 PhePheSerAsnAsnGlyGlyLys 110
|||:|||||:|||||:|||||:
30731 TTCGTTGCCCGAAGCGCGCGGAG 30708
|||||:|||||:|||||:|||||:

seq_name: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:us-09-620-392-22857

seq_documentation_block:
; Sequence 22857, Application US/09620392
; GENERAL INFORMATION:
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Liu, Jingdong
; APPLICANT: McIninch, James
; TITLE OF INVENTION: Plant Genome Sequence And Uses Thereof
; FILE REFERENCE: 38-21(51237)E
; CURRENT APPLICATION NUMBER: US/09/620,392
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 69652
; SEQ ID NO 22857
; LENGTH: 50625
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-620-392-22857

alignment_scores:
  Quality: 74.00      Length: 79
  Ratio: 1.542      Gaps: 5
  Percent Similarity: 60.759      Percent Identity: 34.177

alignment_block:
US-09-528-682-4 x US-09-620-392-22857 ..

Align seg 1/1 to: US-09-620-392-22857 from: 1 to: 50625

10 AlaTyrgluProile...AlaAsnThrAsnThrThrGlnPheLeuAs 25
|||||:|||||:|||||:|||||:|||||:

```


alignment_scores:		
Quality:	74.00	Length: 108
Ratio:	1.138	Gaps: 5
Percent Similarity:	60.185	Percent Identity: 25.000

3 varargilegim...asparylgduplloleatlaasimasmim in 20
|||||::: ||| ||||: |||||||||::: |
49958 GTGCGCCTCGAGCTCGATGAATAAAGCGCATGCCAACACCGATCGCT 50007

20 rThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgTyr

50008 GACGGC.....CCTCCACCGCGCGCTTCGACGACCGCGTGG 50048
 37 eAsnTyrAlaLeuIleSerAlaGluGlyMetAspArgAspLeuPhe 53
 50049 CC.....TCGGTTATGACAGCTCCATCGCGCTGCAATATACCAACGCTC 50092
 54 GlySerAlaAsnIleAspGlyPheProGluValArgGlu...PheAsnSps 69

50093 GTCCTTCGGATATCGATCACTTCAAGCGAATCAACGATACGTTTCGGCCA 50142
69 rLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnH 86
50143 TCCGTCGGCGACAAAGATTCCGACACGTCGCCTCCGTC..... 50182
86 iAspAlaAspPheIsvstsvrilleLysLeuLeuIleAsnAsnAspGlv 102

```

50193 .....ATCCGCCCAATGTGCGCAAGATGGT 50209
103 PhePheSerAsnAsnGlyGlyLys 110
111 .....
50210 TTCGTGTGCCCAAGCGCGCGGAG 50233
seq_name: /cqn2_6/ptodata/2/pna/US100.COMB.seq:US-10-085-959-35

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seq_documentation_block:
; Sequence 35, Application US/10085959
; GENERAL INFORMATION:
```

APPLICANT: BLAGOJEVIC, FREDERICK K.
APPLICANT: Welch, Rodney A.

; APPLICANT: BURLAND, Valerie D.
 ; TITLE OF INVENTION: Novel Sequence of E. Coli CFT073
 ; FILE REFERENCE: 960296.97648
 ; CURRENT APPLICATION NUMBER: US/10/085.959

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?
? CURRENT FILING DATE: 2002-03-01
? PRIOR APPLICATION NUMBER: 60/242,412
? PRIOR FILING DATE: 2000-10-19
? NUMBER OF SEQ ID NOS: 255
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 35
? LENGTH: 5225
? TYPE: DNA
? ORGANISM: Escherichia coli
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (377)..(377)
? OTHER INFORMATION: Unsure
?
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; LOCATION: (1204)..(1204)
; OTHER INFORMATION: Unsure
US-10-085-959-35

alignment_scores:
    Quality: 73.50
Length: 126

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```
20 rThrGlnPheLeuAsnMet...GlyAsnGluVal..... 30
   :::::||||:::|||||
393 GCGGATTTGTTGAGGTGAGGCAATGATATTCGTGTTGTTGTAAC 442
   :::::||||:::|||||
31 .....AlaLeuAspGlyArgTyrSerAsnTyrAlaLeuIle 42
   ||:::|||||
443 GTGGAAGGAGAGGTGCAATGGAGGATCGTTATTCT.....GCAC TTGTC 486
   ||:::|||||
43 SerAlaGluGlyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAs 59
   :::::||||:::|||||
487 AATTTCACAGGAGATTCAAAACAGGGTATTTTGGTGTATTGATGGACA 536
   ||| |||:::|||||
59 pGlyPheProGluValArgGluPheAsnSerLeuProAsnAsnLysAlas 76
   ||| |||:::|||||
537 TGGAGGACCTAAGCTGCAGAGTTTCAGCAGACGACCTTGAATGAACA 586
   ||| |||:::|||||
76 erSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLysLys 92
   ||| |||:::|||||
587 TTATGGAT.....GAATTAGTAAGGAGGAATGATGAAGATGTTGTGGAA 630
   ||| |||:::|||||
93 TyrIleLys 95
   :::::
631 GTGCTGAAA 639
```


OM of: US-09-528-682-4 to: Pending_Patents_NA_New: * out_format : pfs

Date: Jun 18, 2002 9:49 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL=framet.p2n.model -DEV=xlp
-Q/cgn2.1/USPTO.spool/US09528682/runat_18062002.082444_7900/app_query.fasta_1.689
-DB=Pending_Patents_NA_New -QPMT=fastap -SUFFIX=pan.rnpn
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -FGAPOP=4.500 -FGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -XGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=1000 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09528682@cgn1_1_572 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-528-682-4

Query length: 110

Database: Pending_Patents_NA_New: *

Database sequences: 1014543

Database length: 727792371

Search time (sec): 403.930000

score_list:

Sequence	Strid Orig	zScore	EScore	Len	Documentation
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-540-209B-3042	79.50	177.47	0.0900	
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-540-209B-3340	78.00	166.42	0.3715	
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-540-209B-517	72.50	158.27	1.06	
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-770-105A-3	69.50	161.69	0.6813	59
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-770-105A-1	69.50	157.40	1.18	91
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-10-041-018-103	69.50	145.93	5.14	2
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-721-544-8479	69.00	165.26	0.4309	
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-919-002-2707	69.00	144.57	6.05	
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	PCT-US02-09188-363	69.00	143.22	7.29	3
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	PCT-US02-09370-379	69.00	143.22	7.29	3
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-10-105-299-500	69.00	143.22	7.29	3
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-935-632-13145	69.00	139.18	12.23	
/cgn2.6/ptodata/1/pna/US60_NEW_COMB.seq	US-60-360-039-25380	67.00	149.54	3.24	
/cgn2.6/ptodata/1/pna/US60_NEW_COMB.seq	US-60-360-039-43631	67.00	144.35	6.30	
/cgn2.6/ptodata/1/pna/US60_NEW_COMB.seq	US-60-360-039-43853	66.50	137.50	15.16	
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/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-540-209B-4674	66.00	150.12	3.00	
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-10-027-632-19402	65.50	151.14	2.64	
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-10-027-632-19403	65.50	151.14	2.64	
/cgn2.6/ptodata/1/pna/US60_NEW_COMB.seq	US-60-360-039-46339	65.50	137.04	16.09	
/cgn2.6/ptodata/1/pna/US60_NEW_COMB.seq	US-60-360-039-46343	65.50	134.16	23.28	
/cgn2.6/ptodata/1/pna/US60_NEW_COMB.seq	US-60-360-039-25817	65.50	126.99	58.39	
/cgn2.6/ptodata/1/pna/US60_NEW_COMB.seq	US-60-360-039-42700	65.00	148.47	3.71	
/cgn2.6/ptodata/1/pna/US60_NEW_COMB.seq	US-60-360-039-45623	64.50	134.28	22.93	
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-539-3310-15353	64.00	155.37	1.53	
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-540-209B-3507	64.00	140.46	10.38	
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-09-882-272-619	64.00	133.69	24.71	2
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-10-027-632-110883	64.00	133.59	25.05	
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-975-254-22987	63.50	154.22	1.78	
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-10-027-632-268304	63.50	147.34	4.29	
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-620-393B-4281	63.50	146.36	4.87	
/cgn2.6/ptodata/1/pna/US09_NEW_COMB.seq	US-09-935-625-6253	63.50	146.13	5.01	
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-10-027-632-201696	63.50	144.18	6.44	
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-10-027-632-201697	63.50	144.18	6.44	
/cgn2.6/ptodata/1/pna/PCT_NEW_COMB.seq	PCT-US02-13142-2019	63.50	138.52	13.31	

/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-10-128-714-2019	63.50	138.52	13.31	
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/cgn2.6/ptodata/1/pna/PCT_NEW_COMB.seq	PCT-US02-13142-7019	63.50	136.46	17.33	
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-10-128-714-7019	63.50	136.46	17.33	
/cgn2.6/ptodata/1/pna/PCT_NEW_COMB.seq	PCT-US02-13142-6019	63.50	135.70	19.11	
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-10-128-714-6019	63.50	135.70	19.11	
/cgn2.6/ptodata/1/pna/PCT_NEW_COMB.seq	PCT-US02-13142-19	63.50	135.18	20.41	
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-10-128-714-19	63.50	128.19	50.02	
/cgn2.6/ptodata/1/pna/PCT_NEW_COMB.seq	PCT-US02-13142-5019	63.50	127.83	52.43	
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-10-128-714-5019	63.50	127.83	52.43	
/cgn2.6/ptodata/1/pna/PCT_NEW_COMB.seq	PCT-US02-13142-437	63.00	147.59	4.16	
/cgn2.6/ptodata/1/pna/US60_NEW_COMB.seq	US-60-360-039-26725	63.00	140.77	9.96	
/cgn2.6/ptodata/1/pna/US10_NEW_COMB.seq	US-10-027-632-164418	63.00	140.71	10.05	
/cgn2.6/ptodata/1/pna/PCT_NEW_COMB.seq	PCT-US02-09237-136	63.00	133.80	24.38	
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/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-10-057-312-1 - 53.50 65.50 1.5e+05
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/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-09-704-302A-1032 + 53.00 124.82 77.09
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-10-011-154-179 + 53.00 122.15 108.65
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-75433 - 53.00 121.68 115.31
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-10-027-632-313578 - 53.00 121.68 115.31
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-09-539-800C-9341 + 53.00 119.77 147.34
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-10-068-965-1 + 53.00 119.73 148.05
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-113-872-14 - 53.00 119.68 149.11
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-991-936-1439 + 53.00 119.51 152.31
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-09-539-331D-31430 + 53.00 119.39 154.8
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-10-027-632-35622 - 53.00 119.35 155.52
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-113-872-72 + 53.00 119.30 156.60
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-620-330B-6690 + 53.00 119.05 161.63
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-60-360-039-42570 + 53.00 118.47 174.01
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-60-377-240-6921 + 53.00 118.34 176.95
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-60-360-039-25189 + 53.00 117.76 190.68


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; SEQ ID NO 3340
; LENGTH: 3381
; TYPE: DNA
; ORGANISM: B.fragilis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2997)..(3209)
; OTHER INFORMATION: Identity of nucleotide sequences at the above
US-09-540-209B-3340

alignment_scores:
    Quality: 78.00      Length: 112
    Ratio: 1.322      Gaps: 7
    Percent Similarity: 52.679      Percent Identity: 29.464

alignment_block:
US-09-528-682-4 x US-09-540-209B-3340 ..

Align seg 1/1 to: US-09-540-209B-3340 from: 1 to: 3381

10 AlaTyrGluProIleAlaAsnThrAsnThrThrThrGlnPheLeuAsn.. 25
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
281 GCTTATCGGAATCGTGAATTTGACTGAAAGCCGCTTATACAAACGG 2330

26 ...MetGlyAsnGluValAlaLeuAspGly.....ArgTyrS 37
||||| ||||| ||||| ||||| ||||| ||||| |||||
2331 ATATCGGTGGTAGTACCACCTTCATTATCAGGACCTACTTATAATCGATTCC 2380

37 erAsnTyrAlaLeuIleSerAlaGluGly.....GlyMet 48
||||| ||||| ||||| ||||| ||||| ||||| |||||
2381 AGAATAATGAATCTACGTGGGAAGTCGGAATAAACTGAATGTGGGTGTC 2430

49 AspArgAspLeuPheGlySerAlaAsnIle.....AspGlyPheProG1 63
||||| ||||| ||||| ||||| ||||| ||||| |||||
2431 GATTACAGCTTCTCAATTCATTAATATCATCTGTCGACGGATTACAGGA 2480

63 uValArg.....GluPheAsnSerLeuProAsnAsnLysA 75
||||| ||||| ||||| ||||| ||||| ||||| |||||
2481 GATTAGAGATAATATTTTCAGCAGAAAAATCCATACCGAATTATCTGG 2530

75 laSerSerAspThrAlaSerLeuAsnLysGlnHisAspAlaAspPheLys 91
||||| ||||| ||||| ||||| ||||| ||||| |||||
2531 GAATCGCCAGTACTAAAATCTAC.....GGCAATTTTCGCT 2565

92 LysTyrIleLysLeuLeuIleAsnAsnAspGlyPhe 103
||||| ||||| ||||| ||||| ||||| ||||| |||||
2566 AAA.....GTGAAGAATACAGGATTT 2586

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-540-209B-517

seq_documentation_block:
; Sequence 517, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATIN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540, 209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 517
; LENGTH: 1824
; TYPE: DNA
; ORGANISM: B.fragilis
US-09-540-209B-517

alignment_scores:
    Quality: 72.50      Length: 114
    Ratio: 1.189      Gaps: 3
    Percent Similarity: 53.509      Percent Identity: 23.684

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alignment_block:

US-09-528-682-4 x US-09-540-209B-517 ..

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: : : : : ||| : : : : : |||

61 TTCATACCGTTCATGTACCGCTAAATTAGAGAAACAGACATATACGAA 110

: : : : : ||| : : : : : |||

18 nThrThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeu..... 32

: : : : : ||| : : : : : |||

111 TGTATATGATTTACATTTTGCATTCGGCTGTGATTCGGGTGGTTTATC 160

: : : : : ||| : : : : : |||

33AspGlyArgTyrSerAsnTyrAlaLeuIleLeuLeuLeuLeu 45

: : : : : ||| : : : : : |||

161 CGTGGCGTCAAAATGAGCATATAGCAATATATCTATCCCTGCTTATATA 210

: : : : : ||| : : : : : |||

46 GlyGlyMetAspArgAspLeuPheGlySerAlaAsnIleAspGlyPhePr 62

: : : : : ||| : : : : : |||

211 CAAGATTCAAAATCGAAATTTGTTCGCTAAAAAATATTTTAAAGGATTC 260

: : : : : ||| : : : : : |||

62 OGUValArgGluPheAsnSer.....LeuProA 72

: : : : : ||| : : : : : |||

261 TTTTCTAAGCGGTTAAGATCAGAGTACGACAGAGAATTTTCTTCCCA 310

: : : : : ||| : : : : : |||

72 snAsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnHisAspAla 88

: : : : : ||| : : : : : |||

311 ATATAACATAAAAGAA.....GCTGTAATCGGATTTGAAGGTAAGGT 354

: : : : : ||| : : : : : |||

89 AspPheLysLysTyrIleLysLeuLeuIleAsnAsnAspGly 102

: : : : : ||| : : : : : |||

355 GATAATATAAAATCTCTCTATCATCTTGGATCGCATAGGT 396

: : : : : ||| : : : : : |||

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-770-105A-3

seq_documentation_block:

; Sequence 3, Application US/09770105A

; GENERAL INFORMATION:

; APPLICANT: Acton, Susan

; TITLE OF INVENTION: Novel Phospholipase Molecule and Uses Therefor

; FILE REFERENCE: mnl-059

; CURRENT APPLICATION NUMBER: US/09/770,105A

; CURRENT FILING DATE: 2001-01-25

; PRIOR APPLICATION NUMBER: US/09/163,833

; PRIOR FILING DATE: 1998-09-30

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 3

; LENGTH: 594

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(594)

US-09-770-105A-3

alignment_scores:

Quality: 69.50 Length: 70

Ratio: 1.448 Gaps: 3

Percent Similarity: 68.571 Percent Identity: 30.000

alignment_block:

US-09-528-682-4 x US-09-770-105A-3/rev ..

Align seg 1/1 to reverse of: US-09-770-105A-3 from: 1 to: 594

32 LeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGlyGlyMe 48

: : : : : ||| : : : : : |||

498 CTGGATGGCCTCTACCAGCGTCATGTCTCATAGATCATGAGGAAGGCCA 449

: : : : : ||| : : : : : |||

48 tAspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGlu.... 63

: : : : : ||| : : : : : |||

448 GGACAAG.....TGTGGCAGAGCG.....GCTTACCCCATGGCA 414

: : : : : ||| : : : : : |||

64 ..ValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspThr 79

: : : : : ||| : : : : : |||

413 CAGTGTACCAAGCAGCGGCTTGGGAACACTAGGGCAGCTCGGATGTA 364

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80 AlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysLe 96

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363 TCAGCAACAGCAGAAAGTAGACACTGAGTGCAGAGAGGGGTTGTCGT 314

: : : : : ||| : : : : : |||

96 uLeuIleAsn 99

: : : : : ||| : : : : : |||

313 CCGCCTCAAT 304

: : : : : ||| : : : : : |||

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-770-105A-1

seq_documentation_block:

; Sequence 1, Application US/09770105A

; GENERAL INFORMATION:

; APPLICANT: Acton, Susan

; TITLE OF INVENTION: Novel Phospholipase Molecule and Uses Therefor

; FILE REFERENCE: mnl-059

; CURRENT APPLICATION NUMBER: US/09/770,105A

; CURRENT FILING DATE: 2001-01-25

; PRIOR APPLICATION NUMBER: US/09/163,833

; PRIOR FILING DATE: 1998-09-30

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 1

; LENGTH: 912

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (52)..(645)

US-09-770-105A-1

alignment_scores:

Quality: 69.50 Length: 70

Ratio: 1.448 Gaps: 3

Percent Similarity: 68.571 Percent Identity: 30.000

alignment_block:

US-09-528-682-4 x US-09-770-105A-1/rev ..

Align seg 1/1 to reverse of: US-09-770-105A-1 from: 1 to: 912

32 LeuAspGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGlyGlyMe 48

: : : : : ||| : : : : : |||

549 CTGGATGGCCTCTACCAGCGTCATGTCTCATAGATCATGAGGAAGGCCA 500

: : : : : ||| : : : : : |||

48 tAspArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGlu.... 63

: : : : : ||| : : : : : |||

499 GGACAAG.....TGTGGCAGAGCG.....GCTTACCCCATGGCA 465

: : : : : ||| : : : : : |||

64 ..ValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSerAspThr 79

: : : : : ||| : : : : : |||

464 CAGTGTACCAAGCAGCGGCTTGGGAACACTAGGGCAGCTCGGATGTA 415

: : : : : ||| : : : : : |||

80 AlaSerLeuAsnLysGlnHisAspAlaAspPheLysLysTyrIleLysLe 96

: : : : : ||| : : : : : |||

414 TCAGCAACAGCAGAAAGTAGACACTGAGTGCAGAGAGGGGTTGTCGT 365

: : : : : ||| : : : : : |||

96 uLeuIleAsn 99

: : : : : ||| : : : : : |||

364 CCGCCTCAAT 355

: : : : : ||| : : : : : |||

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-041-018-103

seq_documentation_block:

; Sequence 103, Application US/10041018

; GENERAL INFORMATION:


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; APPLICANT: Matsuda, Seichi P.T.
; APPLICANT: Hart, Elizabeth A.
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism
; FILE REFERENCE: P02080US1/10025547
; CURRENT APPLICATION NUMBER: US/10/041,018
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259880
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 2869
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-10-041-018-103

alignment_scores:
  Quality: 69.50      Length: 132
  Ratio: 1.053        Gaps: 8
  Percent Similarity: 50.000      Percent Identity: 27.273

alignment_block:
US-09-528-682-4 x US-10-041-018-103/rev ..

Align seg 1/1 to reverse of: US-10-041-018-103 from: 1 to: 2869

3 PheThrValArgIleGlnAspAlaTyrGluProIleAlaAsn.....Th 17
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563 TTCACCAAAATGGGACAAAGCTTTAGATTCTATTATTATCATGCGGA 514

17 rAsnThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspG 34
:::||||| ::| ||||| ::| ::| ::| |||||
513 TGAACATACACAAGCGCTTACTTACTAGTTACCAAGATGCAGTTGAT. 465

34 lyArgTyrSerAsnTyr..... 39
||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
464 .....TATAATCGTTATGTCGGTAATATTACACAGGTCCTTATATTTA 420

40 AlaLeuIleSer.....AlaGluGlyGlyMetAspAr 50
:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
419 AGTCTCATCTCTTTATTAGAACACGTGATTAAAGCGGACAAACGAT 370

50 gAspLeuPhe.....GlySerAlaAsn..... 57
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
369 TGGTCTCTTTAGTTAGTTCTGTTCTGTAGCGGAGTCTTTAGTGGA 320

58 .....IleAspGlyPheProGlu.....ValArgGluPheAsnSer 69
:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
319 CATTAGTAGATGGATTCAAGAGCAATTAGATTGTGAGCGCCACAAATCT 270

70 LeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnHi 86
||| ||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
269 TTATTAATATAGAAATAGAGTTCTTGT.....GATGAATA 232

86 sAspAlaAspPheLysLysTyrIleLysLeuLeuIleAsnAsnAsp 101
::: ||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
231 TGAACATTTCTTCAACGCTTGACCAATTAGAAATTGAATCATGAA 186

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-721-544-8479

seq_documentation_block:
; Sequence 8479, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica

```

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; APPLICANT: Giedt, Gretchen
; APPLICANT: Hunter, Kelly
; APPLICANT: Jessen, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroja, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fei
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 728CIP
; CURRENT APPLICATION NUMBER: US/09/721,544
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/034,341
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8479
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-721-544-8479

alignment_scores:
  Quality: 69.00      Length: 72
  Ratio: 1.683        Gaps: 4
  Percent Similarity: 56.944      Percent Identity: 31.944

alignment_block:
US-09-528-682-4 x US-09-721-544-8479 ..

Align seg 1/1 to: US-09-721-544-8479 from: 1 to: 365

13 ProIleAlaAsnThrAsnThrThrGlnPheLeuAsnMetGlyAsnG 29
||| ::| ||||| ::| ::| ::| ||| |||
75 CCGCGAGATTCAACAAATCCAGTGACATCTACACAATGATTATTC 124

29 uValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeu..... 41
||| ||| ||||| ::| ::|
125 AGTCCGCGCTGGAGGAGCGCGTCCCAACTTCCCGATGGTCCCGGCTCG 174

42 .....IleSerAlaGluGlyGlyMetAsp.....ArgAsp 51
::: ::| ::| ||||| ::| ::| ::|
175 ACGTCCGATGGCGCGATGGGTGGCATGGCCACACCATGAATGGA 224

52 LeuPheGlySerAlaAsnIleAspGlyPheProGluValArgGluPhe 68
::: ||||| ::| ||||| ::| ||||| ::| |||||
225 TCATTAGGGTCAGGCGACATAGACGGACTTCCAAA.....AA 262

68 nSerLeuProAsnAsn 73
||| ||||| |||||
263 TTCT...CCTAACAC 275

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-919-002-2707

seq_documentation_block:
; Sequence 2707, Application US/09919002
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin

```



```

13  ProLeuAlaAsnThrAsnThrThrThrGlnPheLeuAsnMetGlyAsnG1 29
14  |||  ::::::::::::::::::::  ::::  ::::  |||
15  938  CCCGAGATTCAACAATTCAGTGACAACATCTACACATGATTATCC 987
16  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
17  29  uValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeu..... 41
18  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
19  988  AGTCCGCCTGGAGCGACCGCGTCCAACTTCCCGATGGTCCCGCTCGG 1037
20  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
21  42  .....IleSerAlaGluGlyMetAsp.....ArgAsp 51
22  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
23  1038  ACGTCCGATGGCGCGATGGTGGCGATGGAGCCACACCATGAATGGA 1087
24  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
25  52  LeuPheGlySerAlaAsnIleAspGlyPheProGluValArgGluPheAs 68
26  ::::::::::::::::::::  ::::  ::::  |||
27  1088  TCATTAGGTCAGCGACATAGACGGACTTCCAAAA.....AA 1125
28  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
29  68  nSerLeuProAsnAsn 73
30  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
31  1126  TTCT...CCTAACAAAC 1138
32  seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-105-299-500
33
34  seq_documentation_block:
35  ; Sequence 500, Application US/10105299
36  ; GENERAL INFORMATION:
37  ; APPLICANT: Rosen, et. al
38  ; TITLE OF INVENTION: Human Secreted Proteins
39  ; FILE REFERENCE: PS950
40  ; CURRENT APPLICATION NUMBER: US/10/105,299
41  ; CURRENT FILING DATE: 2002-03-26
42  ; NUMBER OF SEQ ID NOS: 15197
43  ; Prior Application removed - See File Wrapper or Palm
44  ; SOFTWARE: PatentIn Ver. 2.0
45  ; SEQ ID NO 500
46  ; LENGTH: 3303
47  ; TYPE: DNA
48  ; ORGANISM: Homo sapiens
49  ; FEATURE:
50  ; NAME/KEY: misc.feature
51  ; LOCATION: (2355)..(2355)
52  ; OTHER INFORMATION: n equals a,t,g, or c
53  ;
54  US-10-105-299-500
55
56  alignment_scores:
57  Quality: 69.00 Length: 72
58  Ratio: 1.683 Gaps: 4
59  Percent Similarity: 56.944 Percent Identity: 31.944
60
61  alignment_block:
62  US-09-528-682-4 x US-10-105-299-500 ..
63
64  Align seg 1/1 to: US-10-105-299-500 from: 1 to: 3303
65
66  13  ProLeuAlaAsnThrAsnThrThrThrGlnPheLeuAsnMetGlyAsnG1 29
67  |||  ::::::::::::::::::::  ::::  ::::  |||
68  938  CCCGAGATTCAACAATTCAGTGACAACATCTACACATGATTATCC 987
69  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
70  29  uValAlaLeuAspGlyArgTyrSerAsnTyrAlaLeu..... 41
71  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
72  988  AGTCCGCCTGGAGCGACCGCGTCCAACTTCCCGATGGTCCCGCTCGG 1037
73  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
74  42  .....IleSerAlaGluGlyMetAsp.....ArgAsp 51
75  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
76  1038  ACGTCCGATGGCGCGATGGTGGCGATGGAGCCACACCATGAATGGA 1087
77  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
78  52  LeuPheGlySerAlaAsnIleAspGlyPheProGluValArgGluPheAs 68
79  ::::::::::::::::::::  ::::  ::::  |||
80  1088  TCATTAGGTCAGCGACATAGACGGACTTCCAAAA.....AA 1125
81  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
82  68  nSerLeuProAsnAsn 73
83  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
84  1126  TTCT...CCTAACAAAC 1138

```

```

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-935-625-13145
seq_documentation_block:
; Sequence 13145, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 13145
; LENGTH: 4944
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: Misc.feature
; LOCATION: 1..4944
; OTHER INFORMATION: Ceres Seq. ID no. 3037797
;
US-09-935-625-13145

alignment_scores:
Quality: 69.00 Length: 90
Ratio: 1.211 Gaps: 2
Percent Similarity: 63.333 Percent Identity: 25.556

alignment_block:
US-09-528-682-4 x US-09-935-625-13145 ..
Align seg 1/1 to: US-09-935-625-13145 from: 1 to: 4944

21  ThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgTyrSe 37
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
3184  ACGCAGAGACTCGGACTGGGA.....GCTTGTCTGCTGTGTTTC 3224
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
37  rAsnTyrAlaLeuIleSerAlaGluGlyGlyMetAspArgAspLeuPheG 54
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
3225  AAAAGATATACAATTAGGAGGAGAAAGAGCTTTGATTCATTCGATTG 3274
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
54  lySerAlaAsnIleAspGlyPheProGluValArgGluPheAsnSerLeu 70
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
3275  CTTCTACTAAACGCTGAAGCTGTGCCAAGATTTTACGAGATCTCTCTTG 3324
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
71  ProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnHisAs 87
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
3325  AGTAATCGTGCTCTTTCTCCAGTGTGGCACTAAAGTATCAAGAGGA 3374
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
87  pAlaAspPheLysLysTyrIleLysLeuLeuIleAsnAsnAspGlyPheP 104
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
3375  AGACGACCTCGAA.....GACGGTTTCT 3397
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
104  heSerAsnAsnGlyGlyLys 110
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
3398  CAGAACTGGAAGGTTCAAAG 3417
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||

seq_name: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:US-60-360-039-25380
seq_documentation_block:
; Sequence 25380, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21

```


Align seq 1/1 to reverse of: US-10-027-632-43498 from: 1 to: 618

Align seq 1/1 to reverse of: US-10-027-632-43499 from: 1 to: 618


```

1  APPLICANT: Wang, David G.
2  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
3  : Polymorphisms in the Human Genome
4  :
5  : TITLE OF INVENTION: Polymorphisms in the Human Genome
6  :
7  : FILE REFERENCE: 10827.129
8  :
9  : CURRENT APPLICATION NUMBER: US/10/027,632
10 :
11 : CURRENT FILING DATE: 2002-04-30
12 :

```


;; TITLE OF INVENTION: EXPRESSION OF MICROPLANTS WITH IMPROVED

;; TITLE OF INVENTION: EXPRESSION OF MICROPLANTS WITH IMPROVED


```
alignment_scores:
  Quality: 64.00      Length: 68
  Ratio: 1.641        Gaps: 4
  Percent Similarity: 57.353  Percent Identity: 32.353

alignment_block:
US-09-528-682-4 x US-09-539-331D-15353 ..
Align seg 1/1 to: US-09-539-331D-15353 from: 1 to: 267

17 ThrAsnThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAs 33
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 ACAAAATCCAGTGCACAACTACACAAATGATTAATCCAGTCCGCCCTGG 50
33 pGlyArgTyrSerAsnTyrAlaLeu.....IleS 43
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 AGGCAGCGCGTCCAACTCCCGATGGTCCCGGCTCNGACGGTCCGATGG 100
43 erAlaGluGlyGlyMetAsp.....ArgAspLeuPheGlySer 55
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 GCGGCATGGTGGCATGGAGCCACACACATCAATGGATCATTAGGTCA 150
56 AlaAsnIleAspGlyPheProGluValArgGluPheAsnSerLeuProAs 72
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 GCGGACATAGCGGACTTCCAAA.....AATTCT...CCTAA 185
72 nAsn 73
|||||
186 CAAC 189
```

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-540-209B-3507

```
seq_documentation_block:
; Sequence 3507, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FRA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 3507
; LENGTH: 1185
; TYPE: DNA
; ORGANISM: B. fragilis
US-09-540-209B-3507
```

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alignment_scores:
  Quality: 64.00      Length: 49
  Ratio: 1.882        Gaps: 0
  Percent Similarity: 69.388  Percent Identity: 30.612

alignment_block:
US-09-528-682-4 x US-09-540-209B-3507 ..
Align seg 1/1 to: US-09-540-209B-3507 from: 1 to: 1185

3 PheThrValArgIleGlnAspAlaTyrGluProIleAlaAsnThrAsnTh 19
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
613 TGGACCATCAATGAGCGCCATCTATTCCAGCTGAGCCGGAAGCAAGCT 662
19 rThrThrGlnPheLeuAsnMetGlyAsnGluValAlaLeuAspGlyArgT 36
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
663 GACACAGCGCTATCTAAGCAACGACGAGGAGGAGCATCTATACCCGCA 712
36 yrSerAsnTyrAlaLeuIleSerAlaGluGlyMetAspArgAsp 51
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
713 TTTTCATCTACTCCCGCATACAGTGAAGAAAGGACGCGCGGGGAC 759
```

seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-882-227-619

```
seq_documentation_block:
; Sequence 619, Application US/09882227
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding Novel Helicobacter Polypeptides in the Helicobacter
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/047002
; CURRENT APPLICATION NUMBER: US/09/882,227
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/902,615
; PRIOR FILING DATE: 1997-07-29
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 619
; LENGTH: 2329
; TYPE: DNA
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)...(2274)
US-09-882-227-619
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alignment_scores:
  Quality: 64.00      Length: 107
  Ratio: 1.255        Gaps: 6
  Percent Similarity: 47.664  Percent Identity: 24.299
```

alignment_block:
US-09-528-682-4 x US-09-882-227-619 ..

```
Align seg 1/1 to: US-09-882-227-619 from: 1 to: 2329

11 TyrGluProIleAla...AsnThrAsnThrThrGlnPhe.....Le 24
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
892 TATGAACCTTCTCCTTAAAAACACACCGATTTAATCCTTCGCTTATGT 941
24 uAsnMetGlyAsnGluValAlaLeu.....A 33
|||||:|||||:|||||:|||||:|||||:|||||:
942 GGATTTTGTAATGATGGTGGTTTGACCGAAGACATACTCTCAAAATG 991
33 spGlyArgTyrSerAsnTyrAlaLeuIleSerAlaGluGlyGlyMetAsp 49
|||||:|||||:|||||:|||||:|||||:|||||:
992 ACACACGCCCTAAAGGCGATGGCATGGTGGTAGTGGAGGGGATTTTTC 1041
50 ArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgI 66
|||||:|||||:|||||:|||||:|||||:|||||:
1042 ACTCAATCTTTGGATTAGCAAGCTC...GTGTTCCCTGAA..... 1080
66 uPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeu 83
|||||:|||||:|||||:|||||:|||||:|||||:
1081 .....AGACCTAATGAAAAA..... 1095
83 snLysGlnHisAspAlaAspPheLysLysTyrIleLysLeuIleAsn 99
|||||:|||||:|||||:|||||:|||||:|||||:
1095 ..... 1095
100 AsnAspGlyPhePheSerAsn 106
|||||:|||||:|||||:|||||:|||||:
1096 ...GATCCTTTCTTAGCAAT 1113
```

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-027-632-110883

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seq_documentation_block:
; Sequence 110883, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```



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; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: fastseq for Windows version 4.0
; SEQ ID NO 110884
; LENGTH: 2354
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-110884

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alignment_scores:		
Quality:	64.00	Length: 102
Ratio:	1.164	Gaps: 3
Percent Similarity:	53.922	Percent Identity: 23.529

arrangement block.
US-09-528-682-4 x US-10-027-632-110884

Align seq 1/1 to: US-10-027-632-110884 from: 1 to: 2354

16 AsnThrAsnThrThrGlnPheLeuAsnMetClyAsnGluValAlaLe 32
||||| |||| | ||||| : : :
780 AACACAAATAAAAACTCTCTTCTTAATATTGCTGAAAAATAGACCTT 829
32 uAspGlyArgTyrSerAsnTyrrAlaLeuIleSerAlaGluGlyGlyMeta 49
| ||||| : : : : : : :
830 GTACAGAACCCTATTCAACTACAGTAACAACAACTCTCATATGAACAACGG 879
49 spArgAspLeupheGlySerAlaAsnIleAspGlyPheProGluValArg 65
: : : : : : : : : : : : :
880 ATAGAAATATGTTT.....TCTGGATATCCACATCATCAGA 914

```

66  GluPheAsnSerLeuProAsnAsnLysAla..... 75
      :::::  |||||  |||
915  AATTTTGAC.....CCAAATTTTAAAAATAAAATTGTGCTTTCAACTCC 958

```

76SerSerAspThrAlaSerLeuAsnLysGlnH 86
 ::: : :::::::::::::: |
959 ATAGCATTCCTGTAGTTTGAACACTATTGGTCTCAATGACTTCTGCAC 100

86 isAspAlaaspPheLysLysTyrIleLysLeuLeuIleAsnAsnAspGly 102
 || ::::||| ||-| :: ::::: |||
 109 ATATTTTCCTTCATATAGGGAATCTTAGTCACCTTAGAAGAGAAAGGC 105

103 PhePhe 104

1059 TTTCTTT 106A

seq name: /can2 6/ptodata/1/pna/US09 NEW COMB.seq:US-09-975-254-29497

```
seq_documentation_block:
; Sequence 29497, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molec
```


Align seg 1/1 to: US-10-027-632-268304 from: 1 to: 523

```

36 TyrSerAsnTyrAlaLeuIleSerAlaGluGlyMetAspArgAspie 52
||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
297 TATCCAGATTCTCCCTGGAGGCGCTGCAGGCTGTGTCTTCAAGAGCT 346

```

52 uPhe.....GlySerAlaAsn...IleAspGlyP 61
||||| :|||:
:||||:

347 GTTTGAAGATCAGAGCAGAGCCCTGTCCACAGCAAACTAAAAATGATGGCT 396

61 heProGluValArgGluPheAsnSerLeuProAsnAsnLysAlaSerSer 77
:: ::::: ::|||::|::: ||||||: |||::: |:::
397 ATGTGGACATGAGCAGCTTCAACACCTTTTAGACACAATCAGCAGAGCAC 446

78 AspThrAlaSerLeuasnLysGlnHisaspAlaaspPheLysLysLysTyrTrl 94
 447GACCAGGACGCGAAGAAGTACCT 469

94 e 94
:
470 G 470

```
seq_name: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:US-09-620-393B
seq_documentation_block:
; Sequence 4281, Application US/09620393B
```

```

; GENERAL INFORMATION:
;
; APPLICANT: ALEXANDROV, Nikolai et al.
;
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND COMPOSITIONS THEREOF
;
; TITLE OF INVENTION: THEREBY

```

```

; FILE REFERENCE: 2750-1068P
; CURRENT APPLICATION NUMBER: US/09/620,393B

```

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; CURRENT FILING DATE: 2000-07-21
;
; NUMBER OF SEQ ID NOS: 9948
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4281

```

```

; LENGTH: 577
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:

```

```
; NAME/KEY: misc_feature
; LOCATION: 1..577
; OTHER INFORMATION: any n = a, g, c, t, unknown, or other
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: 1.577
; OTHER INFORMATION: Ceres Seq. ID 1387475
US-09-620-393B-4281

```

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alignment_scores:
  Quality: 63.50      Length: 77
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Ratio: 1.984 Gaps: 4
Percent Similarity: 41.558 Percent Identity: 28.571
alignment_block:

US-09-528-682-4 x US-09-620-393B-4281 ..
Align seg 1/1 to: US-09-620-393B-4281 from: 1 to: 577

Percent Similarity: 57.798 Percent Identity: 25.688

alignment_block:

US-09-528-682-4 x US-10-128-714-2019/rev ..

Align seg 1/1 to reverse of: US-10-128-714-2019 from: 1 to: 1263

```
5 ValArgileGlnAspAlaTyrGluProIleAlaAsnThrAsnThrThr 21
||||:||||| :||| |||:| |||:|||||
726 GTTCAGCTTCAGCACACCATGAGGATAGAGCCACCTGCACACCCCT 677
21 rGlnPheLeuAsnMetGlyAsnGlu...ValAlaLeuAspGlyArgTyr 37
||||:||||| :||| |||:| |||:|||||
676 TCAACTCATCGATCTCGCACCGGGTTGTGACGTCGAAGGAACGAATG 627
37 erAsnTyrAlaLeuIleSerAlaGlu.....GlyGlyMetAsp... 49
||||:||||| :||| |||:| |||:|||||
626 ACAATCATGTGAGCGGAAGCAGTGAAGTCACGGACGGAACTGGGATGTG 577
50 ArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgG 66
||||| :||| :||| :||| :|||
576 CGAGAC.....AAGGTATTCTGTGACAGCGTCGATGTTGACTTGA 536
66 uPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeu 83
||||| :||| :||| :||| :|||
535 GCTGACGACAGATGGGAATGATAGGAGAGCCATCGGCAACAGTACCAC 486
83 snLysGlnHisAsp.....AlaAspPheLysLys 92
||||| :||| :||| :||| :|||
485 ATGAACCTTCAGGATTTGATGTTGATGTTGCAGAGCACCGCTTCCCTCAT 436
93 TyrIleLysLeuLeuIleAsnAsnAsp 101
||||:||||| :||| |||:| |||:|||||
435 CAGATCAACCTTGTTCGACAGATGAT 409
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seq_name: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:PCT-US02-13142-1019

seq_documentation_block:

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; Sequence 1019, Application PC/TUS0213142
; GENERAL INFORMATION:
; APPLICANT: Elitra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-228
; CURRENT APPLICATION NUMBER: PCT/US02/13142
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1019
; TYPE: DNA
; LENGTH: 1542
; ORGANISM: Aspergillus fumigatus
PCT-US02-13142-1019
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alignment_scores:

Quality: 63.50 Length: 109
Ratio: 1.008 Gaps: 5
Percent Similarity: 57.798 Percent Identity: 25.688

alignment_block:

US-09-528-682-4 x PCT-US02-13142-1019/rev ..

Align seg 1/1 to reverse of: PCT-US02-13142-1019 from: 1 to: 1542

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5 ValArgileGlnAspAlaTyrGluProIleAlaAsnThrAsnThrThr 21
||||:||||| :||| |||:| |||:|||||
948 GTTCAGCTTCAGCACACCATGAGGATAGAGCCACCTGCACACCCCT 899
21 rGlnPheLeuAsnMetGlyAsnGlu...ValAlaLeuAspGlyArgTyr 37
||||:||||| :||| |||:| |||:|||||
898 TCAACTCATCGATCTCGCACCGGGTTGTGACGTCGAAGGAACGAATG 849
37 erAsnTyrAlaLeuIleSerAlaGlu.....GlyGlyMetAsp... 49
||||:||||| :||| |||:| |||:|||||
848 ACAATCATGTGAGCGGAAGCAGTGAAGTCACGGACGGAACTGGGATGTG 799
50 ArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgG 66
||||| :||| :||| :||| :|||
798 CGAGAC.....AAGGTATTCTGTGACAGCGTCGATGTTGACTTGA 758
66 uPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeu 83
||||| :||| :||| :||| :|||
757 GCTGACGACAGATGGGAATGATAGGAGAGCCATCGGCAACAGTACCAC 708
83 snLysGlnHisAsp.....AlaAspPheLysLys 92
||||| :||| :||| :||| :|||
707 ATGAACCTTCAGGATTTGATGTTGATGTTGCAGAGCACCGCTTCCCTCAT 658
93 TyrIleLysLeuLeuIleAsnAsnAsp 101
||||:||||| :||| |||:| |||:|||||
657 CAGATCAACCTTGTTCGACAGATGAT 631
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seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-128-714-1019

seq_documentation_block:

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; Sequence 1019, Application US/10128714
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Hu, Wengqi
; APPLICANT: Zamudio, Carlos
; APPLICANT: Broshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1019
; TYPE: DNA
; LENGTH: 1542
; ORGANISM: Aspergillus fumigatus
US-10-128-714-1019
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alignment_scores:

Quality: 63.50 Length: 109
Ratio: 1.008 Gaps: 5
Percent Similarity: 57.798 Percent Identity: 25.688

alignment_block:

US-09-528-682-4 x US-10-128-714-1019/rev ..

Align seg 1/1 to reverse of: US-10-128-714-1019 from: 1 to: 1542

5 ValArgileGlnAspAlaTyrGluProIleAlaAsnThrAsnThrTh 21
|||||:|||||:|:| ||| |||||:|
948 GTTCAGCTTCAGCACACACAGTGGATAGAGCCACCTGCAACACCACT 899

21 rGlnPheLeuAsnMetGlyAsnGlu...ValAlaLeuAspGlyArgTyrS 37
|||||:|||||:|:| ||| |||||:|
898 TCAACTCATCGATCCCGCAGCGGTTTGTTCACGTCGAAGGAACGAATG 849

37 erAsnTyrAlaLeuIleSerAlaGlu.....GlyGlyMetAsp... 49
:|||||:|:|:|:|:|:|:| |||||:|
848 ACAATCATGTGAGCGAGCAGTGAAGTCACGCGGGAACCTGGGATGTG 799

50 ArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgG1 66
|||||:|:|:|:|:|:|:| |||||:|
798 CGAGAC.....AAGTATTCTGTCACAGCGTCGATGTTGTACTTGA 758

66 uPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuA 83
|||||:|:|:|:|:|:|:| |||||:|
757 GCTGAGCAGAGATGGGAATGATAGGAGAGCCATCGGCAACAGTACCACGA 708

83 snLysGlnHisAsp.....AlaAspPheLysLys 92
|||||:|:|:|:|:|:|:| |||||:|
707 ATGAACCTTCAGGATTGATTGTAATGTCAGAGACCGCTCTCCCTCAT 658

93 TyrIleLysLeuLeuIleAsnAsnAsp 101
|||||:|:|:|:|:|:|:| |||||:|
657 CAGATCAACCTTGTTCTGCAGAATGAT 631

seq_name: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:PCT-US02-13142-7019

seq_documentation_block:
; Sequence 7019, Application PC/TUS0213142
; GENERAL INFORMATION:
; APPLICANT: Elitra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-228
; CURRENT APPLICATION NUMBER: PCT/US02/13142
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7019
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
PCT-US02-13142-7019

alignment_scores:
Quality: 63.50 Length: 109
Ratio: 1.008 Gaps: 5
Percent Similarity: 57.798 Percent Identity: 25.688

alignment_block:
US-09-528-682-4 x PCT-US02-13142-7019/rev ..

Align seg 1/1 to reverse of: PCT-US02-13142-7019 from: 1 to: 1551

5 ValArgileGlnAspAlaTyrGluProIleAlaAsnThrAsnThrTh 21
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1014 GTTCAGCTTCAGCACACACAGTGGATAGAGCCACCTGCAACACCACT 965

21 rGlnPheLeuAsnMetGlyAsnGlu...ValAlaLeuAspGlyArgTyrS 37
|||||:|||||:|:| ||| |||||:|
964 TCAACTCATCGATCCCGCAGCGGTTTGTTCACGTCGAAGGAACGAATG 915

37 erAsnTyrAlaLeuIleSerAlaGlu.....GlyGlyMetAsp... 49
:|||||:|:|:|:|:|:|:| |||||:|
914 ACAATCATGTGAGCGAGCAGTGAAGTCACGCGGGAACCTGGGATGTG 865

50 ArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgG1 66
|||||:|:|:|:|:|:|:| |||||:|
864 CGAGAC.....AAGTATTCTGTCACAGCGTCGATGTTGTACTTGA 824

66 uPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuA 83
|||||:|:|:|:|:|:|:| |||||:|
823 GCTGAGCAGAGATGGGAATGATAGGAGAGCCATCGGCAACAGTACCACGA 774

83 snLysGlnHisAsp.....AlaAspPheLysLys 92
|||||:|:~|:~|:~|:~|:~| |||||:|
773 ATGAACCTTCAGGATTGATTGTAATGTCAGAGACCGCTCTCCCTCAT 724

93 TyrIleLysLeuLeuIleAsnAsnAsp 101
|||||:|:~|:~|:~|:~|:~| |||||:|
723 CAGATCAACCTTGTTCTGCAGAATGAT 697

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-128-714-7019

seq_documentation_block:
; Sequence 7019, Application US/10128714
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7019
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-7019

alignment_scores:
Quality: 63.50 Length: 109
Ratio: 1.008 Gaps: 5
Percent Similarity: 57.798 Percent Identity: 25.688

alignment_block:
US-09-528-682-4 x US-10-128-714-7019/rev ..

Align seg 1/1 to reverse of: US-10-128-714-7019 from: 1 to: 1551

5 ValArgileGlnAspAlaTyrGluProIleAlaAsnThrAsnThrTh 21
|||||:|||||:|:~|:~|:~|:~|:~| |||||:|
1014 GTTCAGCTTCAGCACACACAGTGGATAGAGCCACCTGCAACACCACT 965


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37 erAsnTyrAlaLeuIleSerAlaGlu.....GlyGlyMetAsp... 49
   |||:||||: |||:||||: |||:||||:
980 ACAATCATGTGAGCGAAGCACTGAAGTCACGCGACGGAACCTGGGATGTG 931
   |||:||||: |||:||||: |||:||||:
50 ArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgG1 66
   |||:||||: |||:||||: |||:||||:
930 CGAGAC.....AAGGTATTCGTTGACACGCGTCGATGTGTACTTGA 890
   |||:||||: |||:||||: |||:||||:
66 uPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuA 83
   |||:||||: |||:||||: |||:||||:
889 CTTGAGCAGAGATGGATGATGATGAGAGACCATCGCAACAGTACCACGA 840
   |||:||||: |||:||||: |||:||||:
83 snLysGlnHisAsp.....AlaAspPheLysLys 92
   |||:||||: |||:||||: |||:||||:
839 ATGAACCTTCAGGATTCGATGTTGTAATGTTGCAGACGACCGTCTTCCTCAT 790
   |||:||||: |||:||||: |||:||||:
93 TyrIleLysLeuLeuIleAsnAsnAsp 101
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789 CAGATCAACCTTGTTCTGCAGAATGAT 763
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seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-106-698-225

seq_documentation_block:

; Sequence 225, Application US/10106698

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

; FILE REFERENCE: PA005P1

; CURRENT APPLICATION NUMBER: US/10/106,698

; CURRENT FILING DATE: 2002-03-27

; PRIOR APPLICATION NUMBER: PCT/US00/26524

; PRIOR FILING DATE: 2000-09-28

; PRIOR FILING DATE: 1999-09-29

; PRIOR FILING DATE: 1999-11-03

; NUMBER OF SEQ ID NOS: 8564

; SOFTWARE: PatentIn Ver. 3.0

; SEQ ID NO 225

; LENGTH: 1762

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-106-698-225

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alignment_scores:
  Quality: 63.50      Length: 114
  Ratio: 1.058       Gaps: 5
  Percent Similarity: 52.632  Percent Identity: 21.930

alignment_block:
US-09-528-682-4 x US-10-106-698-225 ..

Align seg 1/1 to: US-10-106-698-225 from: 1 to: 1762
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11 TyrGluProIleAlaAsnThrAsnThrThrGlnPheLeuAsnMetG1 27
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744 TACCAGCCCATCCGCGCGG.....CTCAACGTGG 775

27 yAsnGluValAlaLeuAspGlyArgTyrSerAsnTyrAla..... 40
   |||:||||: |||:||||: |||:||||:
776 AATGTCGTCTTACATCCAAAGAGTGGTCAGCGAGCACATGAAGCGTTCT 825
   |||:||||: |||:||||: |||:||||:
41 .....LeuIleSerAlaGluGlyGlyMetAspArgAspLeuPhe 53
   |||:||||: |||:||||: |||:||||:
826 TCGTCAACTTGTGGTGGGAGATCCGGCTCAGACGTCGCTTCAC 875

54 GlySerAlaAsnIleAspGlyPheProGluValArgGluPheAsnSerIe 70
   |||:||||: |||:||||: |||:||||:
876 TTCATCCGCGGTTTGACGCGTGGGACAAGTG...GTCTTCAACACGTT 922

70 uProAsnAsnLysAlaSerSerAspThrAlaSerLeuAsnLysGlnHisA 87
   |||:||||: |||:||||: |||:||||:
```

```
923 GCAGGCGGGGAAGTGGGCGCAGCGAG.....GAGAGGAAGAGGA 960
   |||:||||: |||:||||: |||:||||:
87 spAlaAspPheLysLys..... 92
   |||:||||: |||:||||: |||:||||:
961 GCATGCCCTTCAAAAAGGTCGCCCTTTGAGCTGGTCTTCATAGTCCCTG 1010
   |||:||||: |||:||||: |||:||||:
93 .....TyrIleLysLeuLeuIleAsnAsnAspGlyPhePhe 104
   |||:||||: |||:||||: |||:||||:
1011 GCTGAGCAGTACAAAGTGGTGGTAAATGGAATCCCTTCTAT 1052
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seq_name: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:PCT-US02-13142-19

seq_documentation_block:

; Sequence 19, Application PC/TUS0213142

; GENERAL INFORMATION:

; APPLICANT: Elitra Pharmaceuticals, Inc.

; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and

; FILE REFERENCE: 10182-018-228

; CURRENT APPLICATION NUMBER: PCT/US02/13142

; CURRENT FILING DATE: 2002-04-23

; PRIOR APPLICATION NUMBER: US 60/285,697

; PRIOR FILING DATE: 2001-04-23

; PRIOR APPLICATION NUMBER: US 60/287,066

; PRIOR FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/295,890

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/303,899

; PRIOR FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: US 60/316,362

; PRIOR FILING DATE: 2001-08-31

; NUMBER OF SEQ ID NOS: 8603

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 3542

; TYPE: DNA

; ORGANISM: Aspergillus fumigatus

PCT-US02-13142-19

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alignment_scores:
  Quality: 63.50      Length: 109
  Ratio: 1.008       Gaps: 5
  Percent Similarity: 57.798  Percent Identity: 25.688
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alignment_block:
US-09-528-682-4 x PCT-US02-13142-19/rev ..

Align seg 1/1 to reverse of: PCT-US02-13142-19 from: 1 to: 3542

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5 ValArgIleGlnAspAlaTyrGluProIleAlaAsnThrAsnThrThr 21
   |||:||||: |||:||||: |||:||||:
1948 GTTCAGCTTCAGCACACCACTGAGGATAGAGCCACTGCACACACCCT 1899

21 rGlnPheLeuAsnMetGlyAsnGlu...ValAlaLeuAspGlyArgTyr 37
   |||:||||: |||:||||: |||:||||:
1898 TCAACTCATCGATCTCCGCGCGGTTGTTGACGTCGAAAGAACGAATG 1849

37 erAsnTyrAlaLeuIleSerAlaGlu.....GlyGlyMetAsp... 49
   |||:||||: |||:||||: |||:||||:
1848 ACAATCATGTGAGCGCAAGCAGTGAAGTCACGCGACGGGAACCTGGGATGTG 1799
   |||:||||: |||:||||: |||:||||:
1798 CGAGAC.....AAGGTATTCGTTGACAGCGTCGATGTTGTTACTTGA 1758
   |||:||||: |||:||||: |||:||||:
66 uPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuA 83
   |||:||||: |||:||||: |||:||||:
1757 GCTGAGCAGAGATGGGAATGATAGGAGAGCCATCGGCAACAGTACCACGA 1708

83 snLysGlnHisAsp.....AlaAspPheLysLys 92
   |||:||||: |||:||||: |||:||||:
1707 ATGAACCTTCAGGATTCGATGTTGTAATGTTGCAGACGACCGTCTTCCCTCAT 1658
```


93 TyrIleLysLeuLeuIleAsnAsp 101
|||::|||::|||::|||::|||::|||::|||
1657 CAGATCAACCTTGTCTGCAGATGAT 1631

93 TyrIleLysLeuLeuIleAsnAsp 101
|||::|||::|||::|||::|||::|||::|||
1657 CAGATCAACCTTGTCTGCAGATGAT 1631

seq_name: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:US-10-128-714-19

seq_documentation_block:
; Sequence 19, Application US/10128714
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lenieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 3542
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-19

alignment_scores:
Quality: 63.50 Length: 109
Ratio: 1.008 Gaps: 5
Percent Similarity: 57.798 Percent Identity: 25.688

alignment_block:
US-09-528-682-4 x US-10-128-714-19/rev ..

Align seg 1/1 to reverse of: US-10-128-714-19 from: 1 to: 3542

5 ValArgIleGlnAspAlaTyrGluProIleAlaAsnThrAsnThrThr 21
|||::|||::|||::|||::|||::|||::|||
1948 GTTCAGCTTCAGCACACCATGAGATAGAGCCACCTGCAACACCCCT 1899
21 rGlnPheLeuAsnMetGlyAsnGlu...ValAlaLeuAspGlyArgTyrS 37
|||::|||::|||::|||::|||::|||::|||
1898 TCAACTCATCGATCTCCGACCGGGTTGTGACGTCGAAGGACGATG 1849
37 erAsnTyrAlaLeuIleSerAlaGlu.....GlyGlyMetAsp... 49
:||||::|||::|||::|||::|||::|||::|||
1848 ACAATCATGTGAGCGGAAGCAGTGAAGTCACGGACGGGAACTGGGATGTG 1799
50 ArgAspLeuPheGlySerAlaAsnIleAspGlyPheProGluValArgG 66
|||||::|||::|||::|||::|||::|||::|||
1798 CGAGAC.....AAGGTATTCTGTTGACAGCGCTCGATGTTGTACTTGA 1758
66 uPheAsnSerLeuProAsnAsnLysAlaSerSerAspThrAlaSerLeuA 83
|::|::|::|||::|||::|||::|||::|||::|||
1757 GCTGACGACAGATGGGANTATAGGAGAGCGCATCGGCAACAGTACCACGA 1708
83 snLysGlnHisAsp.....AlaAspPheLysLys 92
|||::|||::|||::|||::|||::|||::|||
1707 ATGAACCTCAGGATTGATTGGTAAATGTTGCAGAGCACCGCTCTTCCTCAT 1658

